```
40S RIBOSOMAL PROTEIN S16 >gi_538428 (L36313) ribosomal
NCBI Description
                  protein S16 [Oryza sativa] >gi_1096552_prf__2111468A
                  ribosomal protein S16 [Oryza sativa]
                  410283
Seq. No.
                  uC-osflcyp031f11b1
Seq. ID
Method
                  BLASTX
                  g4678204
NCBI GI
                  147
BLAST score
                  2.0e-09
E value
                  91
Match length
                  38
% identity
                  (AC007134) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  410284
                  uC-osflcyp031g01b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4006829
BLAST score
                  666
                  5.0e-70
E value
                  156
Match length
                  82
% identity
                  (AC005970) putative protein kinase [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  410285
                  uC-osflcyp031g02b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3024122
BLAST score
                   653
                  2.0e-68
E value
                  124
Match length
                  100
% identity
                  S-ADENOSYLMETHIONINE SYNTHETASE 2 (METHIONINE
NCBI Description
                   ADENOSYLTRANSFERASE 2) (ADOMET SYNTHETASE 2) >gi_1778821
                   (U82833) S-adenosyl-L-methionine synthetase [Oryza sativa]
                   410286
Seq. No.
                  uC-osflcyp031g03b1
Seq. ID
Method
                  BLASTX
                   g5051771
NCBI GI
                   471
BLAST score
                   3.0e-47
E value
                   135
Match length
                   70
% identity
NCBI Description (AL078637) putative protein [Arabidopsis thaliana]
                   410287
Seq. No.
                   uC-osflcyp031g07b1
Seq. ID
Method
                   BLASTX
```

Method BLASTX
NCBI GI g2723471
BLAST score 914
E value 4.0e-99
Match length 169
% identity 99

NCBI Description (D87819) sucrose transporter [Oryza sativa]

Seq. No. 410288

% identity



```
Seq. ID
                  uC-osflcyp031g08b1
Method
                  BLASTX
NCBI GI
                  g1203832
BLAST score
                  828
                  5.0e-89
E value
Match length
                  169
                  91
% identity
                  (U46003) beta-D-glucan exohydrolase, isoenzyme ExoII
NCBI Description
                   [Hordeum vulgare] >gi 1588407 prf 2208395A beta-D-glucan
                  exohydrolase [Hordeum vulgare]
Seq. No.
                   410289
                  uC-osflcyp031g09b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1352613
BLAST score
                  323
                  8.0e-30
E value
Match length
                  75
                  89
% identity
                  OCS-ELEMENT BINDING FACTOR 1 (OCSBF-1)
NCBI Description
                  >qi 444047 emb CAA44607 (X62745) ocs-binding factor 1 [Zea
                  mays]
                   410290
Seq. No.
Seq. ID
                  uC-osflcyp031g11b1
                  BLASTX
Method
NCBI GI
                   g1777312
BLAST score
                   337
E value
                   2.0e-31
                   90
Match length
                   69
% identity
                  (D30622) novel serine/threonine protein kinase [Arabidopsis
NCBI Description
                   thaliana]
                   410291
Seq. No.
                   uC-osflcyp031g12b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   q401140
BLAST score
                   642
                   3.0e-67
E value
                   129
Match length
                   99
% identity
                  SUCROSE SYNTHASE 2 (SUCROSE-UDP GLUCOSYLTRANSFERASE 2)
NCBI Description
                   >gi_20095_emb_CAA41774_ (X59046) sucrose-UDP
                   glucosyltransferase (isoenzyme 2) [Oryza sativa]
                   >gi_1587662_prf__2207194A sucrose synthase:ISOTYPE=2 [Oryza
                   sativa]
                   410292
Seq. No.
                   uC-osflcyp031h02b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   q115787
BLAST score
                   547
E value
                   4.0e-56
                   131
Match length
```

NCBI Description CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I

```
CAB-2) (LHCP) >gi_82461_pir__S03706 chlorophyll a/b-binding protein 2R precursor - rice >gi_20182_emb_CAA32109_
(X13909) chlorophyll a/b-binding preprotein (AA -28 to 235)
[Oryza sativa]
410293
```

Seq. ID uC-osflcyp031h04b1
Method BLASTX
NCBI GI g4126809
BLAST score 768
E value 5.0e-82
Match length 143

Seq. No.

% identity

NCBI Description (AB017042) glyoxalase I [Oryza sativa]

Seq. No. 410294

Seq. ID uC-osflcyp031h06b1

55

Method BLASTX
NCBI GI g5802606
BLAST score 809
E value 8.0e-87
Match length 163
% identity 93

NCBI Description (AF174486) methylenetetrahydrofolate reductase [Zea mays]

Seq. No. 410295

Seq. ID uC-osflcyp031h07b1

Method BLASTX
NCBI GI g4741931
BLAST score 462
E value 9.0e-50
Match length 126
% identity 82

NCBI Description (AF130975) plasma membrane intrinsic protein [Zea mays]

Seq. No. 410296

Seq. ID uC-osflcyp031h08b1

Method BLASTX
NCBI GI g2911358
BLAST score 196
E value 3.0e-15
Match length 79
% identity 52

NCBI Description (AF041043) NADPH HC toxin reductase [Zea mays]

Seq. No. 410297

Seq. ID uC-osflcyp032a07b1

Method BLASTX
NCBI GI 94538913
BLAST score 261
E value 2.0e-22
Match length 85
% identity 64

NCBI Description (AL049482) putative protein [Arabidopsis thaliana]

Seq. No. 410298

Seq. ID uC-osflcyp032a09b1

Method

BLASTX

```
Method
                  BLASTX
                  g1519253
NCBI GI
BLAST score
                  335
E value
                  3.0e-31
Match length
                  97
                  73
% identity
NCBI Description
                  (U65958) GF14-d protein [Oryza sativa]
Seq. No.
                  410299
                  uC-osflcyp032a10b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2501189
BLAST score
                  445
                  3.0e-44
E value
Match length
                  121
                  74
% identity
                  THIAMINE BIOSYNTHETIC ENZYME 1-1 PRECURSOR
NCBI Description
                  >qi 2130146 pir S61419 thiamine biosynthetic enzyme thil-1
                  - maize >qi 596078 (U17350) thiamine biosynthetic enzyme
                  [Zea mays]
                  410300
Seq. No.
Seq. ID
                  uC-osflcyp032a12b1
Method
                  BLASTX
NCBI GI
                  g4894628
BLAST score
                  153
E value
                  5.0e-10
Match length
                  103
% identity
                  28
NCBI Description (AF124369) NT3 [Nicotiana tabacum]
                  410301
Seq. No.
                  uC-osflcyp032b01a1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4559339
BLAST score
                  273
                  7.0e-24
E value
Match length
                  58
                  88
% identity
                  (AC007087) putative ATP-dependent RNA helicase [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                   410302
                  uC-osflcyp032b01b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2088647
BLAST score
                   365
E value
                   9.0e-35
Match length
                  124
% identity
                   52
NCBI Description
                   (AF002109) hypothetical protein [Arabidopsis thaliana]
                   >gi 3158394 (AF036340) LRR-containing F-box protein
                   [Arabidopsis thaliana]
                   410303
Seq. No.
                  uC-osflcyp032b02b1
Seq. ID
```

NCBI GI q115787 BLAST score 210 E value 6.0e-23 Match length 111 % identity 64 CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I NCBI Description CAB-2) (LHCP) >gi 82461 pir S03706 chlorophyll a/b-binding protein 2R precursor - rice >gi 20182 emb CAA32109 (X13909) chlorophyll a/b-binding preprotein (AA -28 to 235) [Oryza sativa] Seq. No. 410304 uC-osflcyp032b03b1 Seq. ID Method BLASTX NCBI GI g4753659 BLAST score 460 E value 7.0e-46 Match length 96 88 % identity NCBI Description (AL049751) putative protein [Arabidopsis thaliana] Seq. No. 410305 Seq. ID uC-osflcyp032b07b1 Method BLASTX NCBI GI g4559339 BLAST score 613 E value 8.0e-64 Match length 152 % identity 78 NCBI Description (AC007087) putative ATP-dependent RNA helicase [Arabidopsis thaliana]

Seq. No. 410306

uC-osflcyp032b08b1 Seq. ID

Method BLASTX NCBI GI g1076724 BLAST score 678 E value 2.0e-71 137 Match length 87 % identity

LHCI-680, photosystem I antenna protein - barley NCBI Description

>gi_666054_emb_CAA59049_ (X84308) LHCI-680, photosystem I

antenna protein [Hordeum vulgare]

410307 Seq. No.

uC-osflcyp032b09b1 Seq. ID

Method BLASTX NCBI GI g3695403 BLAST score 497 E value 3.0e-50Match length 122 % identity

NCBI Description (AF096373) contains similarity to the pfkB family of

> carbohydrate kinases (Pfam: PF00294, E=1.6e-75) [Arabidopsis thaliana] >gi 4538955 emb CAB39779.1

(AL049488) fructokinase-like protein [Arabidopsis thaliana]



Seq. No. 410308 uC-osflcyp032b10b1 Seq. ID Method BLASTX g2673912 NCBI GI 330 BLAST score 1.0e-30 E value 90 Match length 68 % identity (AC002561) unknown protein [Arabidopsis thaliana] NCBI Description 410309 Seq. No. uC-osflcyp032c04b1 Seq. ID Method BLASTX g2960364 NCBI GI

BLAST score 516 E value 2.0e-52 159 Match length % identity 62

(AJ224986) cinnamoyl CoA reductase [Populus balsamifera NCBI Description

subsp. trichocarpa]

410310 Seq. No.

Seq. ID uC-osflcyp032c09b1

Method BLASTX q283008 NCBI GI BLAST score 691 6.0e-73E value Match length 152 % identity 89

sucrose synthase (EC 2.4.1.13) - rice NCBI Description

>gi_20366_emb_CAA46017_ (X64770) sucrose synthase [Oryza

sativa]

410311 Seq. No.

uC-osflcyp032c10b1 Seq. ID

Method BLASTX NCBI GI g2149127 BLAST score 219 E value 1.0e-17 Match length 139 39 % identity

NCBI Description (U81293) UDP-glucose:indole-3-acetate

beta-D-glucosyltransferase [Arabidopsis thaliana]

410312 Seq. No.

uC-osflcyp032d01a1 Seq. ID

Method BLASTN NCBI GI g5091496 172 BLAST score E value 5.0e-92 260 Match length 92 % identity

NCBI Description Oryza sativa genomic DNA, chromosome 6, clone P0680A03,

complete sequence

410313 Seq. No.

uC-osflcyp032d01b1 Seq. ID

Method BLASTX
NCBI GI g320618
BLAST score 514
E value 2.0e-52
Match length 110
% identity 90

NCBI Description chlorophyll a/b-binding protein I precursor - rice

>gi 218172 dbj BAA00536 (D00641) type I light-harvesting

chlorophyll a/b-binding protein [Oryza sativa]

>gi 227611 prf 1707316A chlorophyll a/b binding protein 1

[Oryza sativa]

Seq. No. 410314

Seq. ID uC-osflcyp032d04b1

Method BLASTX
NCBI GI g2829887
BLAST score 428
E value 4.0e-42
Match length 118
% identity 64

NCBI Description (AC002396) Hypothetical protein [Arabidopsis thaliana]

Seq. No. 410315

Seq. ID uC-osflcyp032d05b1

Method BLASTX
NCBI GI g2982453
BLAST score 704
E value 2.0e-74
Match length 160
% identity 85

NCBI Description (AL022223) fructose-bisphosphate aldolase-like protein

[Arabidopsis thaliana]

Seq. No. 410316

Seq. ID uC-osflcyp032d07b1

Method BLASTX
NCBI GI g5091509
BLAST score 771
E value 2.0e-82
Match length 166
% identity 90

NCBI Description (AB023482) EST AU065533(C2174) corresponds to a region of

the predicted gene.; Similar to Homo sapiens splicing factor Prp8 mRNA, complete cds.(AF092565) [Oryza sativa]

Seq. No. 410317

Seq. ID uC-osflcyp032d08b1

Method BLASTX
NCBI GI g2341032
BLAST score 153
E value 5.0e-10
Match length 115
% identity 40

NCBI Description (AC000104) EST gb ATTS0956 comes from this gene.

[Arabidopsis thaliana]

Seq. No. 410318

Method

BLASTX

```
uC-osflcyp032d09b1
Seq. ID
Method
                  BLASTX
                  q517500
NCBI GI
BLAST score
                  296
                  1.0e-26
E value
                  140
Match length
                  47
% identity
                  (M87435) precursor of the oxygen evolving complex 17 kDa
NCBI Description
                  protein [Zea mays] >gi 444338 prf 1906386A photosystem II
                  OE17 protein [Pisum sativum]
                   410319
Seq. No.
Seq. ID
                  uC-osflcyp032d10b1
Method
                  BLASTX
                  g4519539
NCBI GI
BLAST score
                   245
                   4.0e-23
E value
Match length
                  120
                   54
% identity
                  (AB016256) NAD-dependent sorbitol dehydrogenase [Malus
NCBI Description
                  domestica]
                   410320
Seq. No.
Seq. ID
                   uC-osflcyp032d11b1
Method
                   BLASTX
NCBI GI
                   q1705629
                   768
BLAST score
                   6.0e-82
E value
Match length
                   140
% identity
                   99
NCBI Description CATALASE ISOZYME B (CAT-B) >gi 516839 dbj BAA05494
                   (D26484) catalase [Oryza sativa]
                   410321
Seq. No.
                   uC-osflcyp032e04b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g5430749
               3,60 لىنىمىيىنىد
BLAST score
                   4.0e-34
E value
Match length
                   121
% identity
NCBI Description (AC007504) Hypothetical Protein [Arabidopsis thaliana]
Seq. No.
                   410322
Seq. ID
                   uC-osflcyp032e09b1
Method
                   BLASTX
NCBI GI
                   g3928084
BLAST score
                   374
                   6.0e-36
E value
Match length
                   132
% identity
                   55
                  (AC005770) retrotransposon-like protein [Arabidopsis
NCBI Description
                   thaliana]
                   410323
Seq. No.
                   uC-osflcyp032e12b1
Seq. ID
```

```
NCBI GI
                  q82263
BLAST score
                  807
                  1.0e-86
E value
Match length
                  159
% identity
                  96
NCBI Description ubiquinol--cytochrome-c reductase (EC 1.10.2.2) cytochrome
                  c1 precursor (clone pC(1)3II) - potato
                  410324
Seq. No.
                  uC-osflcyp032f04b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g320618
BLAST score
                  607
                  3.0e-63
E value
                  143
Match length
% identity
                  82
NCBI Description
                  chlorophyll a/b-binding protein I precursor - rice
                  >gi 218172_dbj_BAA00536_ (D00641) type I light-harvesting
                  chlorophyll a/b-binding protein [Oryza sativa]
                  >gi 227611 prf 1707316A chlorophyll a/b binding protein 1
                   [Oryza sativa]
Seq. No.
                  410325
Seq. ID
                  uC-osflcyp032f06b1
Method
                  BLASTX
NCBI GI
                  q3046693
BLAST score
                  403
                  3.0e-39
E value
Match length
                  93
% identity
                  77
NCBI Description
                  (AL022140) receptor like protein (fragment) [Arabidopsis
                  thaliana]
Seq. No.
                  410326
Seq. ID
                  uC-osflcyp032f08b1
Method
                  BLASTX
NCBI GI
                  g4586054
BLAST score
                  219
E value
                  1.0e-17
Match length
                  81
% identity
                  52
NCBI Description (AC007020) unknown protein [Arabidopsis thaliana]
Seq. No.
                  410327
Seq. ID
                  uC-osflcyp032f09b1
Method
                  BLASTX
NCBI GI
                  g3386614
BLAST score
                  439
                  2.0e-43
E value
Match length
                  126
% identity
                  41
NCBI Description
                  (AC004665) putative transcription factor SF3 [Arabidopsis
                  thaliana]
```

Seq. No. 410328

Seq. ID uC-osflcyp032f11b1

Method BLASTX



```
NCBI GI
                  g871931
BLAST score
                  526
                  1.0e-53
E value
Match length
                  131
% identity
                  82
                 (D30763) ferredoxin [Oryza sativa]
NCBI Description
Seq. No.
                  410329
Seq. ID
                  uC-osflcyp032f12b1
                  BLASTX
Method
NCBI GI
                  g2407281
BLAST score
                  787
E value
                  3.0e-84
                  149
Match length
% identity
                  99
                 (AF017363) ribulose 1,5-bisphosphate carboxylase small
NCBI Description
                  subunit [Oryza sativa]
Seq. No.
                  410330
                  uC-osflcyp032g01b1
Seq. ID
                  BLASTX
Method
                  q2293480
NCBI GI
BLAST score
                  252
E value
                  3.0e - 34
                  84
Match length
% identity
                  94
NCBI Description (AF011331) glycine-rich protein [Oryza sativa]
Seq. No.
                  410331
Seq. ID
                  uC-osflcyp032g02b1
                  BLASTX
Method
NCBI GI
                  q3043428
BLAST score
                  481
E value
                  1.0e-48
Match length
                  106
% identity
                  83
                 (AJ005346) 40S ribosomal protein S5 [Cicer arietinum]
NCBI Description
Seq. No.
                   410332
                  uC-osflcyp032g03b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3757522
                  245
BLAST score
                  8.0e-21
E value
                  55
Match length
```

84 % identity

NCBI Description (AC005167) putative splicing factor [Arabidopsis thaliana]

Seq. No. 410333

uC-osflcyp032g04b1 Seq. ID

Method BLASTN NCBI GI g5852170 180 BLAST score 2.0e-96 E value 463 Match length 85 % identity

NCBI Description Oryza sativa indica(GLA4) genomic DNA, chromosome 4, BAC

```
clone:t17804
```

Seq. No. 410334 uC-osflcyp032g05a1 Seq. ID Method BLASTX q4884526 NCBI GI BLAST score 416 1.0e-40 E value 99 Match length 83 % identity (AB027428) beta 1,3-glucanase [Oryza sativa] NCBI Description 410335 Seq. No. uC-osflcyp032g05b1 Seq. ID Method BLASTX g2765140 NCBI GI BLAST score 628 E value 1.0e-65 Match length 151 76 % identity (Y11931) 1-phosphatidylinositol-4,5-bisphosphate NCBI Description phosphodiesterase [Nicotiana rustica] Seq. No. 410336 uC-osflcyp032g06b1 Seq. ID BLASTX Method NCBI GI g5031281 BLAST score 317 4.0e-29 E value 109 Match length 60 % identity NCBI Description (AF139499) unknown [Prunus armeniaca] Seq. No. 410337 uC-osflcyp032g08b1 Seq. ID BLASTX Method NCBI GI g4454033 BLAST score 187 6.0e-14E value Match length 147 33 % identity NCBI Description (AL035394) putative potassium transport protein [Arabidopsis thaliana] 410338 Seq. No. uC-osflcyp032g10b1 Seq. ID BLASTX Method g2252860 NCBI GI 173 BLAST score E value 2.0e-12 54 Match length % identity 65 NCBI Description (AF013294) No definition line found [Arabidopsis thaliana]

Seq. No. 410339

Seq. ID uC-osflcyp032g11b1

Method BLASTX

```
NCBI GI
                  q4097940
BLAST score
                  596
                  8.0e-62
E value
Match length
                  137
                  87
% identity
NCBI Description (U72251) beta-1,3-glucanase precursor [Oryza sativa]
                  410340
Seq. No.
                  uC-osflcyp032g12b1
Seq. ID
Method
                  BLASTX
                  g1076791
NCBI GI
BLAST score
                  672
                  1.0e-70
E value
Match length
                  125
                  97
% identity
NCBI Description calcium-binding protein - maize >gi_2119370_pir___$58170
                  Calreticulin precursor - maize >gi_577612_emb_CAA86728_
                  (Z46772) calcium-binding protein [Zea mays]
                  >gi 927572 emb CAA61939 (X89813) Calreticulin precursor
                  [Zea mays] >gi 1587033 prf 2205314A calreticulin [Zea
                  mays]
                  410341
Seq. No.
Seq. ID
                  uC-osflcyp032h02b1
Method
                  BLASTN
NCBI GI
                  g5091597
BLAST score
                  164
                  6.0e-87
E value
Match length
                  353
% identity
                  99
NCBI Description Oryza sativa chromosome 1 BAC 10A19I, complete sequence
Seq. No.
                  410342
Seq. ID
                  uC-osflcyp032h03b1
Method
                  BLASTX
NCBI GI
                  g283442
BLAST score
                  146
E value
                  5.0e-09
Match length
                  133
% identity
                  30
NCBI Description TcD antigen - Trypanosoma cruzi
Seq. No.
                  410343
                  uC-osflcyp032h04b1
Seq. ID
Method
                  BLASTN
NCBI GI
                  q5420609
                  39
BLAST score
                  2.0e-12
E value
Match length
                  67
% identity
                  90
```

NCBI Description Genomic sequence for Arabidopsis thaliana BAC F28C11 from chromosome I, complete sequence

410344 Seq. No.

uC-osflcyp032h05b1 Seq. ID

Method BLASTX NCBI GI g2832641



```
BLAST score
                  379
                  2.0e-36
E value
Match length
                  129
% identity
                  55
                  (AL021710) glycolate oxidase - like protein [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  410345
Seq. ID
                  uC-osflcyp032h09a1
Method
                  BLASTN
NCBI GI
                  g2196541
BLAST score
                  93
E value
                  8.0e-45
Match length
                  189
                  88
% identity
NCBI Description Oryza sativa glycine-rich protein mRNA, complete cds
                  410346
Seq. No.
Seq. ID
                  uC-osflcyp033a01b1
Method
                  BLASTX
NCBI GI
                  q3152568
BLAST score
                  449
E value
                  1.0e-44
Match length
                  139
                  63
% identity
                  (AC002986) Similar to hypothetical protein product
NCBI Description
                  gb Z97337 from A. thaliana. EST gb H76597 comes from this
                  gene. [Arabidopsis thaliana]
Seq. No.
                  410347
                  uC-osflcyp033a04b1
Seq. ID
Method
                  BLASTN
                  g5852170
NCBI GI
BLAST score
                  306
                  1.0e-172
E value
Match length
                  372
                  97
% identity
NCBI Description Oryza sativa indica(GLA4) genomic DNA, chromosome 4, BAC
                  clone:t17804
                  410348
Seq. No.
                  uC-osflcyp033a06b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1173027
                  259
BLAST score
                  3.0e-22
E value
                  83
Match length
                  69
% identity
NCBI Description 60S RIBOSOMAL PROTEIN L31 >gi_915313 (U23784) ribosomal
                  protein L31 [Nicotiana glutinosa]
```

Seq. No. 410349
Seq. ID uC-osflcyp033a07b1
Method BLASTX

Method BLASTX NCBI GI g82708 BLAST score 186 E value 9.0e-14



Match length 38 100 % identity

NCBI Description Ocs-element binding factor 1 - maize

Seq. No.

410350

Seq. ID

uC-osflcyp033a08b1

Method NCBI GI BLASTX

BLAST score

q1449179 286

E value

2.0e-25

Match length

107

% identity

56

NCBI Description

(D86506) N-ethylmaleimide sensitive fusion protein

[Nicotiana tabacum]

Seq. No.

410351

Seq. ID

uC-osflcyp033a09b1

Method NCBI GI BLASTX g1041710

BLAST score

394

E value

3.0e-40

Match length % identity

100 76

NCBI Description (U30477) expansin Os-EXP2 [Oryza sativa]

Seq. No.

410352

Seq. ID

uC-osflcyp033a12b1

Method NCBI GI BLASTX g3193290

BLAST score

451

E value

8.0e-45

Match length

157

% identity

55

NCBI Description

(AF069298) contains similarity to a protein kinase domain (Pfam: pkinase.hmm, score: 165.48), to legume lectins beta domain (Pfam: lectin legB.hmm, score: 125.64) and legume lectins alpha domain (Pfam: lectin legA.hmm, score: 16.72)

[Arabido

Seq. No.

410353

Seq. ID Method

uC-osflcyp033b01b1

NCBI GI

BLASTX q5922612

309

BLAST score

3.0e-28

E value Match length

134

% identity

51

NCBI Description

(AP000492) EST AU078118(E3904) corresponds to a region of the predicted gene.; similar to Arabidopsis thaliana BAC

IG002P16; No definition line found. (AF007270) [Oryza

sativa]

Seq. No.

410354

Seq. ID

uC-osflcyp033b04b1

Method

BLASTN

NCBI GI

g2773153

BLAST score

E value 0.0e+00 Match length 476 % identity 100

NCBI Description Oryza sativa abscisic acid- and stress-inducible protein

(Asr1) mRNA, complete cds

Seq. No. 410355

Seq. ID uC-osflcyp033b07b1

Method BLASTX
NCBI GI g3560531
BLAST score 562
E value 7.0e-58
Match length 123
% identity 89

NCBI Description (AF042332) cycloartenol-C24-methyltransferase [Oryza sativa

subsp. japonica]

Seq. No. 410356

Seq. ID uC-osflcyp033b08b1

Method BLASTX
NCBI GI g3913427
BLAST score 619
E value 1.0e-64
Match length 153
% identity 81

NCBI Description S-ADENOSYLMETHIONINE DECARBOXYLASE PROENZYME (ADOMETDC)

(SAMDC) >gi_1532073_emb_CAA69075_ (Y07767) S-adenosylmethionine decarboxylase [Zea mays]

Seq. No. 410357

Seq. ID uC-osflcyp033b09a1

Method BLASTX
NCBI GI g1362009
BLAST score 504
E value 6.0e-51
Match length 119
% identity 44

NCBI Description ubiquitin-like protein 7 - Arabidopsis thaliana

Seq. No. 410358

Seq. ID uC-osflcyp033b09b1

Method BLASTX
NCBI GI g1362009
BLAST score 452
E value 6.0e-45
Match length 109
% identity 51

NCBI Description ubiquitin-like protein 7 - Arabidopsis thaliana

Seq. No. 410359

Seq. ID uC-osflcyp033b10b1

Method BLASTX
NCBI GI g1762945
BLAST score 250
E value 3.0e-21
Match length 86
% identity 53

NCBI Description (U66269) ORF; able to induce HR-like lesions [Nicotiana tabacum] Seq. No. 410360 Seq. ID uC-osflcyp033b12b1 Method BLASTX NCBI GI q5042413 BLAST score 184 E value 2.0e-13 Match length 117 36 % identity NCBI Description (AC006193) Hypothetical Protein [Arabidopsis thaliana] Seq. No. 410361 Seq. ID uC-osflcyp033c01b1 Method BLASTX NCBI GI q4895197 BLAST score 194 E value 9.0e-15 Match length 92 39 % identity NCBI Description (AC007661) hypothetical protein [Arabidopsis thaliana] Seq. No. 410362 Seq. ID uC-osflcyp033c04b1 Method BLASTX NCBI GI q137476 BLAST score 528 E value 7.0e-54Match length 124 86 % identity NCBI Description VACUOLAR ATP SYNTHASE 16 KD PROTEOLIPID SUBUNIT >gi 82334 pir A40814 H+-transporting ATPase (EC 3.6.1.35) proteolipid chain, vacuolar - oat >gi 166549 (M73232) H+-ATPase [Avena sativa] Seq. No. 410363 uC-osflcyp033c05a1 Seq. ID Method BLASTN NCBI GI q968995 95 BLAST score E value 6.0e-46 Match length 328 % identity 80 NCBI Description Oryza sativa clone glyceraldehyde-3-phosphate dehydrogenase (Gpc) mRNA, complete cds Seq. No. 410364 Seq. ID uC-osflcyp033c05b1 Method BLASTX NCBI GI g3023816 BLAST score 664 E value 8.0e-70 Match length 144 90 % identity

53250

>gi_968996 (U31676) glyceraldehyde-3-phosphate

NCBI Description GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC



dehydrogenase [Oryza sativa]

Seq. No. 410365 Seq. ID uC-osflcyp033c07b1 Method BLASTX NCBI GI q82080 BLAST score 501 E value 1.0e-50 137 Match length 69 % identity chlorophyll a/b-binding protein type III precursor - tomato NCBI Description >gi 226872 prf 1609235A chlorophyll a/b binding protein [Lycopersicon esculentum] 410366 Seq. No. uC-osflcyp033c10b1 Seq. ID Method BLASTN NCBI GI g3885881 BLAST score 255 1.0e-141 E value 259 Match length 100 % identity NCBI Description Oryza sativa inorganic pyrophosphatase (IPP) mRNA, complete cds 410367 Seq. No. Seq. ID uC-osflcyp033d03b1 BLASTX Method NCBI GI q6006270 BLAST score 175 2.0e-12 E value 71 Match length 39 % identity NCBI Description (AB022692) TAF-Ibeta2 [Xenopus laevis] Seq. No. 410368 uC-osflcyp033d04b1 Seq. ID Method BLASTX NCBI GI g4454464 BLAST score 484 E value 1.0e-48 Match length 158 % identity 56 NCBI Description (AC006234) unknown protein [Arabidopsis thaliana] Seq. No. 410369 uC-osflcyp033d05b1 Seq. ID Method BLASTX g2130069 NCBI GI BLAST score 804 3.0e-86 E value Match length 149 % identity 100 NCBI Description catalase (EC 1.11.1.6) catA - rice

Seq. No. 410370

>gi 1261858 dbj BAA06232 (D29966) catalase [Oryza sativa]

NCBI GI

g68843

```
Seq. ID
                   uC-osflcyp033d09b1
Method
                   BLASTX
NCBI GI
                   q4895197
BLAST score
                   182
E value
                   3.0e-13
Match length
                   92
                   39
% identity
NCBI Description (AC007661) hypothetical protein [Arabidopsis thaliana]
                   410371
Seq. No.
                   uC-osflcyp033d10b1
Seq. ID
                   BLASTX
Method
NCBI GI
                   g1885310
BLAST score
                   623
                   4.0e-65
E value
                   124
Match length
% identity
                   90
NCBI Description (X91659) Endoxyloglucan transferase (EXT) [Hordeum vulgare]
                   410372
Seq. No.
                   uC-osflcyp033d12b1
Seq. ID
                   BLASTX
Method
                   q1169382
NCBI GI
BLAST score
                   598
                   3.0e-67
E value
                   157
Match length
                   82
% identity
NCBI Description DNAJ PROTEIN HOMOLOG 2 >gi 542196 pir S42031 LDJ2 protein
                   - leek >gi 454303 emb CAA5\overline{4}720 (\overline{X}776\overline{32}) LDJ2 [Allium
                   porrum]
Seq. No.
                   410373
Seq. ID
                   uC-osflcyp033e02b1
Method
                   BLASTX
NCBI GI
                   g5541721
                   656
BLAST score
                   7.0e-69
E value
Match length
                   152
% identity
                   77
NCBI Description (AL096856) cell division cycle protein 23 homolog
                   [Arabidopsis thaliana]
                   410374
Seq. No.
                   uC-osflcyp033e03b1
Seq. ID
Method
                   BLASTN
                   g2773153
NCBI GI
                   310
BLAST score
                   1.0e-174
E value
                   398
Match length
                   94
% identity
NCBI Description Oryza sativa abscisic acid- and stress-inducible protein
                   (Asr1) mRNA, complete cds
                   410375
Seq. No.
                   uC-osflcyp033e04b1
Seq. ID
Method
                   BLASTX
```

BLAST score 275 E value 3.0e-24 81 Match length % identity 68 NCBI Description phospholipid transfer protein homolog - rice >gi_4139635_pdb_1RZL_ Rice Nonspecific Lipid Transfer Protein >gi 5107522 pdb 1BV2 Lipid Transfer Protein From Rice Seeds, Nmr, 14 Structures 410376 Seq. No. Seq. ID uC-osflcyp033e05a1 BLASTN Method NCBI GI g1519250 BLAST score 480 0.0e + 00E value

Match length 517 99 % identity

NCBI Description Oryza sativa GF14-c protein mRNA, complete cds

410377 Seq. No.

uC-osflcyp033e05b1 Seq. ID

Method BLASTX NCBI GI q1519251 BLAST score 573 8.0e-62 E value Match length 129 % identity 94

NCBI Description (U65957) GF14-c protein [Oryza sativa]

Seq. No. 410378

uC-osflcyp033e06b1 Seq. ID

Method BLASTX NCBI GI q1351357 BLAST score 438 E value 3.0e-43Match length 123 % identity 67

UBIQUINOL-CYTOCHROME C REDUCTASE COMPLEX 14 KD PROTEIN NCBI Description

(CR14) >gi 633681 emb CAA55863 (X79276)

ubiquinol--cytochrome c reductase [Solanum tuberosum]

410379 Seq. No.

uC-osflcyp033e07b1 Seq. ID

Method BLASTX NCBI GI g3435196 249 BLAST score E value 3.0e-21 Match length 110 % identity 46

NCBI Description (AF067773) glutamyl-tRNA synthetase [Arabidopsis thaliana]

410380 Seq. No.

Seq. ID uC-osflcyp033e08b1

Method BLASTX NCBI GI g5123708 BLAST score 434 7.0e-43E value

Match length

% identity

126

NCBI Description ubiquitin precursor - maize (fragment)

30





```
Match length
                  151
% identity
NCBI Description (AL079347) RNA helicase (RH16) [Arabidopsis thaliana]
                  410381
Seq. No.
Seq. ID
                  uC-osflcyp033e09b1
                  BLASTX
Method
NCBI GI
                  g2286153
BLAST score
                  212
                  7.0e-17
E value
Match length
                  92
                  54
% identity
NCBI Description (AF007581) cytoplasmic malate dehydrogenase [Zea mays]
                  410382
Seq. No.
Seq. ID
                  uC-osflcyp033e11b1
Method
                  BLASTX
NCBI GI
                  g3294469
BLAST score
                  646
E value
                  1.0e-67
                  131
Match length
                  96
% identity
NCBI Description (U89342) phosphoglucomutase 2 [Zea mays]
Seq. No.
                  410383
Seq. ID
                  uC-osflcyp033f01b1
                  BLASTN
Method
NCBI GI
                  g3721941
BLAST score
                  278
E value
                  1.0e-155
                  418
Match length
                  93
% identity
NCBI Description Oryza sativa mRNA for chitinase, complete cds
Seq. No.
                  410384
                  uC-osflcyp033f02b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g6016872
BLAST score
                  370
E value
                  2.0e-35
Match length
                  117
% identity
                  (AP000570) EST AU058127(S5254) corresponds to a region of
NCBI Description
                  the predicted gene.; Similar to dynein light chain 1,
                  cytoplasmic. (Q24117) [Oryza sativa]
Seq. No.
                  410385
                  uC-osflcyp033f04b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g82734
BLAST score
                  622
                  7.0e-65
E value
```

53254

>gi 226763 prf 1604470A poly-ubiquitin [Zea mays]

Seq. No. 410386 uC-osflcyp033f06b1 Seq. ID Method BLASTX NCBI GI g2130073 BLAST score 466 1.0e-78 E value Match length 153 % identity 100 NCBI Description fructose-bisphosphate aldolase (EC 4.1.2.13) isoenzyme C-1, cytosolic - rice >gi_786178 dbj BAA08845 (D50307) aldolase C-1 [Oryza sativa] >gi 790970 dbj BAA08830 (D50301) aldolase C-1 [Oryza sativa] Seq. No. 410387 Seq. ID uC-osflcyp033f08b1 Method BLASTX NCBI GI g2624328 BLAST score 577 E value 1.0e-59 Match length 124 % identity 90 NCBI Description (AJ002894) OsGRP2 [Oryza sativa] Seq. No. 410388 Seq. ID uC-osflcyp033f09b1 Method BLASTX NCBI GI q4760553 BLAST score 802 E value 5.0e-86 Match length 152 99 % identity NCBI Description (AB019533) Nad-dependent formate dehydrogenase [Oryza sativa] Seq. No. 410389 Seq. ID uC-osflcyp033f10b1 Method BLASTX NCBI GI g2696804 BLAST score 731 E value 1.0e-77 Match length 154 % identity NCBI Description (AB009665) water channel protein [Oryza sativa]

Seq. No. 410390

Seq. ID uC-osflcyp033f12b1

Method BLASTN
NCBI GI g4097337
BLAST score 340
E value 0.0e+00
Match length 348
% identity 99

NCBI Description Oryza sativa metallothionein-like protein mRNA, complete

cds

Seq. No. 410391

Seq. ID uC-osflcyp033g01b1

Method BLASTX NCBI GI g2286153 BLAST score 606 E value 5.0e-63 Match length 124 97 % identity NCBI Description (AF007581) cytoplasmic malate dehydrogenase [Zea mays] 410392 Seq. No. uC-osflcyp033g03b1 Seq. ID BLASTX Method NCBI GI g3559805 BLAST score 237 9.0e-20 E value 65 Match length 68 % identity NCBI Description (AJ006787) putative phytochelatin synthetase [Arabidopsis thaliana] Seq. No. 410393 uC-osflcyp033g04b1 Seq. ID BLASTX Method NCBI GI g4107276 BLAST score 556 4.0e-57 E value Match length 118 92 % identity NCBI Description (X98506) acetyl-CoA synthetase [Solanum tuberosum] Seq. No. 410394 uC-osflcyp033g06b1 Seq. ID Method BLASTX g462195 NCBI GI BLAST score 478 5.0e-48 E value 107 Match length % identity 88 NCBI Description PROTEIN TRANSLATION FACTOR SUI1 HOMOLOG (GOS2 PROTEIN) >gi 100682 pir S21636 GOS2 protein - rice >gi_20238_emb_CAA36190_ (X51910) GOS2 [Oryza sativa] >gi 3789950 (AF094774) translation initiation factor [Oryza sativa] 410395 Seq. No. uC-osflcyp033g07b1 Seq. ID Method BLASTN

Method BLASTN
NCBI GI g5042437
BLAST score 170
E value 1.0e-90
Match length 210
% identity 95

NCBI Description Oryza sativa BAC T49B20 genomic sequence, complete sequence

Seq. No. 410396

Seq. ID uC-osflcyp033g08b1

Method BLASTX NCBI GI g3850587

271 BLAST score 5.0e-24 E value Match length 103 % identity 54 (AC005278) Strong similarity to gi 2244780 hypothetical NCBI Description protein from Arabidopsis thaliana chromosome 4 contig gb Z97335. [Arabidopsis thaliana] 410397 Seq. No. Seq. ID uC-osflcyp033g09b1 BLASTX Method NCBI GI q115787 BLAST score 471 2.0e-47 E value 119 Match length 80 % identity CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I NCBI Description CAB-2) (LHCP) >gi 82461_pir__S03706 chlorophyll a/b-binding protein 2R precursor - rice >gi 20182 emb CAA32109 (X13909) chlorophyll a/b-binding preprotein (AA -28 to 235) [Oryza sativa] 410398 Seq. No. uC-osflcyp033g11b1 Seq. ID BLASTX Method NCBI GI g4567273 488 BLAST score 3.0e-49 E value 155 Match length 61 % identity NCBI Description (AC006841) putative vacuolar proton ATPase subunit [Arabidopsis thaliana] 410399 Seq. No. uC-osflcyp033g12b1 Seq. ID Method BLASTN g3789949 NCBI GI BLAST score 169

6.0e-90 E value Match length 317 89 % identity

NCBI Description Oryza sativa translation initiation factor (GOS2) mRNA,

complete cds

410400 Seq. No.

Seq. ID uC-osflcyp033h03b1

BLASTX Method NCBI GI q5262777 BLAST score 316 5.0e-29E value Match length 86 % identity

NCBI Description (AL080282) fatty acid hydroxylase-like protein [Arabidopsis

thaliana]

Seq. No. 410401

uC-osflcyp033h04b1 Seq. ID

```
BLASTX
Method
NCBI GI
                  g4826572
BLAST score
                  685
                  3.0e-72
E value
                  151
Match length
                  81
% identity
NCBI Description (AJ238848) polygalacturonase [Phleum pratense]
                  410402
Seq. No.
                  uC-osflcyp033h05b1
Seq. ID
                  BLASTX
Method
NCBI GI
                  q1946372
BLAST score
                  243
E value
                  2.0e-20
                  62
Match length
                  76
% identity
NCBI Description (U93215) yeast hypothetical protein YDB1_SCHPO isolog
                  [Arabidopsis thaliana]
Seq. No.
                  410403
                  uC-osflcyp033h09b1
Seq. ID
                  BLASTX
Method
                  g4100433
NCBI GI
                  156
BLAST score
E value
                  2.0e-10
                  57
Match length
                  53
% identity
NCBI Description (AF000378) beta-glucosidase [Glycine max]
                  410404
Seq. No.
Seq. ID
                  uC-osflcyp033h10b1
                  BLASTX
Method
NCBI GI
                  q4585882
                  533
BLAST score
E value
                  2.0e-54
Match length
                  146
% identity
                  71
NCBI Description (AC005850) PSI type III chlorophyll a/b-binding protein
                  [Arabidopsis thaliana]
                  410405
Seq. No.
Seq. ID
                  uC-osflcyp034a01b1
                  BLASTX
Method
NCBI GI
                  q132105
BLAST score
                  722
E value
                  1.0e-76
Match length
                  153
                  90
% identity
NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
                  (RUBISCO SMALL SUBUNIT C) >gi 68094 pir RKRZS9
                  ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                  precursor (clone pOSSS1139) - rice >gi 218208 dbj BAA00538
                  (D00643) small subunit of ribulose-1,5-bisphosphate
                  carboxylase (RuBPC) [Oryza sativa] >gi 2407283 (AF017364)
                  ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
                  sativa] >gi 226375 prf 1508256A ribulose bisphosphate
```

carboxylase S [Oryza sativa]

Seq. No.

410406

```
Seq. ID
                  uC-osflcyp034a03b1
Method
                  BLASTX
                  q4584527
NCBI GI
BLAST score
                  152
E value
                  1.0e-09
Match length
                  101
                  35
% identity
NCBI Description (AL049607) putative protein [Arabidopsis thaliana]
Seq. No.
                  410407
Seq. ID
                  uC-osflcyp034a04b1
Method
                  BLASTX
NCBI GI
                  g2130069
BLAST score
                  287
                  9.0e-60
E value
Match length
                  123
% identity
                  98
NCBI Description catalase (EC 1.11.1.6) catA - rice
                  >gi_1261858_dbj_BAA06232 (D29966) catalase [Oryza sativa]
Seq. No.
                  410408
Seq. ID
                  uC-osflcyp034a05b1
Method
                  BLASTX
NCBI GI
                  g4126403
BLAST score
                  260
                  2.0e-22
E value
Match length
                  110
% identity
                  46
NCBI Description
                  (AB011796) flavonol synthase [Citrus unshiu]
Seq. No.
                  410409
Seq. ID
                  uC-osflcyp034a06b1
Method
                  BLASTX
NCBI GI
                  g3885882
BLAST score
                  407
E value
                  1.0e-39
Match length
                  85
% identity
                  94
                  (AF093629) inorganic pyrophosphatase [Oryza sativa]
NCBI Description
Seq. No.
                  410410
                  uC-osflcyp034a07a1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2454182
BLAST score
                  190
E value
                  3.0e-14
Match length
                  39
% identity
                  87
                  (U80185) pyruvate dehydrogenase E1 alpha subunit
NCBI Description
                  [Arabidopsis thaliana]
Seq. No.
                  410411
Seq. ID
                  uC-osflcyp034a07b1
Method
                  BLASTX
NCBI GI
```

53259

g2454182

BLAST score 551 E value 2.0e-56 Match length 126 % identity 83

NCBI Description (U80185) pyruvate dehydrogenase E1 alpha subunit

[Arabidopsis thaliana]

Seq. No. 410412

Seq. ID uC-osflcyp034a08b1

Method BLASTX
NCBI GI g548605
BLAST score 608
E value 3.0e-63
Match length 133
% identity 91

NCBI Description PHOTOSYSTEM I REACTION CENTRE SUBUNIT X PRECURSOR

(LIGHT-HARVESTING COMPLEX I 7 KD PROTEIN) (PSI-K)

>gi_539055_pir__A48527 photosystem I protein psaK precursor - barley >gi_304220 (L12707) photosystem I PSI-K subunit

[Hordeum vulgare]

Seq. No. 410413

Seq. ID uC-osflcyp034a09b1

Method BLASTX
NCBI GI g4218151
BLAST score 191
E value 3.0e-14
Match length 86
% identity 44

NCBI Description (AJ132705) hypothetical protein [Anabaena variabilis]

Seq. No. 410414

Seq. ID uC-osflcyp034a11b1

Method BLASTX
NCBI GI g4204281
BLAST score 154
E value 6.0e-10
Match length 73
% identity 38

NCBI Description (AC004146) Hypothetical protein [Arabidopsis thaliana]

Seq. No. 410415

Seq. ID uC-osflcyp034b01b1

Method BLASTX
NCBI GI g4836883
BLAST score 342
E value 6.0e-32
Match length 151
% identity 40

NCBI Description (AC007260) lcl prt seq No definition line found

[Arabidopsis thaliana]

Seq. No. 410416

Seq. ID uC-osflcyp034b03b1

Method BLASTX NCBI GI g4585882 BLAST score 649

E value 6.0e-68
Match length 169
% identity 73

NCBI Description (AC005850) PSI type III chlorophyll a/b-binding protein

[Arabidopsis thaliana]

Seq. No. 410417

Seq. ID uC-osflcyp034b04b1

Method BLASTX
NCBI GI g2130069
BLAST score 848
E value 2.0e-91
Match length 157
% identity 100

NCBI Description catalase (EC 1.11.1.6) catA - rice

>gi_1261858_dbj_BAA06232_ (D29966) catalase [Oryza sativa]

Seq. No. 410418

Seq. ID uC-osflcyp034b10b1

Method BLASTX
NCBI GI g3980378
BLAST score 719
E value 3.0e-76
Match length 150
% identity 85

NCBI Description (AC004561) putative RNA binding protein [Arabidopsis

thaliana]

Seq. No. 410419

Seq. ID uC-osflcyp034c02b1

Method BLASTX
NCBI GI g4996646
BLAST score 362
E value 2.0e-34
Match length 81
% identity 80

NCBI Description (AB028132) Dof zinc finger protein [Oryza sativa]

Seq. No. 410420

Seq. ID uC-osflcyp034c05b1

Method BLASTN
NCBI GI g607894
BLAST score 99
E value 2.0e-48
Match length 170
% identity 99

NCBI Description Oryza sativa IR54 anther specific (RTS2) gene, complete cds

Seq. No. 410421

Seq. ID uC-osflcyp034c07a1

Method BLASTN
NCBI GI g20280
BLAST score 108
E value 1.0e-53
Match length 364
% identity 82

NCBI Description Rice gene for phenylalanine ammonia-lyase (EC 4.3.1.5)

Seq. No.

410427

```
410422
Seq. No.
                  uC-osflcyp034c07b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g82496
                  549
BLAST score
                  2.0e-56
E value
                  136
Match length
                  76
% identity
NCBI Description phenylalanine ammonia-lyase (EC 4.3.1.5) - rice
Seq. No.
                  410423
                  uC-osflcyp034c08b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3646373
BLAST score
                  803
                  5.0e-86
E value
                  150
Match length
                  99
% identity
NCBI Description (AJ011078) RGP1 protein [Oryza sativa]
Seq. No.
                  410424
Seq. ID
                  uC-osflcyp034c09b1
Method
                  BLASTX
NCBI GI
                  g2388585
BLAST score
                  172
                  2.0e-26
E value
                  119
Match length
% identity
                  61
                  (AC000098) Similar to Caenorhabditis unknown protein
NCBI Description
                  T03F1.1 (gb_U88169). [Arabidopsis thaliana]
Seq. No.
                  410425
                  uC-osflcyp034c10b1
Seq. ID
                  BLASTX
Method
                  g283008
NCBI GI
                  995
BLAST score
                  1.0e-108
E value
                  190
Match length
                  99
% identity
NCBI Description sucrose synthase (EC 2.4.1.13) - rice
                  >gi 20366 emb CAA46017 (X64770) sucrose synthase [Oryza
                   sativa]
Seq. No.
                   410426
Seq. ID
                  uC-osflcyp034c11b1
                  BLASTX
Method
NCBI GI
                  g1346109
                   827
BLAST score
                  7.0e-89
E value
Match length
                  167
                   93
% identity
NCBI Description GUANINE NUCLEOTIDE-BINDING PROTEIN BETA SUBUNIT-LIKE
                   PROTEIN (GPB-LR) (RWD) >gi 540535 dbj BAA07404 (D38231)
                   RWD [Oryza sativa]
```

Seq. ID

Method

```
uC-osflcyp034d01b1
Seq. ID
Method
                  BLASTX
                  q6018458
NCBI GI
BLAST score
                  350
                  6.0e-33
E value
Match length
                  170
                  45
% identity
NCBI Description (AJ243972) 6-phosphogluconolactonase [Homo sapiens]
                  410428
Seq. No.
Seq. ID
                  uC-osflcyp034d03b1
                  BLASTX
Method
NCBI GI
                  g2257756
BLAST score
                  152
                  9.0e-10
E value
                  95
Match length
                  35
% identity
                  (U82815) nucleolar histone deacetylase HD2-p39 [Zea mays]
NCBI Description
                  >gi 3650466 (AF026917) histone deacetylase HD2-p39 [Zea
                  mays]
                   410429
Seq. No.
Seq. ID
                  uC-osflcyp034d07b1
                  BLASTX
Method
NCBI GI
                  g3914899
                  502
BLAST score
                   6.0e-64
E value
                  152
Match length
% identity
                  82
NCBI Description 40S RIBOSOMAL PROTEIN S4 >gi 2331301 (AF013487) ribosomal
                  protein S4 type I [Zea mays]
                   410430
Seq. No.
                   uC-osflcyp034d08b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g6016174
BLAST score
                   185
E value
                   2.0e-13
Match length
                   132
% identity
                   33
NCBI Description GLUTATHIONE-S-TRANSFERASE HOMOLOG
                   >gi 2393724 gb AAB70110.1 (U80819)
                   glutathione-S-transferase homolog [Mus musculus]
Seq. No.
                   410431
                   uC-osflcyp034d09b1
Seq. ID
Method
                   BLASTN
                   g607894
NCBI GI
                   106
BLAST score
                   1.0e-52
E value
Match length
                   192
                   100
% identity
NCBI Description Oryza sativa IR54 anther specific (RTS2) gene, complete cds
                   410432
Seq. No.
```

53263

uC-osflcyp034d10b1

BLASTX

g165414 309

NCBI GI g1654144
BLAST score 309
E value 3.0e-28
Match length 102
% identity 68

NCBI Description (U38471) small GTP-binding protein rab [Brassica rapa]

Seq. No. 410433

Seq. ID uC-osflcyp034d12b1

Method BLASTX
NCBI GI g1235664
BLAST score 698
E value 1.0e-73
Match length 144
% identity 47

NCBI Description (U37936) novel calmodulin-like protein [Oryza sativa]

>gi 3171148 (AF064456) calmodulin-like protein [Oryza

sativa subsp. indica]

Seq. No. 410434

Seq. ID uC-osflcyp034e01b1

Method BLASTX
NCBI GI g2245001
BLAST score 438
E value 3.0e-43
Match length 99
% identity 84

NCBI Description (Z97341) hypothetical protein [Arabidopsis thaliana]

Seq. No. 410435

Seq. ID uC-osflcyp034e09b1

Method BLASTX
NCBI GI g2181180
BLAST score 273
E value 6.0e-24
Match length 172
% identity 35

NCBI Description (Z84377) xylosidase [Aspergillus niger]

Seq. No. 410436

Seq. ID uC-osflcyp034e10b1

Method BLASTX
NCBI GI g2501190
BLAST score 493
E value 1.0e-49
Match length 120
% identity 84

NCBI Description THIAMINE BIOSYNTHETIC ENZYME 1-2 PRECURSOR

>gi_2130147_pir__S61420 thiamine biosynthetic enzyme thi1-2
- maize >gi_596080 (U17351) thiamine biosynthetic enzyme

[Zea mays]

Seq. No. 410437

Seq. ID uC-osflcyp034e11b1

Method BLASTX NCBI GI g1703380 BLAST score 747

Match length

% identity

84

93

```
2.0e-79
E value
Match length
                  148
                  99
% identity
NCBI Description ADP-RIBOSYLATION FACTOR >gi_1132483 dbj BAA04607 (D17760)
                  ADP-ribosylation factor [Oryza sativa]
                  410438
Seq. No.
Seq. ID
                  uC-osflcyp034e12b1
Method
                  BLASTX
NCBI GI
                  q4538902
BLAST score
                  325
                  4.0e-39
E value
Match length
                  102
% identity
                  82
NCBI Description (AL049482) rab7-like protein [Arabidopsis thaliana]
                  410439
Seq. No.
Seq. ID
                  uC-osflcyp034f01b1
Method
                  BLASTX
NCBI GI
                  g1732406
BLAST score
                  164
                  3.0e-11
E value
Match length
                  34
                  85
% identity
NCBI Description (U81157) S25-XP1 DNA binding protein [Nicotiana tabacum]
Seq. No.
                  410440
Seq. ID
                  uC-osflcyp034f02b1
Method
                  BLASTX
NCBI GI
                  g417154
BLAST score
                  866
                  2.0e-93
E value
                  173
Match length
                  98
% identity
NCBI Description HEAT SHOCK PROTEIN 82 >gi 100685 pir S25541 heat shock
                  protein 82 - rice (strain Taichung Native One)
                  >gi 20256 emb CAA77978 (Z11920) heat shock protein 82
                  (HSP82) [Oryza sativa]
Seq. No.
                  410441
                  uC-osflcyp034f03a1
Seq. ID
Method
                  BLASTX
                  g3721942
NCBI GI
BLAST score
                  594
                  1.0e-61
E value
Match length
                  153
                  73
% identity
NCBI Description (AB018248) chitinase [Oryza sativa]
                  410442
Seq. No.
Seq. ID
                  uC-osflcyp034f03b1
Method
                  BLASTX
NCBI GI
                  g3721942
BLAST score
                  409
E value
                  6.0e-40
```

NCBI Description (AB018248) chitinase [Oryza sativa]

Seq. No. 410443

Seq. ID uC-osflcyp034f05b1

Method BLASTX
NCBI GI g131192
BLAST score 512
E value 7.0e-52
Match length 142
% identity 72

NCBI Description PHOTOSYSTEM I REACTION CENTRE SUBUNIT V PRECURSOR

(PHOTOSYSTEM I 9 KD PROTEIN) (PSI-G) >gi 100606 pir S20937

photosystem I chain V precursor - barley

>gi_19091_emb_CAA42727 (X60158) photosystem I polypeptide

PSI-G precursor [Hordeum vulgare]

Seq. No. 410444

Seq. ID uC-osflcyp034f08b1

Method BLASTX
NCBI GI g544242
BLAST score 463
E value 3.0e-46
Match length 132
% identity 72

NCBI Description ENDOPLASMIN HOMOLOG PRECURSOR (GRP94 HOMOLOG)

>gi_485498_pir__S33533 heat shock protein 90 homolog
precursor - barley >gi_22652 emb CAA48143 (X67960) GRP94

homologue [Hordeum vulgare]

Seq. No. 410445

Seq. ID uC-osflcyp034f09b1

Method BLASTX
NCBI GI g1402918
BLAST score 365
E value 6.0e-43
Match length 116
% identity 79

NCBI Description (X98320) peroxidase [Arabidopsis thaliana]

>gi_1429215_emb_CAA67310_ (X98774) peroxidase ATP6a

[Arabidopsis thaliana]

Seq. No. 410446

Seq. ID uC-osflcyp034f10b1

Method BLASTN
NCBI GI g4097337
BLAST score 478
E value 0.0e+00
Match length 495
% identity 99

NCBI Description Oryza sativa metallothionein-like protein mRNA, complete

cds

Seq. No. 410447

Seq. ID uC-osflcyp034f12b1

Method BLASTX NCBI GI g2286153 BLAST score 775

```
2.0e-82
E value
Match length
                  177
                  88
% identity
NCBI Description (AF007581) cytoplasmic malate dehydrogenase [Zea mays]
                  410448
Seq. No.
                  uC-osflcyp034g01b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g5701965
BLAST score
                  224
                  1.0e-18
E value
                  79
Match length
                  44
% identity
NCBI Description (AL109736) WD repeat protein [Schizosaccharomyces pombe]
                  410449
Seq. No.
Seq. ID
                  uC-osflcyp034g03b1
                  BLASTX
Method
                  g485517
NCBI GI
BLAST score
                  700
E value
                  6.0e-74
Match length
                  140
                  99
% identity
NCBI Description ADP, ATP carrier protein - rice
                  410450
Seq. No.
Seq. ID
                  uC-osflcyp034g04b1
                  BLASTX
Method
                  g6014701
NCBI GI
BLAST score
                  333
E value
                  9.0e-47
                  160
Match length
% identity
                  61
NCBI Description (AF190450) enoyl-CoA-hydratase [Avicennia marina]
Seq. No.
                  410451
Seq. ID
                  uC-osflcyp034g05b1
Method
                  BLASTX
NCBI GI
                  g2492834
BLAST score
                  181
                  4.0e-13
E value
Match length
                  104
% identity
                  43
NCBI Description PUTATIVE AMIDASE >gi 1224069 (U49269) amidase [Moraxella
                  catarrhalis]
                  410452
Seq. No.
                  uC-osflcyp034g06b1
Seq. ID
Method
                  BLASTX
                  q548605
NCBI GI
BLAST score
                  599
                  4.0e-62
E value
Match length
                  131
% identity
```

53267

(LIGHT-HARVESTING COMPLEX I 7 KD PROTEIN) (PSI-K)

>gi 539055 pir A48527 photosystem I protein psaK precursor

NCBI Description PHOTOSYSTEM I REACTION CENTRE SUBUNIT X PRECURSOR

.



- barley >gi_304220 (L12707) photosystem I PSI-K subunit [Hordeum vulgare]

Seq. No. 410453

Seq. ID uC-osflcyp034g08b1

Method BLASTX
NCBI GI g3386622
BLAST score 183
E value 2.0e-13
Match length 37
% identity 86

NCBI Description (AC004665) unknown protein [Arabidopsis thaliana]

Seq. No. 410454

Seq. ID uC-osflcyp034g09b1

Method BLASTX
NCBI GI g2130069
BLAST score 750
E value 6.0e-80
Match length 139
% identity 100

NCBI Description catalase (EC 1.11.1.6) catA - rice

>gi_1261858_dbj_BAA06232_ (D29966) catalase [Oryza sativa]

Seq. No. 410455

Seq. ID uC-osflcyp034g10b1

Method BLASTX
NCBI GI g1778093
BLAST score 344
E value 1.0e-32
Match length 96
% identity 68

NCBI Description (U64902) putative sugar transporter; member of major

facilitative superfamily; integral membrane protein [Beta

vulgaris]

Seq. No. 410456

Seq. ID uC-osflcyp034g12b1

Method BLASTN
NCBI GI g1154858
BLAST score 45
E value 4.0e-16
Match length 128
% identity 84

NCBI Description H.vulgare mRNA for L24 ribosomal protein

Seq. No. 410457

Seq. ID uC-osflcyp034h02b1

Method BLASTX
NCBI GI g1136122
BLAST score 700
E value 5.0e-74
Match length 130
% identity 98

NCBI Description (X91807) alfa-tubulin [Oryza sativa]

Seq. No. 410458

```
uC-osflcyp034h03b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g6013233
BLAST score
                  180
E value
                  5.0e-17
                  102
Match length
                  46
% identity
                  (AF183932) ionotropic glutamate receptor homolog
NCBI Description
                   [Arabidopsis thaliana]
                  410459
Seq. No.
                  uC-osflcyp034h04b1
Seq. ID
Method
                  BLASTX
                  q5803205
NCBI GI
                  153
BLAST score
                  8.0e-10
E value
Match length
                  111
                  31
% identity
                  outer mitochondrial membrane translocase (34kD) >gi 1399813
NCBI Description
                   (U58970) hTOM34p [Homo sapiens]
                   410460
Seq. No.
Seq. ID
                  uC-osflcyp034h06b1
                  BLASTN
Method
                  g2773153
NCBI GI
                   463
BLAST score
                   0.0e + 00
E value
                   475
Match length
                   100
% identity
NCBI Description Oryza sativa abscisic acid- and stress-inducible protein
                   (Asr1) mRNA, complete cds
Seq. No.
                   410461
                   uC-osflcyp034h09b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2130069
BLAST score
                   767
                   7.0e-82
E value
Match length
                   142
% identity
                   100
NCBI Description
                   catalase (EC 1.11.1.6) catA - rice
                   >gi 1261858 dbj BAA06232 (D29966) catalase [Oryza sativa]
Seq. No.
                   410462
Seq. ID
                   uC-osflcyp034h10b1
Method
                   BLASTX
                   g5263313
NCBI GI
BLAST score
                   363
                   2.0e-34
E value
Match length
                   148
% identity
                   51
                  (AC007727) Contains similarity to gb U07707 epidermal
NCBI Description
```

Seq. No. 410463

and gb_AA395440 come from this gene. [Arabidop

growth factor receptor substrate (eps15) from Homo sapiens and contains 2 PF 00036 EF hand domains. ESTs gb_T44428

Match length

```
uC-osflcyp034h11b1
Seq. ID
                  BLASTX
Method
                  g4581164
NCBI GI
BLAST score
                  251
                  2.0e-21
E value
                  143
Match length
                  37
% identity
NCBI Description (AC006220) putative polyprotein [Arabidopsis thaliana]
                  410464
Seq. No.
                  uC-osflcyp034h12b1
Seq. ID
                  BLASTX
Method
                  q5541723
NCBI GI
                  412
BLAST score
                  2.0e-40
E value
                  139
Match length
                  59
% identity
NCBI Description (AL096856) betaine aldehyde dehydrogenase-like protein
                  [Arabidopsis thaliana]
Seq. No.
                  410465
Seq. ID
                  uC-osflcyp035a01b1
                  BLASTN
Method
                  q2196541
NCBI GI
                  73
BLAST score
                  2.0e-33
E value
Match length
                  85
                  96
% identity
NCBI Description Oryza sativa glycine-rich protein mRNA, complete cds
                  410466
Seq. No.
Seq. ID
                  uC-osflcyp035a02b1
                  BLASTX
Method
                  g5123547
NCBI GI
                  408
BLAST score
                  1.0e-39
E value
                  151
Match length
                  52
% identity
NCBI Description (AL079344) putative protein [Arabidopsis thaliana]
                  410467
Seq. No.
                  uC-osflcyp035a04b1
Seq. ID
                  BLASTX
Method
NCBI GI
                  g5262154
                  184
BLAST score
                  1.0e-13
E value
Match length
                  121
                  37
% identity
NCBI Description (AL080237) putative protein [Arabidopsis thaliana]
                  410468
Seq. No.
Seq. ID
                  uC-osflcyp035a07b1
                  BLASTX
Method
NCBI GI
                  q4126809
BLAST score
                  783
                  1.0e-83
E value
```

53270

711. -



```
% identity
                  (AB017042) glyoxalase I [Oryza sativa]
NCBI Description
                  410469
Seq. No.
Seq. ID
                  uC-osflcyp035a09b1
Method
                  BLASTX
                  q2880051
NCBI GI
BLAST score
                  329
                  2.0e-30
E value
                  99
Match length
                  59
% identity
                  (AC002340) putative protein kinase [Arabidopsis thaliana]
NCBI Description
                  410470
Seq. No.
Seq. ID
                  uC-osflcyp035a10b1
                  BLASTX
Method
NCBI GI
                  g320618
BLAST score
                  661
E value
                  2.0e-69
Match length
                  144
                  88
% identity
                  chlorophyll a/b-binding protein I precursor - rice
NCBI Description
                  >gi_218172_dbj_BAA00536_ (D00641) type I light-harvesting
                  chlorophyll a/b-binding protein [Oryza sativa]
                  >gi_227611_prf__1707316A chlorophyll a/b binding protein 1
                   [Oryza sativa]
                  410471
Seq. No.
Seq. ID
                  uC-osflcyp035a12b1
Method
                  BLASTN
NCBI GI
                  q4097337
                   299
BLAST score
                  1.0e-167
E value
                   384
Match length
                   99
% identity
                  Oryza sativa metallothionein-like protein mRNA, complete
NCBI Description
                   410472
Seq. No.
Seq. ID
                  uC-osflcyp035b02b1
Method
                   BLASTX
NCBI GI
                   q320618
BLAST score
                   399
                   8.0e-39
E value
                   115
Match length
% identity
                  chlorophyll a/b-binding protein I precursor - rice
NCBI Description
                   >gi 218172 dbj BAA00536 (D00641) type I light-harvesting
                   chlorophyll a/b-binding protein [Oryza sativa]
                   >gi 227611 prf 1707316A chlorophyll a/b binding protein 1
                   [Oryza sativa]
```

Seq. No. 410473

Seq. ID uC-osflcyp035b03b1

Method BLASTX
NCBI GI g4006978
BLAST score 152

```
7.0e-10
E value
                  87
Match length
                  38
% identity
                 (AJ131335) pollen allergen (group II) [Cynodon dactylon]
NCBI Description
                  410474
Seq. No.
Seq. ID
                  uC-osflcyp035b04b1
                  BLASTX
Method
NCBI GI
                  q320618
BLAST score
                  447
                  2.0e-44
E value
                  113
Match length
                  83
% identity
NCBI Description chlorophyll a/b-binding protein I precursor - rice
                  >gi_218172_dbj_BAA00536_ (D00641) type I light-harvesting
                  chlorophyll a/b-binding protein [Oryza sativa]
                  >gi_227611_prf__1707316A chlorophyll a/b binding protein 1
                  [Oryza sativa]
                  410475
Seq. No.
                  uC-osflcyp035b07b1
Seq. ID
                  BLASTX
Method
NCBI GI
                  q4544422
BLAST score
                  599
E value
                  3.0e-62
                  160
Match length
                  73
% identity
NCBI Description (AC006955) putative fimbrin [Arabidopsis thaliana]
                  410476
Seq. No.
Seq. ID
                  uC-osflcyp035b08b1
                  BLASTX
Method
NCBI GI
                  a3386614
BLAST score
                  417
E value
                  9.0e-41
                  125
Match length
                  40
% identity
NCBI Description
                  (AC004665) putative transcription factor SF3 [Arabidopsis
                  thaliana]
Seq. No.
                  410477
Seq. ID
                  uC-osflcyp035b09b1
                  BLASTX
Method
NCBI GI
                  q3258575
BLAST score
                  373
                  1.0e-35
E value
Match length
                  89
% identity
                  80
NCBI Description (U89959) Hypothetical protein [Arabidopsis thaliana]
                  410478
Seq. No.
                  uC-osflcyp035b11b1
Seq. ID
```

Method BLASTX NCBI GI g3319340 BLAST score 302 2.0e-27 E value 102 Match length

60 % identity (AF077407) contains similarity to E. coli cation transport NCBI Description protein ChaC (GB:D90756) [Arabidopsis thaliana] 410479 Seq. No. uC-osflcyp035c03b1 Seq. ID BLASTX Method g5852181 NCBI GI 409 BLAST score 5.0e-40E value 77 Match length 97 % identity NCBI Description (AL117265) zhb0011.1 [Oryza sativa] 410480 Seq. No. uC-osflcyp035c04b1 Seq. ID BLASTX Method g3582335 NCBI GI BLAST score 738 2.0e-78 E value Match length 158 % identity 84 NCBI Description (AC005496) unknown protein [Arabidopsis thaliana] 410481 Seq. No. Seq. ID uC-osflcyp035c06b1 Method BLASTX g1732411 NCBI GI 322 BLAST score 1.0e-29 E value Match length 140 % identity 46 NCBI Description (U47924) isopeptidase T [Homo sapiens] 410482 Seq. No. Seq. ID uC-osflcyp035c07a1 BLASTN Method NCBI GI g2696239 BLAST score 140 E value 8.0e-73 Match length 293 86 % identity NCBI Description Oryza sativa mRNA for aspartate aminotransferase, complete cds Seq. No. 410483 uC-osflcyp035c07b1 Seq. ID BLASTX Method g2130067 NCBI GI BLAST score 759 E value 5.0e-81 Match length 146 97 % identity

53273

aminotransferase [Oryza sativa]

NCBI Description aspartate transaminase (EC 2.6.1.1), mitochondrial - rice

>gi 2696240 dbj BAA23815.1 (D67043) aspartate

```
410484
Seq. No.
                  uC-osflcyp035c08b1
Seq. ID
                  BLASTX
Method
                  g322854
NCBI GI
                  737
BLAST score
                   2.0e-78
E value
                   148
Match length
                   97
% identity
                  pollen-specific protein - rice >gi 20310 emb CAA78897
NCBI Description
                   (Z16402) pollen specific gene [Oryza satīva]
                   410485
Seq. No.
                   uC-osflcyp035c09b1
Seq. ID
                   BLASTX
Method
                   g2245025
NCBI GI
                   162
BLAST score
                   7.0e-11
E value
                   69
Match length
                   46
% identity
                  (Z97341) decarboxylase like protein [Arabidopsis thaliana]
NCBI Description
                   410486
Seq. No.
                   uC-osflcyp035c10b1
Seq. ID
                   BLASTX
Method
                   g3549667
NCBI GI
BLAST score
                   672
                   1.0e-70
E value
Match length
                   184
                   68
% identity
                   (AL031394) Arabidopsis dynamin-like protein ADL2
NCBI Description
                   [Arabidopsis thaliana]
                   410487
Seq. No.
                   uC-osflcyp035c12b1
 Seq. ID
                   BLASTX
Method
                   g4678297
 NCBI GI
                   452
BLAST score
                   6.0e-45
 E value
                   159
Match length
                   57
 % identity
                   (AL049655) protein disulfide-isomerase-like protein
 NCBI Description
                   [Arabidopsis thaliana]
                   410488
 Seq. No.
                   uC-osflcyp035d01b1
 Seq. ID
                   BLASTX
 Method
                   q4538920
 NCBI GI
                   179
 BLAST score
                   7.0e-18
 E value
                   74
 Match length
                   70
 % identity
                   (AL049483) nitrogen fixation like protein [Arabidopsis
 NCBI Description
                   thaliana]
                    410489
 Seq. No.
 Seq. ID
                    uC-osflcyp035d03a1
                    BLASTN
 Method
```

```
q4887617
NCBI GI
                  289
BLAST score
                  1.0e-161
E value
                  305
Match length
                  99
% identity
NCBI Description Oryza sativa HOS59 mRNA, partial cds
                  410490
Seq. No.
                  uC-osflcyp035d03b1
Seq. ID
                  BLASTX
Method
                  q5689236
NCBI GI
                  368
BLAST score
                  3.0e-35
E value
                  101
Match length
                  79
% identity
                  (AB024291) ZmRR2 [Zea mays] >gi 6009897 dbj BAA85113.1
NCBI Description
                   (AB031012) response regulator 2 [Zea mays]
                   410491
Seq. No.
                  uC-osflcyp035d05b1
Seq. ID
                  {\tt BLASTX}
Method
                  g4769004
NCBI GI
                  513
BLAST score
                  4.0e-52
E value
                  89
Match length
                   98
% identity
                  (AF140598) ring-box protein 1 [Homo sapiens]
NCBI Description
                   >gi_4769006_gb_AAD29716.1_AF140599_1 (AF140599) ring-box
                   protein 1 [Mus musculus]
                   >gi_4809216_gb_AAD30146.1_AF142059 1 (AF142059) RING finger
                   protein [Homo sapiens]
                   410492
Seq. No.
                   uC-osflcyp035d07b1
Seq. ID
                  BLASTX
Method
                   q4836879
NCBI GI
                   402
BLAST score
                   5.0e-39
E value
                   150
Match length
% identity
NCBI Description (AC007260) lcl_prt_seq No definition line found
                   [Arabidopsis thaliana]
                   410493
Seq. No.
Seq. ID
                   uC-osflcyp035d08b1
                   BLASTX
Method
                   g5912299
NCBI GI
                   905
BLAST score
                   6.0e-98
E value
                   184
Match length
% identity
                   97
NCBI Description (AJ133787) gigantea homologue [Oryza sativa]
                   410494
Seq. No.
                   uC-osflcyp035d09b1
Seq. ID
Method
                   BLASTX
                   q6065749
NCBI GI
```



425 BLAST score 9.0e-42E value 161 Match length 54 % identity NCBI Description (AJ250341) beta-amylase enzyme [Arabidopsis thaliana] 410495 Seq. No. uC-osflcyp035d10b1 Seq. ID Method BLASTX q3914394 NCBI GI 570 BLAST score 6.0e-59 E value 127 Match length % identity 86 NCBI Description 2,3-BISPHOSPHOGLYCERATE-INDEPENDENT PHOSPHOGLYCERATE MUTASE (PHOSPHOGLYCEROMUTASE) (BPG-INDEPENDENT PGAM) (PGAM-I) >gi_2118335_pir__S60473 phosphoglycerate mutase (EC 5.4.2.1) - common ice plant >gi_602426 (U16021) phosphoglyceromutase [Mesembryanthemum crystallinum] 410496 Seq. No. Seq. ID uC-osflcyp035d11b1 Method BLASTX q4678297 NCBI GI 537 BLAST score 7.0e-55 E value Match length 180 59 % identity NCBI Description (AL049655) protein disulfide-isomerase-like protein [Arabidopsis thaliana] Seq. No. 410497 Seq. ID uC-osflcyp035d12b1 Method BLASTX g418854 NCBI GI 680 BLAST score E value 1.0e-71 136 Match length 18 % identity NCBI Description ubiquitin precursor - parsley >gi_288112_emb_CAA45621_ (X64344) polyubiquitin [Petroselinum crispum] >gi 288114 emb CAA45622_ (X64345) polyubiquitin [Petroselinum crispum] 410498 Seq. No. uC-osflcyp035e03b1 Seq. ID BLASTX Method NCBI GI q4680207 BLAST score 147 E value 4.0e-09 119 Match length

36 % identity

NCBI Description (AF114171) disease resistance protein RPM1 homolog [Sorghum

bicolor]

410499 Seq. No.

Seq. ID uC-osflcyp035e05b1



```
BLASTX
Method
                  g2258315
NCBI GI
                  215
BLAST score
                  4.0e-17
E value
                  162
Match length
                  33
% identity
                  (AF004878) resistance complex protein I2C-1 [Lycopersicon
NCBI Description
                  esculentum]
                  410500
Seq. No.
                  uC-osflcyp035e06b1
Seq. ID
                  BLASTX
Method
                  g5733874
NCBI GI
                  289
BLAST score
                  9.0e-26
E value
                  130
Match length
                  47
% identity
NCBI Description (AC007932) F11A17.8 [Arabidopsis thaliana]
                  410501
Seq. No.
Seq. ID
                  uC-osflcyp035e07b1
Method
                  BLASTX
                  q1052973
NCBI GI
BLAST score
                  286
                  2.0e-25
E value
                  81
Match length
% identity
                   69
NCBI Description (U37838) fructokinase [Beta vulgaris]
                   410502
Seq. No.
                   uC-osflcyp035e09b1
Seq. ID
Method
                  BLASTX
                  g4587552
NCBI GI
                   541
BLAST score
                   2.0e-55
E value
                  134
Match length
                   81
% identity
                  (AC006577) Strong similarity to gb S77096 aldehyde
NCBI Description
                   dehydrogenase homolog from Brassica napus and is a member
                   of PF 00171 Aldehyde dehydrogenase family. ESTs gb_T46213,
                   gb_T42164, gb_T43682, gb_N96380, gb_T42973, gb
                   410503
Seq. No.
                   uC-osflcyp035e10b1
Seq. ID
                   BLASTX
Method
NCBI GI
                   g2293480
                   224
BLAST score
                   8.0e-19
E value
                   47
Match length
```

89 % identity

NCBI Description (AF011331) glycine-rich protein [Oryza sativa]

410504 Seq. No.

Seq. ID uC-osflcyp035e11b1

Method BLASTX q417103 NCBI GI BLAST score 663

1.0e-69 E value 135 Match length 99 % identity HISTONE H3.2, MINOR >gi 282871 pir S24346 histone NCBI Description H3.3-like protein - Arabidopsis thaliana >gi 16324 emb CAA42957 (X60429) histone H3.3 like protein [Arabidopsis thaliana] >gi_404825_emb_CAA42958_ (X60429) histone H3.3 like protein [Arabidopsis thaliana] >gi 488563 (U09458) histone H3.2 [Medicago sativa] >gi 488567 (U09460) histone H3.2 [Medicago sativa] >gi_488569 (U09461) histone H3.2 [Medicago sativa] >gi 488575 (U09464) histone H3.2 [Medicago sativa] $>gi_488577$ (U09465) histone H3.2 [Medicago sativa] >gi_510911_emb_CAA56153_ (X79714) histone H3 [Lolium temulentum] >gi $1\overline{435157}$ emb_CA $\overline{A58445}$ (X83422) histone H3 variant H3.3 [Lycopersicon esculentum] >gi_2558944 (AF024716) histone 3 [Gossypium hirsutum] >gi_3273350_dbj_BAA31218_ (AB015760) histone H3 [Nicotiana $tab\overline{a}cum$] $>g\overline{i}_38\overline{8}5890$ (AFO93633) histone H3 [Oryza sativa] >gi 4038469 gb AAC97380 (AF109910) histone H3 [Porteresia coarctata] >gi_4490754_emb_CAB38916.1_ (AL035708) histone H3.3 [Arabidopsis thaliana] > gi 4490755 emb CAB38917.1(AL035708) Histon H3 [Arabidopsis thaliana] >gi_6006364_dbj_BAA84794.1_ (AP000559) EST D15300(C0425) corresponds to a region of the predicted gene.; Similar to

Method BLASTX
NCBI GI g4835760
BLAST score 695
E value 2.0e-73
Match length 151
% identity 89

NCBI Description (AC007202) Strong similarity to gb_Y14272

3-deoxy-D-manno-2-octulosonate-8-phosphate synthase from Pisum sativum. ESTs gb_AA067485 and gb_AI100551 come from

this gene. [Arabidopsis thaliana]

histone H3 (AB015760) [Oryza sativa]

Seq. No. 410506

Seq. ID uC-osflcyp035f01b1

Method BLASTX
NCBI GI g5042416
BLAST score 371
E value 2.0e-35
Match length 155
% identity 24

NCBI Description (AC006193) Unknown protein [Arabidopsis thaliana]

Seq. No. 410507

Seq. ID uC-osflcyp035f02b1

Method BLASTN
NCBI GI g5803242
BLAST score 255
E value 1.0e-141
Match length 360
% identity 100

```
NCBI Description Oryza sativa genomic DNA, chromosome 6, clone:P0535G04
                  410508
Seq. No.
Seq. ID
                  uC-osflcyp035f03b1
                  BLASTX
Method
                  g4426964
NCBI GI
                  579
BLAST score
                  8.0e-60
E value
                  157
Match length
                  68
% identity
                  (AF126255) purple acid phosphatase precursor [Anchusa
NCBI Description
                  officinalis]
                  410509
Seq. No.
Seq. ID
                  uC-osflcyp035f04b1
Method
                  BLASTX
                  g126386
NCBI GI
                  193
BLAST score
                  2.0e-14
E value
                  90
Match length
% identity
                   43
                  POLLEN ALLERGEN LOL P 2-A (LOL P II-A)
NCBI Description
                   >gi_82449_pir__A34291 pollen allergen Lol p IIA - perennial
                   ryegrass
                   410510
Seq. No.
                   uC-osflcyp035f07b1
Seq. ID
                  BLASTX
Method
                   g3345477
NCBI GI
BLAST score
                   682
                   7.0e-72
E value
                  163
Match length
                   82
% identity
NCBI Description (AB016283) carbonic anhydrase [Oryza sativa]
                   410511
Seq. No.
Seq. ID
                   uC-osflcyp035f09b1
                   BLASTX
Method
                   g4417283
NCBI GI
BLAST score
                   387
E value
                   3.0e-37
                   152
Match length
                   47
% identity
NCBI Description (AC007019) putative cytochrome p450 [Arabidopsis thaliana]
                   410512
Seq. No.
Seq. ID
                   uC-osflcyp035f12b1
                   BLASTX
Method
                   q418854
NCBI GI
                   732
BLAST score
                   9.0e-78
E value
                   147
Match length
                   18
% identity
NCBI Description ubiquitin precursor - parsley >gi 288112 emb CAA45621
                   (X64344) polyubiquitin [Petroselinum crispum]
                   >gi_288114_emb_CAA45622_ (X64345) polyubiquitin
                   [Petroselinum crispum]
```



```
410513
Seq. No.
                  uC-osflcyp035g02b1
Seq. ID
                  BLASTX
Method
                  q974782
NCBI GI
                  757
BLAST score
                  9.0e-81
E value
                  151
Match length
                  95
% identity
                  (Z49150) cobalamine-independent methionine synthase
NCBI Description
                   [Solenostemon scutellarioides]
                   410514
Seq. No.
                  uC-osflcyp035g03b1
Seq. ID
                  BLASTX
Method
                  g132105
NCBI GI
                   542
BLAST score
                   2.0e-55
E value
                   98
Match length
                   100
% identity
NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
                   (RUBISCO SMALL SUBUNIT C) >gi 68094 pir RKRZS9
                   ribulose-bisphosphate carboxy\overline{l}ase (\overline{E}C 4\overline{.1}.1.39) small chain
                   precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_
                   (D00643) small subunit of ribulose-1,5-bisphosphate
                   carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364)
                   ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
                   sativa] >gi 226375 prf 1508256A ribulose bisphosphate
                   carboxylase S [Oryza sativa]
                   410515
Seq. No.
                   uC-osflcyp035g04b1
Seq. ID
                   BLASTX
Method
                   a671740
NCBI GI
BLAST score
                   538
                   6.0e-55
E value
Match length
                   98
% identity
NCBI Description (X84730) ribulose-bisphosphate carboxylase [synthetic
                   construct]
                   410516
Seq. No.
Seq. ID
                   uC-osflcyp035g05b1
                   BLASTX
Method
                   q1777312
NCBI GI
BLAST score
                   211
                   1.0e-16
E value
                   98
Match length
                   48
% identity
NCBI Description (D30622) novel serine/threonine protein kinase [Arabidopsis
                   thaliana]
```

410517

BLASTX

g4467146 293

uC-osflcyp035g07b1

Seq. No.

Seq. ID Method

NCBI GI

BLAST score

```
2.0e-26
E value
                  143
Match length
                  41
% identity
                   (AL035540) galactosidase like protein [Arabidopsis
NCBI Description
                  thaliana]
                  410518
Seq. No.
                  uC-osflcyp035g08b1
Seq. ID
                  BLASTX
Method
                  g6016691
NCBI GI
BLAST score
                  143
                  6.0e-09
E value
                  62
Match length
                   48
% identity
                  (AC009991) unknown protein [Arabidopsis thaliana]
NCBI Description
                   410519
Seq. No.
                   uC-osflcyp035g09b1
Seq. ID
Method
                   BLASTX
                   g5777618
NCBI GI
BLAST score
                   147
                   3.0e-09
E value
                   50
Match length
                   52
% identity
                  (AJ245900) CAA30376.1 protein [Oryza sativa]
NCBI Description
                   410520
Seq. No.
                   uC-osflcyp035g10b1
Seq. ID
                   {\tt BLASTX}
Method
                   g3643608
NCBI GI
BLAST score
                   151
                   4.0e-10
E value
                   84
Match length
                   45
% identity
                   (AC005395) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   >gi_4874312_gb_AAD31374.1_AC006053 16 (AC006053)
                   hypothetical protein [Arabidopsis thaliana]
                   410521
Seq. No.
Seq. ID
                   uC-osflcyp035g11b1
                   BLASTX
Method
NCBI GI
                   g2662612
BLAST score
                   189
E value
                   4.0e-14
                   111
Match length
                   40
% identity
                   (AF036701) similar to the peptidase family M1 (zinc
NCBI Description
                   metalloproteases) [Caenorhabditis elegans]
                   410522
Seq. No.
Seq. ID
                   uC-osflcyp035g12b1
                   BLASTX
Method
                   q1848225
NCBI GI
BLAST score
                   293
E value
                   3.0e-26
                   62
Match length
% identity
                   79
```

```
(U88090) nonspecific lipid transfer protein [Hordeum
NCBI Description
                  vulgare]
                  410523
Seq. No.
                  uC-osflcyp035h01b1
Seq. ID
                  BLASTX
Method
                  q4581164
NCBI GI
                  294
BLAST score
                  2.0e-26
E value
                  145
Match length
                  46
% identity
                  (AC006220) putative polyprotein [Arabidopsis thaliana]
NCBI Description
                  410524
Seq. No.
                  uC-osflcyp035h02b1
Seq. ID
                  BLASTX
Method
                  g4581164
NCBI GI
                  279
BLAST score
                  1.0e-24
E value
                  128
Match length
% identity
                   48
                  (AC006220) putative polyprotein [Arabidopsis thaliana]
NCBI Description
```

Seq. No. 410525

Seq. ID uC-osflcyp035h03b1

Method BLASTX
NCBI GI g3746903
BLAST score 468
E value 9.0e-47
Match length 148
% identity 68

NCBI Description (AF089724) signal recognition particle 54 kDa subunit

precursor [Pisum sativum]

Seq. No. 410526

Seq. ID uC-osflcyp035h04b1

Method BLASTX
NCBI GI g2648032
BLAST score 723
E value 1.0e-76
Match length 185
% identity 73

NCBI Description (AJ001374) alpha-glucosidase [Solanum tuberosum]

Seq. No. 410527

Seq. ID uC-osflcyp035h05b1

Method BLASTX
NCBI GI g3023816
BLAST score 678
E value 2.0e-71
Match length 157
% identity 87

NCBI Description GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC

>gi_968996 (U31676) glyceraldehyde-3-phosphate

dehydrogenase [Oryza sativa]

Seq. No. 410528

```
uC-osflcyp035h06b1
Seq. ID
                  BLASTX
Method
NCBI GI
                  g4510395
                  158
BLAST score
                  3.0e-11
E value
                  69
Match length
                  45
% identity
                  (AC006587) putative beta-galactosidase precursor
NCBI Description
                  [Arabidopsis thaliana]
                  410529
Seq. No.
                  uC-osflcyp035h09b1
Seq. ID
                  BLASTX
Method
                  g445613
NCBI GI
                  451
BLAST score
                  7.0e-45
E value
                  128
Match length
                   67
% identity
NCBI Description ribosomal protein L7 [Solanum tuberosum]
                   410530
Seq. No.
                  uC-osflcyp035h10b1
Seq. ID
                  BLASTX
Method
                   g1708424
NCBI GI
                   536
BLAST score
                   1.0e-54
E value
                   159
Match length
                   68
% identity
                  ISOFLAVONE REDUCTASE HOMOLOG >gi 1230614 (U48590)
NCBI Description
                   isoflavone reductase-like protein [Lupinus albus]
                   410531
Seq. No.
                   uC-osflcyp035h11a1
Seq. ID
                   BLASTX
Method
                   q3702327
NCBI GI
                   396
BLAST score
                   1.0e-38
E value
                   119
Match length
                   65
% identity
NCBI Description (AC005397) unknown protein [Arabidopsis thaliana]
                   410532
Seq. No.
Seq. ID
                   uC-osflcyp036a07b1
                   BLASTX
Method
                   q2982453
NCBI GI
BLAST score
                   598
                   4.0e-62
E value
Match length
                   142
                   84
% identity
NCBI Description (AL022223) fructose-bisphosphate aldolase-like protein
                   [Arabidopsis thaliana]
Seq. No.
                   410533
                   uC-osflcyp036b03b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   q3135543
```

505

BLAST score





```
3.0e-51
E value
                  102
Match length
                  94
% identity
NCBI Description (AF062393) aquaporin [Oryza sativa]
                  410534
Seq. No.
                  uC-osflcyp036b11b1
Seq. ID
                  BLASTX
Method
                  g1170871
NCBI GI
                  199
BLAST score
                  5.0e-20
E value
                  95
Match length
                  56
% identity
                  MALATE OXIDOREDUCTASE, CHLOROPLAST PRECURSOR (MALIC ENZYME)
NCBI Description
                  (ME) (NADP-DEPENDENT MALIC ENZYME) (NADP-ME)
                  >gi 1076749_pir__S46499 NADP-dependent malic enzyme - rice
                  >gi 415315 dbj BAA03949 (D16499) NADP-dependent malic
                  enzyme [Oryza sativa]
                  410535
Seq. No.
                  uC-osflcyp036c07b1
Seq. ID
                  BLASTX
Method
                  g431154
NCBI GI
                  257
BLAST score
                   4.0e-22
E value
                  75
Match length
                   61
% identity
NCBI Description (D21813) ORF [Lilium longiflorum]
                   410536
Seq. No.
Seq. ID
                   uC-osflcyp036e01b1
                   BLASTX
Method
                   q445613
NCBI GI
                   278
BLAST score
                   2.0e-26
E value
                   99
Match length
                   67
% identity
NCBI Description ribosomal protein L7 [Solanum tuberosum]
                   410537
Seq. No.
                   uC-osflcyp036e02b1
Seq. ID
                   BLASTX
Method
                   q5430747
NCBI GI
                   469
BLAST score
                   4.0e-47
E value
                   126
Match length
                   69
% identity
NCBI Description (AC007504) Hypothetical Protein [Arabidopsis thaliana]
                   410538
Seq. No.
                   uC-osflcyp036e09b1
Seq. ID
                   BLASTX
Method
                   q730456
NCBI GI
BLAST score
                   657
                   5.0e-69
 E value
                   127
Match length
```

98

% identity

Method

BLASTX

```
NCBI Description 40S RIBOSOMAL PROTEIN S19
Seq. No.
                  410539
Seq. ID
                  uC-osflcyp036f05b1
Method
                  BLASTX
                  g5732069
NCBI GI
                  226
BLAST score
                  2.0e-18
E value
Match length
                  61
% identity
                  67
                  (AF147263) contains similarity to Pfam family PF00036 - EF
NCBI Description
                  hand; score=11.7, E=0.66, N=1 [Arabidopsis thaliana]
                  410540
Seq. No.
                  uC-osflcyp036q09b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1001263
BLAST score
                  330
E value
                  1.0e-30
Match length
                  98
                   60
% identity
NCBI Description (D64003) hypothetical protein [Synechocystis sp.]
                   410541
Seq. No.
                  uC-osflcyp036h05b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q5701742
BLAST score
                   358
                   4.0e-34
E value
                  108
Match length
% identity
                   64
NCBI Description (AB030706) LEDI-5b protein [Lithospermum erythrorhizon]
Seq. No.
                   410542
Seq. ID
                  uC-osflcyp037a01b1
Method
                  BLASTX
NCBI GI
                  g485517
BLAST score
                   711
                   3.0e-75
E value
                  140
Match length
                   99
% identity
NCBI Description ADP, ATP carrier protein - rice
                   410543
Seq. No.
Seq. ID
                  uC-osflcyp037a03b1
                  BLASTX
Method
NCBI GI
                   q4154810
BLAST score
                   186
                  1.0e-13
E value
                   82
Match length
                   45
% identity
NCBI Description (AE001465) DIAMINOPIMELATE DECARBOXYLASE [Helicobacter
                  pylori J99]
Seq. No.
                   410544
                   uC-osflcyp037a06b1
Seq. ID
```

Seq. ID

```
g115772
       NCBI GI
       BLAST score
                           145
                           1.0e-09
       E value
                           50
       Match length
                            64
       % identity
                           CHLOROPHYLL A-B BINDING PROTEIN 1 PRECURSOR (LHCII TYPE I
       NCBI Description
                           CAB-1) (LHCP) >gi_82460_pir__S03705 chlorophyll a/b-binding
                           protein 1R precursor - rice >gi_20178_emb_CAA32108
                            (X13908) chlorophyll a/b-binding preprotein (AA -31 to 235)
                            [Oryza sativa]
       Seq. No.
                            410545
                            uC-osflcyp037a08b1
       Seq. ID
                            BLASTX
       Method
       NCBI GI
                            g2760327
       BLAST score
                            389
                            1.0e-37
       E value
                            85
Match le % identi
NCBI Des

Seq. No.
Seq. ID
Method
NCBI GI
BLAST sc
E value
Match le
% identi
NCBI Des

Seq. No
Seq. ID
Method
NCBI GI
       Match length
                            45
        % identity
       NCBI Description (AC002130) F1N21.12 [Arabidopsis thaliana]
                            410546
        Seq. No.
                            uC-osflcyp037a09b1
                            BLASTX
                            q6015065
                            614
        BLAST score
                            7.0e-64
                            128
        Match length
                            92
        % identity
        NCBI Description ELONGATION FACTOR 2 (EF-2) >gi_2369714_emb_CAB09900_
                            (Z97178) elongation factor 2 [Beta vulgaris]
                            410547
        Seq. No.
                            uC-osflcyp037a11b1
                            BLASTX
                            g4835793
        NCBI GI
                            301
        BLAST score
                            1.0e-27
        E value
                            87
        Match length
                            69
        % identity
                            (AC007296) Similar to gb U90212 DNA binding protein ACBF
        NCBI Description
                            from Nicotiana tabacum and contains 3 PF 00076 RNA
                            recognition motif domains. ESTs gb T44278, gb_R65195,
                            gb N65904, gb_H37499, gb_R90487, gb_N95952, gb_T4427
                            410548
        Seq. No.
        Seq. ID
                            uC-osflcyp037a12b1
                            BLASTX
        Method
                            q5902371
        NCBI GI
                            375
        BLAST score
                            4.0e-36
        E value
        Match length
                            94
                            71
        % identity
        NCBI Description (AC009322) Hypothetical protein [Arabidopsis thaliana]
        Seq. No.
                             410549
```

uC-osflcyp037b05a1

Seq. ID Method

```
BLASTX
Method
NCBI GI
                  g2224915
                  337
BLAST score
                  2.0e-31
E value
                  112
Match length
                  59
% identity
NCBI Description (U95968) beta-expansin [Oryza sativa]
Seq. No.
                  410550
                  uC-osflcyp037b05b1
Seq. ID
                  BLASTX
Method
NCBI GI
                  g2224915
BLAST score
                  416
E value
                  9.0e-41
                  92
Match length
                  74
% identity
NCBI Description (U95968) beta-expansin [Oryza sativa]
Seq. No.
                  410551
Seq. ID
                  uC-osflcyp037b06b1
                  BLASTX
Method
NCBI GI
                  q2407281
BLAST score
                  575
                  2.0e-59
E value
Match length
                  115
                  95
% identity
NCBI Description (AF017363) ribulose 1,5-bisphosphate carboxylase small
                  subunit [Oryza sativa]
Seq. No.
                  410552
                  uC-osflcyp037b08b1
Seq. ID
                  BLASTX
Method
                  q115787
NCBI GI
BLAST score
                  713
E value
                  2.0e-75
Match length
                  157
                  90
% identity
NCBI Description CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I
                  CAB-2) (LHCP) >gi_82461_pir__S03706 chlorophyll a/b-binding
                  protein 2R precursor - rice >gi 20182 emb CAA32109
                   (X13909) chlorophyll a/b-binding preprotein (AA -28 to 235)
                   [Oryza sativa]
Seq. No.
                   410553
Seq. ID
                  uC-osflcyp037b09b1
Method
                  BLASTX
                  g4104220
NCBI GI
                  259
BLAST score
                  1.0e-22
E value
                  94
Match length
                   62
% identity
NCBI Description (AF033538) caffeic acid O-methyltransferase; LPOMT1 [Lolium
                  perenne]
                   410554
Seq. No.
```

53287

uC-osflcyp037b10b1

BLASTX

```
NCBI GI
                  g4585976
BLAST score
                  315
E value
                  6.0e-29
Match length
                  90
                  63
% identity
NCBI Description (AC005287) Unknown protein [Arabidopsis thaliana]
Seq. No.
                  410555
Seq. ID
                  uC-osflcyp037b11b1
Method
                  BLASTX
NCBI GI
                  g1871186
                  399
BLAST score
                  8.0e-39
E value
                  139
Match length
                  59
% identity
NCBI Description (U90439) protein kinase isolog [Arabidopsis thaliana]
Seq. No.
                  410556
Seq. ID
                  uC-osflcyp037c01b1
Method
                  BLASTX
NCBI GI
                  g2055230
BLAST score
                  222
E value
                  6.0e-18
Match length
                  137
                  40
% identity
NCBI Description (AB000130) SRC2 [Glycine max]
Seq. No.
                  410557
Seq. ID
                  uC-osflcyp037c04b1
Method
                  BLASTX
NCBI GI
                  g4337175
BLAST score
                  167
E value
                  1.0e-11
Match length
                  68
% identity
                  56
NCBI Description
                  (AC006416) ESTs gb T20589, gb T04648, gb AA597906,
                  gb_T04111, gb_R84180, gb_R65428, gb_T44439, gb_T76570,
                  gb R90004, gb T45020, gb T42457, gb T20921, gb AA042762 and
                  gb_AA720210 come from this gene. [Arabidopsis thaliana]
                  410558
Seq. No.
Seq. ID
                  uC-osflcyp037c05b1
Method
                  BLASTX
NCBI GI
                  g2459448
BLAST score
                  343
E value
                  7.0e-33
Match length
                  148
% identity
NCBI Description
                  (AC002332) putative cinnamoyl-CoA reductase [Arabidopsis
                  thaliana]
Seq. No.
                  410559
Seq. ID
                  uC-osflcyp037c08b1
Method
                  BLASTX
NCBI GI
                  g2582645
BLAST score
                  200
```

5.0e-21

E value

Match length 80 % identity NCBI Description (AJ002378) RSZp22 protein [Arabidopsis thaliana] Seq. No. 410560 Seq. ID uC-osflcyp037c09b1 Method BLASTX NCBI GI q3258575 BLAST score 368 E value 5.0e-35 Match length 114 % identity NCBI Description (U89959) Hypothetical protein [Arabidopsis thaliana] Seq. No. 410561 uC-osflcyp037c10b1 Seq. ID Method BLASTX NCBI GI q4337175 BLAST score 262 E value 2.0e-22 Match length 142 % identity 41 NCBI Description (AC006416) ESTs gb T20589, gb T04648, gb AA597906, gb_T04111, gb_R84180, gb_R65428, gb_T44439, gb_T76570, gb_R90004, gb_T45020, gb_T42457, gb_T20921, gb_AA042762 and gb_AA720210 come from this gene. [Arabidopsis thaliana] Seq. No. 410562 Seq. ID uC-osflcyp037d01b1 Method BLASTX NCBI GI q1296955 BLAST score 636 E value 2.0e-66 Match length 117 % identity 50 NCBI Description (X95402) duplicated domain structure protein [Oryza sativa] Seq. No. 410563 Seq. ID uC-osflcyp037d02b1 Method BLASTX NCBI GI g1839188 BLAST score 362 E value 2.0e-34 Match length 107 % identity 64 NCBI Description (U86081) root hair defective 3 [Arabidopsis thaliana] Seq. No. 410564 Seq. ID uC-osflcyp037d03b1 Method BLASTX

Method BLASTX
NCBI GI g2129675
BLAST score 479
E value 3.0e-48
Match length 107
% identity 87

NCBI Description probable chlorophyll synthetase G4 - Arabidopsis thaliana

>gi_972938 (U19382) putative chlorophyll synthetase

[Arabidopsis thaliana] >gi_3068709 (AF049236) putative chlorophyll synthetase [Arabidopsis thaliana]

Seq. No. 410565

Seq. ID uC-osflcyp037d08b1

Method BLASTX
NCBI GI g3482919
BLAST score 151
E value 1.0e-09
Match length 46

Match length 46 % identity 67

NCBI Description (AC003970) Putative protein kinase [Arabidopsis thaliana]

Seq. No. 410566

Seq. ID uC-osflcyp037d09b1

Method BLASTX
NCBI GI g3327389
BLAST score 602
E value 2.0e-62
Match length 174
% identity 68

NCBI Description (AC004483) putative DNA replication licensing factor, mcm5

[Arabidopsis thaliana]

Seq. No. 410567

Seq. ID uC-osflcyp037d10b1

Method BLASTX
NCBI GI g3360291
BLAST score 459
E value 6.0e-46
Match length 122
% identity 70

NCBI Description (AF023165) leucine-rich repeat transmembrane protein kinase

2 [Zea mays]

Seq. No. 410568

Seq. ID uC-osflcyp037e01b1

Method BLASTX
NCBI GI g3986770
BLAST score 192
E value 2.0e-14
Match length 139
% identity 35

NCBI Description (AF109906) NG22 [Mus musculus]

Seq. No. 410569

Seq. ID uC-osflcyp037e03b1

Method BLASTX
NCBI GI g1076790
BLAST score 201
E value 7.0e-16
Match length 61
% identity 69

NCBI Description asparragine synthetase - maize (fragment)

Seq. No. 410570

Seq. ID uC-osflcyp037e04b1

```
Method
                  BLASTX
NCBI GI
                  g5031275
                  367
BLAST score
                  4.0e-35
E value
Match length
                  88
                  77
% identity
NCBI Description (AF139496) unknown [Prunus armeniaca]
Seq. No.
                  410571
Seq. ID
                  uC-osflcyp037e05b1
Method
                  BLASTX
NCBI GI
                  q5912424
BLAST score
                  337
E value
                  1.0e-31
                  98
Match length
                  68
% identity
NCBI Description (AJ242970) BTF3b-like factor [Arabidopsis thaliana]
Seq. No.
                  410572
Seq. ID
                  uC-osflcyp037e09b1
Method
                  BLASTX
NCBI GI
                  g2827709
BLAST score
                  358
                  6.0e - 34
E value
Match length
                  168
                  45
% identity
NCBI Description (AL021684) predicted protein [Arabidopsis thaliana]
Seq. No.
                  410573
Seq. ID
                  uC-osflcyp037e10b1
Method
                  BLASTX
NCBI GI
                  q4914371
BLAST score
                  148
E value
                  3.0e-09
Match length
                  102
% identity
NCBI Description (AC007584) unknown protein [Arabidopsis thaliana]
Seq. No.
                  410574
Seq. ID
                  uC-osflcyp037e11b1
Method
                  BLASTX
NCBI GI
                  g1351014
BLAST score
                  604
E value
                  1.0e-62
Match length
                  122
% identity
                  97
NCBI Description 40S RIBOSOMAL PROTEIN S8 >gi 968902 dbj BAA07207 (D38010)
                  ribosomal protein S8 [Oryza sativa]
Seq. No.
                  410575
                  uC-osflcyp037e12b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3063697
BLAST score
                  342
E value
                  4.0e-32
                  78
Match length
```

77

% identity

```
NCBI Description (AL022537) putative myb-protein (partial) [Arabidopsis
                  thaliana]
                  410576
Seq. No.
Seq. ID
                  uC-osflcyp037f05b1
                  BLASTX
Method
                  g4895238
NCBI GI
                  288
BLAST score
E value
                  6.0e-26
Match length
                  81
                  70
% identity
NCBI Description (AC007659) unknown protein [Arabidopsis thaliana]
                  410577
Seq. No.
                  uC-osflcyp037f06b1
Seq. ID
                  BLASTX
Method
NCBI GI
                  g2662343
BLAST score
                  669
E value
                  6.0e-80
Match length
                  151
                  99
% identity
NCBI Description (D63581) EF-1 alpha [Oryza sativa]
                  410578
Seq. No.
Seq. ID
                  uC-osflcyp037f07b1
                  BLASTX
Method
                  g2760349
NCBI GI
                  732
BLAST score
                  1.0e-77
E value
Match length
                  147
% identity
                  22
NCBI Description (U84969) ubiquitin [Arabidopsis thaliana]
                  410579
Seq. No.
Seq. ID
                  uC-osflcyp037f08b1
Method
                  BLASTX
                  q4512699
NCBI GI
BLAST score
                  346
                  8.0e-33
E value
Match length
                  104
% identity
                  68
NCBI Description (AC006569) putative NADH-ubiquinone oxireductase
                  [Arabidopsis thaliana]
Seq. No.
                  410580
Seq. ID
                  uC-osflcyp037f09b1
Method
                  BLASTX
NCBI GI
                  q2275210
BLAST score
                  203
                  9.0e-16
E value
Match length
                  99
% identity
NCBI Description
                  (AC002337) peptidyl-prolyl cis-trans isomerase isolog
                  [Arabidopsis thaliana]
Seq. No.
                  410581
Seq. ID
                  uC-osflcyp037f10b1
```

Seq. ID Method

```
Method
                  BLASTN
NCBI GI
                  g218180
BLAST score
                  432
                  0.0e + 00
E value
Match length
                  453
% identity
                  98
NCBI Description Rice mRNA for oryzain alpha (EC 3.4.22)
Seq. No.
                  410582
Seq. ID
                  uC-osflcyp037f11b1
Method
                  BLASTX
NCBI GI
                  g1261917
BLAST score
                  220
                  8.0e-18
E value
Match length
                  68
% identity
                  60
NCBI Description (X96979) lipid transfer protein 7a2b [Hordeum vulgare]
Seq. No.
                  410583
Seq. ID
                  uC-osflcyp037f12b1
                  BLASTX
Method
NCBI GI
                  g4115337
BLAST score
                  738
                  2.0e-78
E value
Match length
                  154
% identity
                  18
NCBI Description (L81141) ubiquitin [Pisum sativum]
Seq. No.
                  410584
Seq. ID
                  uC-osflcyp037g02b1
Method
                  BLASTX
NCBI GI
                  q4886756
BLAST score
                  759
                  7.0e-81
E value
Match length
                  172
                  79
% identity
NCBI Description (AF088917) cellulose synthase catalytic subunit
                  [Arabidopsis thaliana]
Seq. No.
                  410585
Seq. ID
                  uC-osflcyp037g04b1
Method
                  BLASTX
NCBI GI
                  q730923
BLAST score
                  414
E value
                  2.0e-40
Match length
                  139
% identity
                  56
NCBI Description T-COMPLEX PROTEIN 1, ZETA SUBUNIT (TCP-1-ZETA) (CCT-ZETA)
                  >gi 626125 pir S48086 chaperonin TCP20 - yeast
                  (Saccharomyces cerevisiae) >gi 531020 (L27698)
                  chaperonin-like protein [Saccharomyces cerevisiae]
                  >gi_1289304_emb_CAA86694_ (Z46727) Tcp20p [Saccharomyces
                  cerevisiae]
Seq. No.
                  410586
```

53293

uC-osflcyp037g05b1

BLASTN

E value

5.0e-84

```
NCBI GI
                   g4097337
BLAST score
                   425
E value
                   0.0e + 00
Match length
                   506
                   100
% identity
NCBI Description Oryza sativa metallothionein-like protein mRNA, complete
                   410587
Seq. No.
Seq. ID
                   uC-osflcyp037g07a1
Method
                   BLASTX
NCBI GI
                   g4689390
BLAST score
                   307
                   7.0e-28
E value
Match length
                   67
% identity
                   87
NCBI Description
                  (AF139470) chlorophyll a/b-binding protein CP24 precursor
                   [Vigna radiata]
Seq. No.
                   410588
Seq. ID
                   uC-osflcyp037g07b1
Method
                   BLASTX
NCBI GI
                   q4689390
BLAST score
                   459
E value
                   1.0e-67
Match length
                   140
% identity
                   90
NCBI Description
                  (AF139470) chlorophyll a/b-binding protein CP24 precursor
                   [Vigna radiata]
Seq. No.
                   410589
Seq. ID
                   uC-osflcyp037g12b1
Method
                   BLASTN
NCBI GI
                   q433216
BLAST score
                   188
E value
                   1.0e-101
Match length
                   194
% identity
                   99
NCBI Description Rice mRNA for ascorbate peroxidase (gene name SS622),
                  partial cds
Seq. No.
                   410590
Seq. ID
                   uC-osflcyp037h01b1
Method
                  BLASTX
NCBI GI
                   q488571
BLAST score
                   430
E value
                  2.0e-42
Match length
                  87
% identity
                  100
NCBI Description (U09462) histone H3.2 [Medicago sativa]
Seq. No.
                   410591
Seq. ID
                  uC-osflcyp037h04b1
Method
                  BLASTX
NCBI GI
                  q125580
BLAST score
                  786
```

Match length 180 % identity 85 PHOSPHORIBULOKINASE PRECURSOR (PHOSPHOPENTOKINASE) (PRKASE) NCBI Description (PRK) >gi_100839_pir__S15743 phosphoribulokinase (EC 2.7.1.19) - wheat >gi_5924030_emb_CAB56544.1_ (X51608) phosphoribulokinase [Triticum aestivum] Seq. No. 410592 Seq. ID uC-osflcyp037h05b1 Method BLASTX NCBI GI g4415992 BLAST score 601 E value 1.0e-62 Match length 119 97 % identity NCBI Description (AF059288) beta-tubulin 2 [Eleusine indica] Seq. No. 410593 Seq. ID uC-osflcyp037h06b1 Method BLASTX NCBI GI q606817 BLAST score 358 2.0e-34 E value Match length 77 % identity 90 NCBI Description (U08404) carbonic anhydrase [Oryza sativa] >gi_5917783_gb_AAD56038.1_AF182806_1 (AF182806) carbonic anhydrase 3 [Oryza sativa] Seq. No. 410594 Seq. ID uC-osflcyp037h07b1 Method BLASTN NCBI GI q607894 BLAST score 82 E value 1.0e-38 Match length 82 % identity 100 NCBI Description Oryza sativa IR54 anther specific (RTS2) gene, complete cds Seq. No. 410595 Seq. ID uC-osflcyp037h09b1 Method BLASTN NCBI GI q3819472 BLAST score 46 E value 1.0e-16 Match length 82 89 % identity NCBI Description Hordeum vulgare genomic DNA fragment; clone MWG0973.uni

Seq. No. 410596

Seq. ID uC-osflcyp037h11b1

Method BLASTX
NCBI GI g1136120
BLAST score 907
E value 3.0e-98
Match length 170
% identity 100

```
NCBI Description (X91806) alpha-tubulin [Oryza sativa]
Seq. No.
                  410597
Seq. ID
                  uC-osflcyp039a01b1
Method
                  BLASTX
NCBI GI
                  g1173090
BLAST score
                  147
E value
                  4.0e-09
Match length
                  87
                  36
% identity
                  2-5A-DEPENDENT RIBONUCLEASE (2-5A-DEPENDENT RNAASE) (RNASE
NCBI Description
                  L) (RIBONUCLEASE 4) >gi 1083193 pir B45771 2-5A-dependent
                  RNAase - mouse (fragment) >gi 2\overline{93265} (L10382)
                  2-5A-dependent RNase [Mus musculus]
Seq. No.
                  410598
Seq. ID
                  uC-osflcyp039a03b1
                  BLASTX
Method
                  g5103846
NCBI GI
BLAST score
                  157
E value
                  3.0e-10
Match length
                  175
                  29
% identity
NCBI Description (AC007591) F9L1.43 [Arabidopsis thaliana]
                  410599
Seq. No.
Seq. ID
                  uC-osflcyp039a06b1
Method
                  BLASTX
NCBI GI
                  g2274859
BLAST score
                  382
E value
                  8.0e-37
                  73
Match length
                  93
% identity
                  (AJ000016) Cks1 protein [Arabidopsis thaliana]
NCBI Description
                  >gi 4510420 gb AAD21506.1 (AC006929) putative
                  cyclin-dependent kinase regulatory subunit [Arabidopsis
                  thaliana]
Seq. No.
                  410600
Seq. ID
                  uC-osflcyp039a08b1
Method
                  BLASTX
NCBI GI
                  q132105
BLAST score
                  830
                  4.0e-89
E value
                  173
Match length
% identity
                  91
NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
                  (RUBISCO SMALL SUBUNIT C) >qi 68094 pir RKRZS9
                  ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                  precursor (clone pOSSS1139) - rice >gi 218208 dbj BAA00538_
                  (D00643) small subunit of ribulose-1,5-bisphosphate
                  carboxylase (RuBPC) [Oryza sativa] >gi 2407283 (AF017364)
                  ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
```

Seq. No. 410601

carboxylase S [Oryza sativa]

sativa] >gi 226375 prf 1508256A ribulose bisphosphate

```
uC-osflcyp039a12b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   q320618
BLAST score
                   193
                   4.0e-15
E value
Match length
                   57
                   70
% identity
                   chlorophyll a/b-binding protein I precursor - rice
NCBI Description
                   >gi_218172_dbj_BAA00536_ (D00641) type I light-harvesting
chlorophyll a/b-binding protein [Oryza sativa]
                   >gi 227611_prf__1707316A chlorophyll a/b binding protein 1
                   [Oryza sativa]
                   410602
Seq. No.
Seq. ID
                   uC-osflcyp039b03b1
Method
                   BLASTX
NCBI GI
                   g82263
BLAST score
                   361
E value
                   3.0e-34
Match length
                   85
% identity
                   84
NCBI Description ubiquinol--cytochrome-c reductase (EC 1.10.2.2) cytochrome
                   c1 precursor (clone pC(1)3II) - potato
Seq. No.
                   410603
Seq. ID
                   uC-osflcyp039b04b1
Method
                   BLASTX
NCBI GI
                   g5257275
BLAST score
                   552
E value
                   8.0e-57
                   108
Match length
% identity
                   100
                   (AP000364) ESTs AU030740(E60171), AU030739(E60171)
NCBI Description
                   correspond to a region of the predicted gene.; Similar to
                   Populus tremuloides caffeoyl-CoA 3-O-methyltransferase.
                   (U27116) [Oryza sativa]
Seq. No.
                   410604
Seq. ID
                   uC-osflcyp039b07b1
Method
                   BLASTX
NCBI GI
                   q4582434
BLAST score
                   176
E value
                   1.0e-12
Match length
                   88
% identity
NCBI Description (AC007196) unknown protein [Arabidopsis thaliana]
Seq. No.
                   410605
Seq. ID
                   uC-osflcyp039b09b1
Method
                   BLASTX
NCBI GI
                   q2065021
BLAST score
                   391
                   7.0e-38
E value
Match length
                   138
                   52
% identity
NCBI Description (Y12555) alanyl t-RNA synthetase [Arabidopsis thaliana]
```

Seq. No. 410606 Seq. ID uC-osflcyp039b11b1 Method BLASTN NCBI GI g6006355 BLAST score 108 5.0e-54 E value 108 Match length % identity 100 NCBI Description Oryza sativa genomic DNA, chromosome 6, clone:P0493C11 410607 Seq. No. uC-osflcyp039b12b1 Seq. ID Method BLASTX NCBI GI g4115377 BLAST score 397 2.0e-38 E value Match length 121 % identity 68 NCBI Description (AC005967) unknown protein [Arabidopsis thaliana] 410608 Seq. No. uC-osflcyp039c01b1 Seq. ID Method BLASTX NCBI GI g4567210 BLAST score 307 6.0e-28 E value 110 Match length % identity 52 NCBI Description (AC007168) unknown protein [Arabidopsis thaliana] Seq. No. 410609 Seq. ID uC-osflcyp039c02b1 Method BLASTN NCBI GI q1132482 BLAST score 35 E value 7.0e-10 Match length 35 % identity 100 NCBI Description Rice mRNA for ADP-ribosylation factor, complete cds Seq. No. 410610 uC-osflcyp039c03b1 Seq. ID Method BLASTX NCBI GI g3789948 BLAST score 302 8.0e-28 E value Match length 60 % identity 93 NCBI Description (AF094773) translation initiation factor 5A [Oryza sativa] 410611 Seq. No. uC-osflcyp039c06b1 Seq. ID Method BLASTX NCBI GI q3258575 BLAST score 161

53298

2.0e-11

72

E value

Match length

```
% identity
NCBI Description
                  (U89959) Hypothetical protein [Arabidopsis thaliana]
                  410612
Seq. No.
                  uC-osflcyp039c07b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3582335
BLAST score
                  276
E value
                  3.0e-24
Match length
                  104
% identity
                  49
NCBI Description
                  (AC005496) unknown protein [Arabidopsis thaliana]
Seq. No.
                  410613
Seq. ID
                  uC-osflcyp039c10b1
Method
                  BLASTX
NCBI GI
                  q1170937
BLAST score
                  768
E value
                  6.0e-82
Match length
                  148
% identity
                  99
NCBI Description
                  S-ADENOSYLMETHIONINE SYNTHETASE 1 (METHIONINE
                  ADENOSYLTRANSFERASE 1) (ADOMET SYNTHETASE 1)
                  >gi_450549_emb CAA81481 (Z26867) S-adenosyl methionine
                  synthetase [Oryza sativa]
Seq. No.
                  410614
Seq. ID
                  uC-osflcyp039c12b1
Method
                  BLASTX
NCBI GI
                  q5922612
BLAST score
                  285
E value
                  2.0e-25
Match length
                  68
% identity
                  81
                  (AP000492) EST AU078118(E3904) corresponds to a region of
NCBI Description
                  the predicted gene.; similar to Arabidopsis thaliana BAC
                  IG002P16; No definition line found. (AF007270) [Oryza
                  sativa]
Seq. No.
                  410615
Seq. ID
                  uC-osflcyp039d01b1
Method
                  BLASTN
NCBI GI
                  g607894
BLAST score
                  87
                  1.0e-41
E value
                  87
Match length
                  100
% identity
NCBI Description Oryza sativa IR54 anther specific (RTS2) gene, complete cds.
                  410616
Seq. No.
                  uC-osflcyp039d02b1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g473980
BLAST score
                  39
E value
                  3.0e-13
Match length
                  71
```

87

% identity

Seq. No.

```
NCBI Description Rice mRNA, partial homologous to glycine-rich protein gene
Seq. No.
                   410617
Seq. ID
                   uC-osflcyp039d08b1
Method
                   BLASTX
NCBI GI
                   q3421123
BLAST score
                   219
E value
                   1.0e-17
Match length
                   67
% identity
                   60
                   (AF043538) 20S proteasome beta subunit PBG1 [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   410618
Seq. ID
                   uC-osflcyp039d09b1
Method
                   BLASTN
                   q4158229
NCBI GI
BLAST score
                   144
                   4.0e-75
E value
Match length
                   347
% identity
                   86
NCBI Description Triticum aestivum mRNA for amylogenin
Seq. No.
                   410619
Seq. ID
                   uC-osflcyp039d10b1
Method
                   BLASTN
NCBI GI
                   q303834
BLAST score
                   96
E value
                   8.0e-47
Match length
                   153
                   96
% identity
NCBI Description Rice mRNA for 21kd polypeptide, complete cds
Seq. No.
                   410620
Seq. ID
                   uC-osflcyp039e02b1
Method
                   BLASTN
NCBI GI
                   g4097337
BLAST score
                   43
E value
                   5.0e-15
Match length
                   79
% identity
                   89
NCBI Description
                   Oryza sativa metallothionein-like protein mRNA, complete
Seq. No.
                   410621
Seq. ID
                   uC-osflcyp039e07b1
Method
                   BLASTX
NCBI GI
                   g4759280
BLAST score
                   403
E value
                   2.0e-39
Match length
                   106
% identity
                   74
                   U5 snRNP-specific protein, 116 kD >gi 434759 dbj BAA04699
NCBI Description
                   (D21163) similar to human elongation \overline{\text{factor } 2 \text{ mRNA}} (HSEF2).
                   [Homo sapiens]
```

Seq. ID uC-osflcyp039e08b1 Method BLASTX NCBI GI q6103735 BLAST score 158 E value 4.0e-12 Match length 44 % identity 86 NCBI Description (Y15964) ATCDPK2-like protein [Arabidopsis thaliana] Seq. No. 410623 Seq. ID uC-osflcyp039f03b1 Method BLASTX NCBI GI q417154 BLAST score 408 E value 6.0e-40 Match length 81 % identity 94 NCBI Description HEAT SHOCK PROTEIN 82 >gi 100685 pir S25541 heat shock protein 82 - rice (strain Taichung Native One) >gi_20256_emb_CAA77978_ (Z11920) heat shock protein 82 (HSP82) [Oryza sativa] Seq. No. 410624 Seq. ID uC-osflcyp039f04b1 Method BLASTX NCBI GI g4574139 BLAST score 289 E value 2.0e-26 Match length 66 % identity (AF073697) cysteine synthase [Oryza sativa] NCBI Description Seq. No. 410625 Seq. ID uC-osflcyp039f06b1 Method BLASTX NCBI GI g5091509 BLAST score 575 E value 1.0e-72 Match length 146 % identity 95 NCBI Description (AB023482) EST AU065533(C2174) corresponds to a region of the predicted gene.; Similar to Homo sapiens splicing factor Prp8 mRNA, complete cds.(AF092565) [Oryza sativa] Seq. No. 410626 Seq. ID uC-osflcyp039f07b1 Method BLASTX NCBI GI g322854 BLAST score 671 E value 1.0e-70 Match length 139 % identity NCBI Description pollen-specific protein - rice >gi_20310_emb_CAA78897_ (Z16402) pollen specific gene [Oryza satīva] Seq. No. 410627

Seq. ID uC-osflcyp039f10b1

```
Method
                  BLASTX
NCBI GI
                  q4335735
BLAST score
                   424
                  1.0e-41
E value
Match length
                   151
% identity
NCBI Description (AC006248) hypothetical protein [Arabidopsis thaliana]
                   410628
Seq. No.
                  uC-osflcyp039f11b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3676296
BLAST score
                  175
                   9.0e-25
E value
                  71
Match length
                  72
% identity
                  (U96497) mitochondrial ATPase beta subunit [Nicotiana
NCBI Description
                  sylvestris]
                   410629
Seq. No.
                  uC-osflcyp039g02b1
Seq. ID
Method
                  BLASTX
                  g1002796
NCBI GI
BLAST score
                   395
                  2.0e-38
E value
Match length
                  86
% identity
                  86
NCBI Description (U33915) Cpm10 [Craterostigma plantagineum]
Seq. No.
                  410630
Seq. ID
                  uC-osflcyp039g04b1
Method
                  BLASTX
NCBI GI
                  q4406780
BLAST score
                   470
E value
                  3.0e-47
Match length
                  97
                  92
% identity
NCBI Description (AC006532) putative multispanning membrane protein
                   [Arabidopsis thaliana]
Seq. No.
                   410631
                  uC-osflcyp039g05b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4097938
BLAST score
                  211
                  1.0e-16
E value
                  49
Match length
                  90
% identity
NCBI Description (U72250) beta-1,3-glucanase precursor [Oryza sativa]
                  410632
Seq. No.
                  uC-osflcyp039g07b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g5081779
BLAST score
                  367
E value
                  3.0e-35
```

71

Match length

Seq. No.

410638

```
% identity
NCBI Description (AF150630) cellulose synthase [Gossypium hirsutum]
Seq. No.
                   410633
Seq. ID
                   uC-osflcyp039g12b1
Method
                  BLASTX
NCBI GI
                   q6093869
BLAST score
                   694
E value
                   3.0e-73
Match length
                  150
% identity
                   87
NCBI Description 60S RIBOSOMAL PROTEIN L13A >gi_2982259 (AF051212) probable
                   60s ribosomal protein L13a [Picea mariana]
Seq. No.
                   410634
Seq. ID
                  uC-osflcyp039h01b1
Method
                  BLASTX
NCBI GI
                  g4531444
BLAST score
                  190
E value
                  2.0e-19
Match length
                  84
% identity
                  49
NCBI Description (AC006224) putative protein kinase [Arabidopsis thaliana]
Seq. No.
                  410635
Seq. ID
                  uC-osflcyp039h06b1
Method
                  BLASTN
NCBI GI
                  g2773153
BLAST score
                  83
E value
                  3.0e-39
Match length
                  111
% identity
                  95
NCBI Description Oryza sativa abscisic acid- and stress-inducible protein
                  (Asr1) mRNA, complete cds
Seq. No.
                  410636
Seq. ID
                  uC-osflcyp039h07b1
Method
                  BLASTX
NCBI GI
                  g4531444
BLAST score
                  486
E value
                  5.0e-49
Match length
                  128
% identity
                  71
NCBI Description (AC006224) putative protein kinase [Arabidopsis thaliana]
Seq. No.
                  410637
Seq. ID
                  uC-osflcyp039h11b1
Method
                  BLASTX
NCBI GI
                  g5051782
BLAST score
                  499
E value
                  2.0e-50
Match length
                  171
% identity
                 (AL078637) serine/threonine kinase-like protein
NCBI Description
                  [Arabidopsis thaliana]
```

Seq. ID uC-osflcyp040a01b1 Method BLASTN NCBI GI g3287498 BLAST score 446 E value 0.0e+00Match length 498 % identity 98 NCBI Description Oryza sativa gene for importin alpha, complete cds Seq. No. 410639 Seq. ID uC-osflcyp040c03b1 Method BLASTX NCBI GI q5031275 BLAST score 564 E value 5.0e-58 Match length 146 % identity 71 NCBI Description (AF139496) unknown [Prunus armeniaca] 410640 Seq. No. Seq. ID uC-osflcyp040d07b1 Method BLASTX NCBI GI g2995990 BLAST score 293 E value 3.0e-26 Match length 125 49 % identity NCBI Description (AF053746) dormancy-associated protein [Arabidopsis thaliana] >gi 2995992 (AF053747) dormancy-associated protein [Arabidopsis thaliana] Seq. No. 410641 Seq. ID uC-osflcyp040f07b1 Method BLASTX NCBI GI g3421413 BLAST score 559 E value 2.0e-57 Match length 116 % identity 90 (AF081922) protein phosphatase 2A 55 kDa B regulatory NCBI Description subunit [Oryza sativa] >gi 3421415 (AF081923) protein phosphatase 2A 55 kDa B regulatory subunit [Oryza sativa] Seq. No. 410642 Seq. ID uC-osflcyp040g03b1 Method BLASTX NCBI GI g1220453 BLAST score 277

E value 2.0e-24 Match length 131 % identity

NCBI Description (M79328) alpha-amylase [Solanum tuberosum]

Seq. No. 410643

Seq. ID uC-osflcyp041a03b1

Method BLASTX NCBI GI q2546988

BLAST score 356 E value 9.0e-44 Match length 149 % identity 63 NCBI Description (Y15113) 2-dehydro-3-deoxyphosphoheptonate aldolase [Morinda citrifolia] Seq. No. 410644 Seq. ID uC-osflcyp041a11b1 Method BLASTX NCBI GI g22240 BLAST score 402 E value 3.0e-39 Match length 82 % identity NCBI Description (X07157) GADPH (383 AA) [Zea mays] Seq. No. 410645 Seq. ID uC-osflcyp041b07b1 Method BLASTX NCBI GI q417745 BLAST score 549 E value 2.0e-56 Match length 125 % identity NCBI Description ADENOSYLHOMOCYSTEINASE (S-ADENOSYL-L-HOMOCYSTEINE HYDROLASE) (ADOHCYASE) >gi 170773 (L11872) S-adenosyl-L-homocysteine hydrolase [Triticum aestivum] Seq. No. 410646 Seq. ID uC-osflcyp041c11b1 Method BLASTX NCBI GI g2827141 BLAST score 712 E value 7.0e-77 Match length 160 % identity 86 (AF027173) cellulose synthase catalytic subunit NCBI Description [Arabidopsis thaliana] >gi_4914447_emb_CAB43650.1 (AL050351) cellulose synthase catalytic subunit (Ath-A) [Arabidopsis thaliana] Seq. No. 410647 Seq. ID uC-osflcyp041d07b1 Method BLASTX NCBI GI g633110 BLAST score 582

E value 3.0e-60 Match length 151 77 % identity

NCBI Description (D31843) plasma membrane H+-ATPase [Oryza sativa]

Seq. No. 410648

Seq. ID uC-osflcyp041d08b1

Method BLASTX NCBI GI g3746581 BLAST score 728

E value 3.0e-77 Match length 147 % identity 95

NCBI Description (AF062403) glutathione S-transferase II [Oryza sativa]

Seq. No. 410649

Seq. ID uC-osflcyp041e03b1

Method BLASTX
NCBI GI g2088647
BLAST score 156
E value 3.0e-10
Match length 51
% identity 55

NCBI Description (AF002109) hypothetical protein [Arabidopsis thaliana]

>gi_3158394 (AF036340) LRR-containing F-box protein

[Arabidopsis thaliana]

Seq. No. 410650

Seq. ID uC-osflcyp041e11b1

Method BLASTX
NCBI GI g1495804
BLAST score 423
E value 2.0e-41
Match length 166
% identity 54

NCBI Description (X96406) 13-lipoxygenase [Solanum tuberosum]

Seq. No. 410651

Seq. ID uC-osflcyp041g03b1

Method BLASTX
NCBI GI g3269287
BLAST score 240
E value 5.0e-20
Match length 65
% identity 65

NCBI Description (AL030978) GH3 like protein [Arabidopsis thaliana]

Seq. No. 410652

Seq. ID uC-osflcyp042b07b1

Method BLASTX
NCBI GI g2507455
BLAST score 190
E value 3.0e-14
Match length 48
% identity 75

NCBI Description FORMATE--TETRAHYDROFOLATE LIGASE (FORMYLTETRAHYDROFOLATE

SYNTHETASE) (FHS) (FTHFS) >gi_322401_pir_A43350

formate--tetrahydrofolate ligase (EC 6.3.4.3) - spinach >gi_170145 (M83940) 10-formyltetrahydrofolate synthetase

[Spinacia oleracea]

Seq. No. 410653

Seq. ID uC-osflcyp042d07b1

Method BLASTX
NCBI GI g1362086
BLAST score 671
E value 1.0e-70

% identity

97



```
Match length
                   159
% identity
NCBI Description
                  5-methyltetrahydropteroyltriglutamate--homocysteine
                  S-methyltransferase (EC 2.1.1.14) - Madagascar periwinkle
                  >gi_2129919_pir__S65957
                  5-methyltetrahydropteroyltriglutamate--homocysteine
                  S-methyltransferase (EC 2.1.1.14) - Madagascar periwinkle
                  >gi_886471_emb_CAA58474_ (X83499) methionine synthase
                   [Catharanthus roseus]
Seq. No.
                  410654
Seq. ID
                  uC-osflcyp042e03b1
Method
                  BLASTX
NCBI GI
                  a548493
BLAST score
                  166
E value
                  2.0e-11
Match length
                  60
                  48
% identity
NCBI Description EXOPOLYGALACTURONASE PRECURSOR (EXOPG) (PECTINASE)
                  (GALACTURAN 1,4-ALPHA-GALACTURONIDASE)
                  >gi_629854_pir__S30067 polygalacturonase - maize
                  >gi_288612_emb_CAA47052_ (X66422) polygalacturonase [Zea
                  mays]
Seq. No.
                  410655
Seq. ID
                  uC-osflcyp042e11b1
Method
                  BLASTX
NCBI GI
                  q1076809
BLAST score
                  229
E value
                  2.0e-39
Match length
                  173
% identity
                  57
NCBI Description H+-transporting ATPase (EC 3.6.1.35) - maize
                  >gi_758355_emb_CAA59800_ (X85805) H(+)-transporting ATPase
                  [Zea mays]
Seq. No.
                  410656
Seq. ID
                  uC-osflcyp042g03b1
Method
                  BLASTX
NCBI GI
                  g5880464
BLAST score
                  608
E value
                  3.0e-63
Match length
                  164
% identity
NCBI Description
                  (AF088901) actin bundling protein ABP135 [Lilium
                  longiflorum]
                  410657
Seq. No.
Seq. ID
                  uC-osflcyp042h07b1
Method
                  BLASTX
NCBI GI
                  g113240
BLAST score
                  499
E value
                  1.0e-50
Match length
                  95
```

53307

>gi_20329_emb_CAA33873 (X15864) actin [Oryza sativa]

NCBI Description ACTIN 2 >gi_71636_pir__ATRZ2 actin 2 - rice

```
Seq. No.
                   410658
Seq. ID
                   uC-osflcyp043a03b1
Method
                   BLASTX
NCBI GI
                   q1498384
BLAST score
                   672
E value
                   2.0e-71
Match length
                   153
% identity
NCBI Description (U60508) actin [Zea mays]
Seq. No.
                   410659
Seq. ID
                   uC-osflcyp043a11b1
Method
                   BLASTX
NCBI GI
                   q3876874
BLAST score
                   350
E value
                   6.0e-33
Match length
                   128
% identity
                   51
NCBI Description
                  (Z81535) Similarity to Human signal recognition particle
                  receptor alpha subunit (SW:P08240) [Caenorhabditis elegans]
Seq. No.
                   410660
Seq. ID
                   uC-osflcyp043b09b1
Method
                   BLASTX
NCBI GI
                   q6093869
BLAST score
                   498
E value
                   2.0e-50
Match length
                  105
% identity
                   89
NCBI Description
                  60S RIBOSOMAL PROTEIN L13A >gi 2982259 (AF051212) probable
                   60s ribosomal protein L13a [Picea mariana]
Seq. No.
                   410661
Seq. ID
                  uC-osflcyp043c05b1
Method
                  BLASTX
NCBI GI
                  g2293480
BLAST score
                  358
E value
                   4.0e-34
Match length
                  88
% identity
NCBI Description (AF011331) glycine-rich protein [Oryza sativa]
Seq. No.
                   410662
Seq. ID
                  uC-osflcyp043d09b1
Method
                  BLASTX
NCBI GI
                  g2501189
BLAST score
                  254
E value
                  1.0e-44
Match length
                  142
% identity
                  74
                  THIAMINE BIOSYNTHETIC ENZYME 1-1 PRECURSOR
NCBI Description
                  >gi 2130146 pir S61419 thiamine biosynthetic enzyme thi1-1
                  - maize >gi_596078 (U17350) thiamine biosynthetic enzyme
                   [Zea mays]
Seq. No.
```

53308

```
Seq. ID
                   uC-osflcyp043f01b1
Method
                   BLASTX
NCBI GI
                   q3820531
BLAST score
                   460
E value
                   6.0e-48
Match length
                   161
% identity
NCBI Description
                  (AF072736) beta-glucosidase [Pinus contorta]
Seq. No.
                   410664
Seq. ID
                   uC-osflcyp043h01b1
Method
                   BLASTX
NCBI GI
                   q4510363
BLAST score
                   295
E value
                   2.0e-45
Match length
                   130
% idehtity
                   76
NCBI Description
                   (AC007017) putative DNA-binding protein [Arabidopsis
                   thaliana]
Seq. No.
                   410665
Seq. ID
                   uC-osflcyp043h09b1
Method
                   BLASTN
NCBI GI
                   g4105560
BLAST score
                   70
E value
                   3.0e-31
                   70
Match length
% identity
                   100
NCBI Description Oryza sativa ribulose-5-phosphate-3-epimerase (RPE) mRNA,
                   complete cds
Seq. No.
                   410666
Seq. ID
                   uC-osflcyp044b09b1
Method
                   BLASTX
NCBI GI
                   g4098331
BLAST score
                   711
E value
                   2.0e-78
Match | length
                  144
                   99
% identity
NCBI Description (U76896) beta-tubulin 5 [Triticum aestivum]
Seq. No.
                   410667
Seq. ID
                  uC-osflcyp044f01b1
Method
                  BLASTX
NCBI GI
                  g4115931
BLAST score
                   452
E value
                   6.0e-45
Match length
                  118
% identity
                  81
NCBI Description
                  (AF118223) contains similarity to Guillardia theta ABC
                  transporter (GB:AF041468) [Arabidopsis thaliana]
Seq. No.
                  410668
Seq. ID
                  uC-osflcyp044g05b1
Method
                  BLASTX
NCBI GI
                  g6016174
                  175
BLAST score
```

Method

BLASTX

```
E value
                   2.0e-12
Match length
                   125
% identity
                   32
NCBI Description
                   GLUTATHIONE-S-TRANSFERASE HOMOLOG
                   >gi_2393724_gb_AAB70110.1_ (U80819)
                   glutathione-S-transferase homolog [Mus musculus]
Seq. No.
                   410669
Seq. ID
                   uC-osflcyp044h01b1
Method
                   BLASTX
NCBI GI
                   q3341511
BLAST score
                   221
E value
                   5.0e-18
Match length
                   44
% identity
                   93
NCBI Description (AJ231134) cinnamoyl-CoA reductase [Saccharum officinarum]
Seq. No.
                   410670
Seq. ID
                  uC-osflcyp044h09b1
Method
                   BLASTX
NCBI GI
                   g2495180
BLAST score
                   495
E value
                   6.0e-50
Match length
                  115
% identity
                   84
NCBI Description
                  PORPHOBILINOGEN DEAMINASE PRECURSOR (PBG)
                   (HYDROXYMETHYLBILANE SYNTHASE) (HMBS) (PRE-UROPORPHYRINOGEN
                   SYNTHASE) >gi_421882_pir__S35873 hydroxymethylbilane
                   synthase (EC 4.3.1.8) - garden pea >gi_541971_pir__JQ2278
                  hydroxymethylbilane synthase (EC 4.3.1.8) precursor -
                   garden pea chloroplast >gi 313724 emb CAA51820 (X73418)
                  hydroxymethylbilane synthase [Pisum sativum]
Seq. No.
                   410671
Seq. ID
                  uC-osflcyp045a05b1
Method
                  BLASTX
NCBI GI
                  q5738365
BLAST score
                  317
E value
                   5.0e-29
Match length
                  161
% identity
                  40
NCBI Description (AL021711) putative protein [Arabidopsis thaliana]
Seq. No.
                  410672
Seq. ID
                  uC-osflcyp045b01b1
Method
                  BLASTX
NCBI GI
                  g6015065
BLAST score
                  878
E value
                  8.0e-95
Match length
                  180
% identity
                  92
NCBI Description ELONGATION FACTOR 2 (EF-2) >gi 2369714 emb CAB09900
                  (Z97178) elongation factor 2 [Beta vulgaris]
Seq. No.
                  410673
Seq. ID
                  uC-osflcyp045b09b1
```

```
NCBI GI
                   g5725649
BLAST score
                   354
E value
                   2.0e-33
Match length
                   110
% identity
                   58
NCBI Description (AF085806) auxin conjugate hydrolase [Arabidopsis thaliana]
Seq. No.
                   410674
Seq. ID
                   uC-osflcyp045c05b1
Method
                   BLASTX
NCBI GI
                   g3819697
BLAST score
                   228
E value
                   1.0e-18
Match length
                   144
% identity
                   42
NCBI Description (AJ009608) BnMAP4K alpha1 [Brassica napus]
Seq. No.
                   410675
Seq. ID
                  uC-osflcyp045d02b1
Method
                  BLASTX
NCBI GI
                   g2498586
BLAST score
                   491
E value
                   1.0e-49
Match length
                  121
% identity
                   78
NCBI Description MAJOR POLLEN ALLERGEN ORY S 1 PRECURSOR (ORY S I)
                  >gi_1173557 (U31771) Ory s 1 [Oryza sativa]
                  410676
Seq. No.
Seq. ID
                  uC-osflcyp045d09b1
Method
                  BLASTX
NCBI GI
                  g584825
BLAST score
                  399
E value
                  1.0e-38
Match length
                  98
% identity
                   76
NCBI Description
                  B2 PROTEIN >gi_322726_pir__S32124 B2 protein - carrot
                  >gi_297889_emb_CAA51078_ (X72385) B2 protein [Daucus
                  carota]
Seq. No.
                   410677
Seq. ID
                  uC-osflcyp045e05b1
Method
                  BLASTX
NCBI GI
                  g4769012
BLAST score
                  422
E value
                  2.0e-49
Match length
                  145
% identity
                  72
NCBI Description (AF143746) CER1 [Oryza sativa]
Seq. No.
                   410678
Seq. ID
```

uC-osflcyp045f09b1

Method BLASTX NCBI GI g3033398 BLAST score 531 E value 3.0e-54 Match length 137

Seq. No.

410684

```
% identity
                   (AC004238) putative phosphoribosylaminoimidazolecarboxamide
NCBI Description
                   formyltransferase [Arabidopsis thaliana]
                   410679
Seq. No.
                  uC-osflcyp045g05b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q82734
BLAST score
                   782
E value
                   1.0e-83
Match length
                  157
% identity
                   36
NCBI Description
                  ubiquitin precursor - maize (fragment)
                  >gi 226763 prf 1604470A poly-ubiquitin [Zea mays]
Seq. No.
                   410680
                  uC-osflcyp045h01b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2262105
BLAST score
                  202
E value
                  1.0e-15
Match length
                  116
% identity
                   39
NCBI Description (AC002343) unknown protein [Arabidopsis thaliana]
                  410681
Seq. No.
                  uC-osflcyp045h09b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3860323
BLAST score
                   156
E value
                  2.0e-10
Match length
                   41
% identity
NCBI Description (AJ012688) hypothetical protein [Cicer arietinum]
Seq. No.
                   410682
Seq. ID
                  uC-osflcyp045h11b1
Method
                  BLASTX
NCBI GI
                  q5360230
BLAST score
                  877
E value
                   1.0e-94
Match length
                  160
% identity
                  99
NCBI Description (AB015287) Ran [Oryza sativa]
Seq. No.
                  410683
Seq. ID
                  uC-osflcyp046b11b1
Method
                  BLASTX
NCBI GI
                  q2621798
BLAST score
                  240
E value
                  5.0e-20
                  63
Match length
                  71
% identity
NCBI Description
                  (AE000850) transcriptional regulator [Methanobacterium
                  thermoautotrophicum]
```

Seq. ID uC-osflcyp046c07b1 Method BLASTX NCBI GI q3395439 BLAST score 263 E value 1.0e-27 Match length 127 % identity 57 NCBI Description (AC004683) hypothetical protein [Arabidopsis thaliana] Seq. No. 410685 Seq. ID uC-osflcyp046d03b1 Method BLASTX NCBI GI q68843 BLAST score 376 E value 5.0e-36 Match length 91 % identity 82 NCBI Description phospholipid transfer protein homolog - rice >gi_4139635_pdb_1RZL_ Rice Nonspecific Lipid Transfer Protein >gi_5107522_pdb_1BV2 Lipid Transfer Protein From Rice Seeds, Nmr, 14 Structures Seq. No. 410686 Seq. ID uC-osflcyp046d11b1 Method BLASTX NCBI GI g5823575 BLAST score 154 E value 5.0e-10 Match length 50 % identity NCBI Description (AL049730) putative protein [Arabidopsis thaliana] Seq. No. 410687 Seq. ID uC-osflcyp046g07b1 Method BLASTN NCBI GI g976256 BLAST score 467 E value 0.0e + 00Match length 508 98 % identity NCBI Description Rice mRNA stearyl-ACP desaturase, complete cds Seq. No. 410688 Seq. ID uC-osflcyp047b03b1 Method BLASTX NCBI GI g3395938 BLAST score 475 E value 1.0e-47 Match length 147 % identity 40 NCBI Description (AF076924) polypyrimidine tract-binding protein homolog

[Arabidopsis thaliana]

Seq. No. 410689

Seq. ID uC-osflcyp047b11b1

Method BLASTX NCBI GI g1084455

BLAST score

```
BLAST score
                    761
E value
                    4.0e-81
Match length
                    158
% identity
                    92
NCBI Description
                   peptidylprolyl isomerase (EC 5.2.1.8) Cyp2 - rice
                    >gi_600767 (L29469) cyclophilin 2 [Oryza sativa]
                    410690
Seq. No.
Seq. ID
                    uC-osflcyp047c07b1
Method
                    BLASTN
NCBI GI
                    g2773153
BLAST score
                    45
E value
                    7.0e-16
Match length
                    89
% identity
                    88
NCBI Description
                   Oryza sativa abscisic acid- and stress-inducible protein
                    (Asr1) mRNA, complete cds
Seq. No.
                    410691
Seq. ID
                   uC-osflcyp047d03b1
Method
                   BLASTX
NCBI GI
                   q478740
BLAST score
                   594
E value
                   8.0e-85
Match length
                   174
% identity
                    99
NCBI Description phenylalanine ammonia-lyase (EC 4.1.3.5) - rice
Seq. No.
                   410692
Seq. ID
                   uC-osflcyp047e07b1
Method
                   BLASTX
NCBI GI
                   g585551
BLAST score
                   223
E value
                   3.0e-18
Match length
                   44
% identity
                   93
NCBI Description NUCLEOSIDE DIPHOSPHATE KINASE I (NDK I) (NDP KINASE I)
                   >gi_629798_pir__S43330 nucleoside-diphosphate kinase (EC
2.7.4.6) - rice >gi_303849_dbj_BAA03798_ (D16292)
                   nucleoside diphosphate kinase [Oryza sativa]
Seq. No.
                   410693
Seq. ID
                   uC-osflcyp047f03b1
Method
                   BLASTX
NCBI GI
                   g2498586
BLAST score
                   181
E value
                   2.0e-13
                   96
Match length
% identity
                   42
NCBI Description MAJOR POLLEN ALLERGEN ORY S 1 PRECURSOR (ORY S I)
                   >gi_1173557 (U31771) Ory s 1 [Oryza sativa]
Seq. No.
                   410694
Seq. ID
                   uC-osflcyp047f11b1
Method
                   BLASTX
NCBI GI
                   g5922612
```

E value 2.0e-23 Match length 141 % identity (AP000492) EST AU078118(E3904) corresponds to a region of NCBI Description the predicted gene.; similar to Arabidopsis thaliana BAC IG002P16; No definition line found. (AF007270) [Oryza sativa] Seq. No. 410695 Seq. ID uC-osflcyp047g07b1 Method BLASTX NCBI GI q3913952 BLAST score 242 E value 3.0e-20 Match length 130 % identity 45 ADENYLATE KINASE (ATP-AMP TRANSPHOSPHORYLASE) >gi_2351578 NCBI Description (U82330) adenylate kinase homolog [Prunus armeniaca] Seq. No. 410696 Seq. ID uC-osflcyp047h03b1 Method BLASTX NCBI GI q4757880 BLAST score 312 E value 4.0e-38 Match length 136 % identity 53 BUB3 (budding uninhibited by benzimidazoles 3, yeast) NCBI Description homolog >gi_2921873 (AF047472) spleen mitotic checkpoint BUB3 [Homo sapiens] >gi_2981231_gb_AAC06258_ (AF053304) mitotic checkpoint component Bub3 [Homo sapiens] >gi_3639060 (AF081496) kinetochore protein BUB3 [Homo sapiens] Seq. No. 410697 Seq. ID uC-osflcyp047h11b1 Method BLASTN NCBI GI g607894 BLAST score 288 E value 1.0e-161 Match length 439 % identity 93 NCBI Description Oryza sativa IR54 anther specific (RTS2) gene, complete cds

Seq. No. 410698

Seq. ID uC-osflcyp048a07b1 Method BLASTX NCBI GI g3287688 BLAST score 457 E value 2.0e-45Match length 115 % identity 80

NCBI Description (AC003979) Contains similarity to ycf37 gene product

gb_1001425 from Synechocystis sp. genome gb_D63999. ESTs gb_T43026, gb_R64902, gb_Z18169 and gb_N37374 come from

this gene. [Arabidopsis thaliana]

Seq. No. 410699 Seq. ID uC-osflcyp048b03b1 Method BLASTX NCBI GI g4006882 BLAST score 329 E value 2.0e-33 Match length 124 % identity 59 NCBI Description (Z99707) UDP-glucuronyltransferase-like protein [Arabidopsis thaliana] 410700 Seq. No. Seq. ID uC-osflcyp048d11b1 Method BLASTX NCBI GI g3122572 BLAST score 669 E value 2.0e-70 Match length 158 83 % identity NCBI Description NADH-UBIQUINONE OXIDOREDUCTASE 75 KD SUBUNIT PRECURSOR (COMPLEX I-75KD) (CI-75KD) (76 KD MITOCHONDRIAL COMPLEX I SUBUNIT) >gi_1084434_pir__S52737 NADH dehydrogenase (ubiquinone) (EC 1.6.5.3) 76K chain precursor - potato >gi_758340_emb_CAA59818_ (X85808) 76 kDa mitochondrial complex I subunit [Solanum tuberosum] Seq. No. 410701 Seq. ID uC-osflcyp048f03b1 Method BLASTX NCBI GI g2662343 BLAST score 648 E value 6.0e-68 Match length 133 % identity 95 NCBI Description (D63581) EF-1 alpha [Oryza sativa] Seq. No. 410702 Seq. ID uC-osflcyp049a02b1 Method BLASTX NCBI GI g4126809 BLAST score 536 E value 6.0e-55 Match length 102 % identity 56 NCBI Description (AB017042) glyoxalase I [Oryza sativa] Seq. No. 410703 Seq. ID uC-osflcyp049a08b1 Method BLASTN NCBI GI g2795840 BLAST score 45 E value 2.0e-16 Match length 85 % identity 89 NCBI Description Cyanella capensis 18S small subunit nuclear ribosomal RNA

gene

```
Seq. No.
                   410704
Seq. ID
                   uC-osflcyp049b03b1
Method
                   BLASTX
NCBI GI
                   q462195
BLAST score
                   524
E value
                   2.0e-53
Match length
                   115
% identity
                   89
NCBI Description
                   PROTEIN TRANSLATION FACTOR SUI1 HOMOLOG (GOS2 PROTEIN)
                   >gi_100682_pir__S21636 GOS2 protein - rice
                   >gi_20238_emb_CAA36190_ (X51910) GOS2 [Oryza sativa]
                   >gi_3789950 (AF094774) translation initiation factor [Oryza
                   sativa]
Seq. No.
                   410705
Seq. ID
                   uC-osflcyp049b08b1
Method
                   BLASTN
NCBI GI
                   q20237
BLAST score
                   84
E value
                   3.0e-39
Match length
                   116
% identity
                   94
NCBI Description O.sativa (rice) constitutive GOS2 gene
Seq. No.
                   410706
Seq. ID
                   uC-osflcyp049b09b1
Method
                   BLASTN
NCBI GI
                   q3789949
BLAST score
                   112
E value
                   3.0e-56
Match length
                   172
% identity
                   92
NCBI Description Oryza sativa translation initiation factor (GOS2) mRNA,
                  complete cds
Seq. No.
                   410707
Seq. ID
                  uC-osflcyp049b12b1
Method
                  BLASTX
NCBI GI
                  q2498586
BLAST score
                  538
E value
                   4.0e-55
Match length
                  134
% identity
                  76
NCBI Description MAJOR POLLEN ALLERGEN ORY S 1 PRECURSOR (ORY S I)
                  >gi_1173557 (U31771) Ory s 1 [Oryza sativa]
Seq. No.
                  410708
Seq. ID
                  uC-osflcyp049c01b1
Method
                  BLASTX
NCBI GI
                  g4582488
BLAST score
                  542
E value
                  2.0e-55
Match length
                  132
% identity
NCBI Description
                 (AL021768) putative protein [Arabidopsis thaliana]
Seq. No.
                  410709
```



Seq. ID uC-osflcyp049c03b1 Method BLASTX NCBI GI q1718097 BLAST score 376 E value 3.0e-36 Match length 105 % identity 63 NCBI Description VACUOLAR ATP SYNTHASE SUBUNIT AC39 (V-ATPASE AC39 SUBUNIT) (41 KD ACCESSORY PROTEIN) (DVA41) >gi_626048_pir A55016 lysosomal membrane protein DVA41 - slime mold(Dictyostelium discoideum) >gi_532733 (U13150) vacuolar ATPase subunit DVA41 [Dictyostelium discoideum] Seq. No. 410710 Seq. ID uC-osflcyp049c07b1 Method BLASTN NCBI GI g303858 BLAST score 74 E value 6.0e - 34Match length 110 % identity 92 Rice mRNA for brain specific protein (S94 gene), complete NCBI Description Seq. No. 410711 Seq. ID uC-osflcyp049c12b1 Method BLASTX NCBI GI g1708108 BLAST score 405 E value 2.0e-39 Match length 119 % identity 71 NCBI Description HISTONE H3.3 >gi_860702 (U28732) similar to histone H3 [Caenorhabditis elegans] Seq. No. 410712 Seq. ID uC-osflcyp049d04b1 Method BLASTX NCBI GI q576886 BLAST score 152 E value 2.0e-10 Match length 55 % identity 58 NCBI Description (L37750) kaurene synthase A [Zea mays] 410713 Seq. ID uC-osflcyp049d07b1 Method BLASTX g2267006

Seq. No.

NCBI GI BLAST score 159 E value 3.0e-11 Match length 33 % identity

NCBI Description (AF006825) endosperm lumenal binding protein [Oryza sativa]

Seq. No. 410714

Seq. ID uC-osflcyp049e05b1

```
Method
                    BLASTX
NCBI GI
                    g2130069
BLAST score
                    732
E value
                    8.0e-78
Match length
                    140
% identity
                    97
NCBI Description catalase (EC 1.11.1.6) catA - rice
                   >gi_1261858_dbj_BAA06232_ (D29966) catalase [Oryza sativa]
Seq. No.
                    410715
Seq. ID
                   uC-osflcyp049e06b1
Method
                   BLASTX
NCBI GI
                   g135483
BLAST score
                   172
E value
                    9.0e-13
Match length
                   38
% identity
                   89
                   TUBULIN BETA CHAIN >gi_84364_pir__B30309 tubulin beta chain
NCBI Description
                   - Euplotes crassus (SG\overline{\text{C9}}) >g\overline{\text{i}}_29\overline{\text{06}}85 (J04534) beta-tubulin
                    [Euplotes crassus]
Seq. No.
                   410716
Seq. ID
                   uC-osflcyp049e09a1
Method
                   BLASTN
NCBI GI
                   g5051932
BLAST score
                   200
E value
                   1.0e-108
Match length
                   254
% identity
                   100
NCBI Description Oryza sativa MADS-box protein FDRMADS8 mRNA, complete cds
Seq. No.
                   410717
Seq. ID
                   uC-osflcyp049e12b1
Method
                   BLASTX
NCBI GI
                   q3334244
BLAST score
                   205
E value
                   1.0e-16
Match length
                   43
% identity
                   79
NCBI Description LACTOYLGLUTATHIONE LYASE (METHYLGLYOXALASE)
                   (ALDOKETOMUTASE) (GLYOXALASE I) (GLX I) (KETONE-ALDEHYDE
                   MUTASE) (S-D-LACTOYLGLUTATHIONE METHYLGLYOXAL LYASE)
                   >gi_2113825_emb_CAA73691.1_ (Y13239) Glyoxalase I [Brassica
                   juncea]
Seq. No.
                   410718
Seq. ID
                   uC-osflcyp049f04b1
Method
                   BLASTX
NCBI GI
                   g482311
BLAST score
                   340
E value
                   2.0e-32
Match length
                   75
% identity
                   89
NCBI Description photosystem II oxygen-evolving complex protein 1 - rice
```

complex protein 1 [Oryza sativa]

(strain Nihonbare) >gi 739292 prf 2002393A oxygen-evolving

BLAST score

Match length

% identity

E value

59

139

86

2.0e-24

Seq. No. 410719 Seq. ID uC-osflcyp049g01b1 Method BLASTX NCBI GI g2129742 BLAST score 263 E value 1.0e-22 Match length 71 % identity 65 NCBI Description stress-induced protein OZI1 precursor - Arabidopsis thaliana >gi_790583 (U20347) mRNA corresponding to this gene accumulates in response to ozone stress and pathogen (bacterial) infection; putative pathogenesis-related protein [Arabidopsis thaliana] >gi_2252869 (AF013294) No definition line found [Arabidopsis thaliana] Seq. No. 410720 Seq. ID uC-osflcyp049q03b1 Method BLASTX g1170937 NCBI GI BLAST score 198 E value 8.0e-16 Match length 42 % identity 98 NCBI Description S-ADENOSYLMETHIONINE SYNTHETASE 1 (METHIONINE ADENOSYLTRANSFERASE 1) (ADOMET SYNTHETASE 1) >gi_450549_emb_CAA81481 (Z26867) S-adenosyl methionine synthetase [Oryza sativa] Seq. No. 410721 Seq. ID uC-osflcyp049h03b1 Method BLASTX NCBI GI q2459443 BLAST score 211 E value 2.0e-17 Match length 57 % identity NCBI Description (AC002332) putative NAD(P)-dependent cholesterol dehydrogenase [Arabidopsis thaliana] Seq. No. Seq. ID uC-osflcyp049h04b1 Method BLASTX NCBI GI g1076678 BLAST score 372 E value 9.0e-36 Match length 76 % identity 97 NCBI Description ubiquitin / ribosomal protein S27a - potato (fragment) Seq. No. 410723 Seq. ID uC-osflcyp049h05b1 Method BLASTN NCBI GI g3851004

% identity

51

NCBI Description Zea mays pyruvate dehydrogenase El alpha subunit RNA, nuclear gene encoding mitochondrial protein, complete cds 410724 Seq. No. Seq. ID uC-osflcyp049h07b1 Method BLASTX NCBI GI q4455274 BLAST score 151 E value 2.0e-10 Match length 38 % identity 76 NCBI Description (AL035527) spliceosome associated protein-like [Arabidopsis thalianal Seq. No. 410725 Seq. ID uC-osflcyp049h08b1 Method BLASTN NCBI GI q4666286 BLAST score 94 E value 9.0e - 46Match length 134 93 % identity NCBI Description Oryza sativa mRNA for cytosolic monodehydroascorbate reductase, complete cds Seq. No. 410726 Seq. ID uC-osflcyp049h09b1 Method BLASTX NCBI GI g710308 BLAST score 210 E value 1.0e-17 Match length 53 % identity 94 NCBI Description (U11693) victorin binding protein [Avena sativa] Seq. No. 410727 Seq. ID uC-osflcyp049h11b1 Method BLASTX NCBI GI q1170937 BLAST score 341 E value 3.0e-32 Match length 69 94 % identity NCBI Description S-ADENOSYLMETHIONINE SYNTHETASE 1 (METHIONINE ADENOSYLTRANSFERASE 1) (ADOMET SYNTHETASE 1) >gi_450549_emb_CAA81481_ (Z26867) S-adenosyl methionine synthetase [Oryza sativa] Seq. No. 410728 Seq. ID uC-osflcyp049h12b1 Method BLASTX NCBI GI g1346396 BLAST score 149 E value 8.0e-10 Match length 69

53321

NCBI Description PUTATIVE RECEPTOR PROTEIN KINASE ZMPK1 PRECURSOR

>gi_100913_pir__S10930 probable receptor protein kinase (EC
2.7.1.-) precursor - maize >gi_22432_emb_CAA36611_ (X52384)
precursor protein (AA -26 to 791) [Zea mays]
>gi_22436_emb_CAA47962_ (X67733) receptor-like protein
kinase [Zea mays] >gi_226927_prf__1611404A receptor protein
kinase [Zea mays]

Seq. No. 410729

Seq. ID uC-osflcyp050a01b1

Method BLASTX
NCBI GI g4567304
BLAST score 288
E value 7.0e-26
Match length 86
% identity 60

NCBI Description (AC005956) unknown protein [Arabidopsis thaliana]

Seq. No. 410730

Seq. ID uC-osflcyp050a05b1

Method BLASTX
NCBI GI g2130069
BLAST score 285
E value 5.0e-26
Match length 54
% identity 91

NCBI Description catalase (EC 1.11.1.6) catA - rice

>gi 1261858 dbj BAA06232 (D29966) catalase [Oryza sativa]

Seq. No. 410731

Seq. ID uC-osflcyp050a06b1

Method BLASTX
NCBI GI g3878044
BLAST score 140
E value 2.0e-10
Match length 69

% identity 50

NCBI Description (Z92835) predicted using Genefinder; similar to elongation

factor; cDNA EST CEMSH83R comes from this gene; cDNA EST EMBL:T00446 comes from this gene; cDNA EST EMBL:C07263 comes from this gene; cDNA EST EMBL:C07825 comes from

Seq. No. 410732

Seq. ID uC-osflcyp050a10b1

Method BLASTX
NCBI GI g2407281
BLAST score 526
E value 1.0e-53
Match length 110
% identity 93

NCBI Description (AF017363) ribulose 1,5-bisphosphate carboxylase small

subunit [Oryza sativa]

Seq. No. 410733

Seq. ID uC-osflcyp050a12b1

Method BLASTX NCBI GI g5729864 BLAST score 255

```
E value
                   2.0e-22
Match length
                   79
                   59
% identity
                   GTP binding protein similar to S. cerevisiae HBS1
NCBI Description
                   >gi_4099482_gb_AAD00645 (U87791) eRFS [Homo sapiens]
                   410734
Seq. No.
                   uC-osflcyp050b04b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g4335760
BLAST score
                   156
                   3.0e-10
E value
Match length
                   128
% identity
                   30
NCBI Description (AC006284) unknown protein [Arabidopsis thaliana]
                   410735
Seq. No.
                   uC-osflcyp050b05a1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g4090884
BLAST score
                   167
E value
                   1.0e-11
                   55
Match length
% identity
                   62
NCBI Description
                  (AF025333) vesicle-associated membrane protein 7B;
                   synaptobrevin 7B [Arabidopsis thaliana]
                   410736
Seq. No.
Seq. ID
                   uC-osflcyp050b07b1
Method
                   BLASTX
NCBI GI
                   g2589162
BLAST score
                   279
E value
                   2.0e-25
Match length
                   66
% identity
                   76
NCBI Description (D88451) aldehyde oxidase [Zea mays]
Seq. No.
                   410737
                   uC-osflcyp050b10b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   q4733939
BLAST score
                   439
E value
                   1.0e-43
Match length
                   98
% identity
NCBI Description (AF068686) geranylgeranyl hydrogenase [Glycine max]
Seq. No.
                   410738
Seq. ID
                  uC-osflcyp050c10b1
Method
                  BLASTN
NCBI GI
                   q5091496
BLAST score
                   162
E value
                   7.0e-86
Match length
                   366
% identity
                   97
NCBI Description
                  Oryza sativa genomic DNA, chromosome 6, clone P0680A03,
                  complete sequence
```

```
Seq. No.
                   410739
Seq. ID
                   uC-osflcyp050c12b1
Method
                   BLASTX
NCBI GI
                   g1841468
BLAST score
                   270
E value
                   7.0e-24
Match length
                   65
% identity
                   72
NCBI Description (Y10990) Tyrosyl-tRNA synthetase [Nicotiana tabacum]
Seq. No.
                   410740
Seq. ID
                   uC-osflcyp050d01b1
Method
                   BLASTX
NCBI GI
                   q133867
BLAST score
                   468
E value
                   7.0e-47
Match length
                   112
                   81
% identity
NCBI Description
                  40S RIBOSOMAL PROTEIN S11 >gi_82722 pir S16577 ribosomal
                   protein S11 - maize >gi_22470_emb CAA39438 (X55967)
                  ribosomal protein S11 [Zea mays]
Seq. No.
                   410741
Seq. ID
                   uC-osflcyp050d02b1
Method
                  BLASTN
                   g20283
NCBI GI
BLAST score
                   72
E value
                   2.0e-32
Match length
                   76
% identity
                   99
NCBI Description
                  Rice (O. sativa) gene for proliferating cell nuclear
                   antigen (PCNA)
Seq. No.
                   410742
Seq. ID
                   uC-osflcyp050d03b1
Method
                  BLASTN
NCBI GI
                  g20283
BLAST score
                  69
E value
                   2.0e-30
Match length
                  105
% identity
                   92
NCBI Description
                  Rice (O. sativa) gene for proliferating cell nuclear
                  antigen (PCNA)
Seq. No.
                   410743
Seq. ID
                  uC-osflcyp050d04b1
Method
                  BLASTN
NCBI GI
                  g2984708
BLAST score
                  55
E value
                  8.0e-23
Match length
                  63
                  97
% identity
NCBI Description
                  Zea mays DnaJ-related protein ZMDJ1 (mdJ1) gene, complete
```

patent $\overline{U}S$

cds >gi_5996689_gb_AR066473.1_AR066473 Sequence 2 from

```
410744
Seq. No.
Seq. ID
                  uC-osflcyp050d05b1
Method
                  BLASTX
NCBI GI
                  q4455323
BLAST score
                  145
E value
                   4.0e-09
Match length
                  74
% identity
                  45
NCBI Description
                  (AL035525) aminopeptidase-like protein [Arabidopsis
                  thaliana]
Seq. No.
                  410745
Seq. ID
                  uC-osflcyp050d11b1
Method
                  BLASTX
NCBI GI
                  g3024122
BLAST score
                  277
E value
                  4.0e-25
Match length
                  63
% identity
                  86
                  S-ADENOSYLMETHIONINE SYNTHETASE 2 (METHIONINE
NCBI Description
                  ADENOSYLTRANSFERASE 2) (ADOMET SYNTHETASE 2) >gi 1778821
                  (U82833) S-adenosyl-L-methionine synthetase [Oryza sativa]
                  410746
Seq. No.
Seq. ID
                  uC-osflcyp050e01b1
Method
                  BLASTX
NCBI GI
                  g4874272
BLAST score
                  222
E value
                  4.0e-18
Match length
                  74
% identity
                  59
NCBI Description
                  (AC007354) Strong similarity to gb Y09533 involved in
                  starch metabolism from Solanum tuberosum and contains a
                  PF_01326 Pyruvate phosphate dikinase, PEP/pyruvate binding
                  domain. EST gb_N96757 comes from this gene. [
Seq. No.
                  410747
Seq. ID
                  uC-osflcyp050e07b1
Method
                  BLASTX
NCBI GI
                  q2792238
BLAST score
                  208
E value
                  2.0e-16
Match length
                  121
% identity
NCBI Description (AF032697) NBS-LRR type resistance protein [Oryza sativa]
Seq. No.
                  410748
Seq. ID
                  uC-osflcyp050e12b1
Method
                  BLASTX
NCBI GI
                  g4680193
BLAST score
                  423
E value
                  1.0e-41
Match length
                  120
                  76
% identity
                  (AF111710) putative farnesyl pyrophosphate synthase [Oryza
NCBI Description
```

sativa subsp. indica]

Seq. No. 410749 Seq. ID uC-osflcyp050f02a1 Method BLASTX NCBI GI g547712 BLAST score 280 E value 7.0e-25 Match length 57 95 % identity NCBI Description EUKARYOTIC INITIATION FACTOR 4A (EIF-4A) >gi_542153_pir__S38358 translation initiation factor eIF-4A - rice >gi 303844 dbj BAA02152 (D12627) eukaryotic initiation factor 4A [Oryza sativa] Seq. No. 410750 Seq. ID uC-osflcyp050f04b1 Method BLASTX NCBI GI g2270994 BLAST score 142 E value 3.0e-09 Match length 55 % identity 51 NCBI Description (AF004809) Ca+2-binding EF hand protein [Glycine max] Seq. No. 410751 uC-osflcyp050g04b1 Seq. ID Method BLASTX NCBI GI g2624328 BLAST score 235 E value 4.0e-20 Match length 58 % identity 79 NCBI Description (AJ002894) OsGRP2 [Oryza sativa] Seq. No. 410752 Seq. ID uC-osflcyp050h02b1 Method BLASTX NCBI GI q4455323 BLAST score 193 E value 4.0e-15 Match length 69 % identity 57 (AL035525) aminopeptidase-like protein [Arabidopsis NCBI Description thaliana] Seq. No. 410753 Seq. ID uC-osflcyp050h06b1 Method BLASTX NCBI GI g2828296 BLAST score 411 E value 3.0e-40Match length 98 % identity 43

Seq. No. 410754

NCBI Description

Seq. ID uC-osflcyp050h08b1

thaliana]

(AL021687) RNase L inhibitor-like protein [Arabidopsis

BLAST score

E value

36

2.0e-11

Method BLASTN g1944204 NCBI GI BLAST score 79 E value 1.0e-36 111 Match length 93 % identity NCBI Description Oryza sativa mRNA for RicMT, complete cds 410755 Seq. No. uC-osflcyp051a05b1 Seq. ID Method BLASTX NCBI GI q1710841 296 BLAST score E value 5.0e-27 Match length 62 % identity 95 NCBI Description ADENOSYLHOMOCYSTEINASE (S-ADENOSYL-L-HOMOCYSTEINE HYDROLASE) (ADOHCYASE) >gi_758247_emb_CAA56278_ (X79905) S-adenosylhomocysteine hydrolase [Phalaenopsis sp.] Seq. No. 410756 Seq. ID uC-osflcyp051a11b1 Method BLASTX NCBI GI g4455192 BLAST score 158 E value 4.0e-15 106 Match length % identity 44 NCBI Description (AL035440) putative protein [Arabidopsis thaliana] Seq. No. 410757 Seq. ID uC-osflcyp051b03b1 Method BLASTX NCBI GI q2708741 BLAST score 419 E value 3.0e-41Match length 129 % identity NCBI Description (AC003952) hypothetical protein [Arabidopsis thaliana] Seq. No. 410758 Seq. ID uC-osflcyp051b04b1 Method BLASTN NCBI GI g20181 BLAST score 76 E value 8.0e-35 Match length 140 % identity 89 NCBI Description Rice cab2R gene for light harvesting chlorophyll a/b-binding protein 410759 Seq. No. Seq. ID uC-osflcyp051b06b1 Method BLASTN NCBI GI g1854636

Seq. No.

410765

```
Match length
                  92
% identity
NCBI Description Oryza sativa gibberellin C-20 oxidase mRNA, complete cds
                  410760
Seq. No.
                  uC-osflcyp051b08b1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g2570514
BLAST score
                  36
                  2.0e-11
E value
Match length
                  36
% identity
                  100
NCBI Description Oryza sativa glycolate oxidase (GOX) mRNA, complete cds
                  410761
Seq. No.
Seq. ID
                  uC-osflcyp051b09b1
Method
                  BLASTX
NCBI GI
                  g4454459
                  230
BLAST score
E value
                  1.0e-19
                  62
Match length
                  76
% identity
NCBI Description (AC006234) unknown protein [Arabidopsis thaliana]
Seq. No.
                  410762
Seq. ID
                  uC-osflcyp051b12b1
Method
                  BLASTX
NCBI GI
                  q4958922
                  197
BLAST score
E value
                  1.0e-15
Match length
                  54
% identity
NCBI Description (AB027757) NADPH oxidoreductase homolog [Cicer arietinum]
Seq. No.
                  410763
Seq. ID
                  uC-osflcyp051c02b1
Method
                  BLASTX
NCBI GI
                  g2130069
BLAST score
                  837
E value
                  4.0e-90
Match length
                  150
% identity
                  99
                  catalase (EC 1.11.1.6) catA - rice
NCBI Description
                  >gi_1261858_dbj_BAA06232_ (D29966) catalase [Oryza sativa]
Seq. No.
                  410764
Seq. ID
                  uC-osflcyp051c03b1
Method
                  BLASTX
NCBI GI
                  g4210332
                  279
BLAST score
E value
                  5.0e-25
Match length
                  71
                  76
% identity
                  (AJ223803) 2-oxoglutarate dehydrogenase E2 subunit
NCBI Description
                   [Arabidopsis thaliana]
```

```
uC-osflcyp051c05b1
Seq. ID
Method
                  BLASTX
                  g4559342
NCBI GI
BLAST score
                  310
                  5.0e-29
E value
Match length
                  65
                  89
% identity
NCBI Description
                  (AC007087) putative copper methylamine oxidase [Arabidopsis
                  thaliana]
                  410766
Seq. No.
                  uC-osflcyp051c06b1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g168587
                  59
BLAST score
E value
                  2.0e-24
                  91
Match length
                  92
% identity
NCBI Description Zea mays cofactor-independent phosphoglycerate mutase mRNA,
                  complete cds
                  410767
Seq. No.
                  uC-osflcyp051c08b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2130069
BLAST score
                  196
E value
                  6.0e-18
Match length
                  57
                  84
% identity
NCBI Description catalase (EC 1.11.1.6) catA - rice
                  >gi_1261858_dbj_BAA06232_ (D29966) catalase [Oryza sativa]
Seq. No.
                  410768
Seq. ID
                  uC-osflcyp051c11b1
Method
                  BLASTX
NCBI GI
                  g2130069
BLAST score
                  163
E value
                  9.0e-12
Match length
                  41
                  76
% identity
NCBI Description catalase (EC 1.11.1.6) catA - rice
                  >gi 1261858 dbj BAA06232 (D29966) catalase [Oryza sativa]
Seq. No.
                  410769
Seq. ID
                  uC-osflcyp051c12b1
Method
                  BLASTX
NCBI GI
                  g551288
BLAST score
                  735
E value
                  4.0e-78
Match length
                  149
% identity
                  93
NCBI Description (Z33611) phosphoglycerate mutase [Zea mays]
                  410770
Seq. No.
Seq. ID
                  uC-osflcyp051d01b1
Method
                  BLASTX
NCBI GI
                  g68843
```

BLAST score 253 E value 7.0e-22 Match length 60 % identity 80

NCBI Description phospholipid transfer protein homolog - rice

>gi_4139635_pdb_1RZL_ Rice Nonspecific Lipid Transfer
Protein >gi_5107522_pdb_1BV2_ Lipid Transfer Protein From

Rice Seeds, Nmr, 14 Structures

Seq. No. 410771

Seq. ID uC-osflcyp051d02b1

Method BLASTX
NCBI GI g4512619
BLAST score 181
E value 2.0e-13
Match length 53
% identity 62

NCBI Description (AC004793) This gene is a member of the formyl transferase

family PF_00551 and may be a pseudogene of gb_X74767 phosphoribosylglycinamide formyl transferase (PUR3) from Arabidopsis thaliana since our sequence differs from

PUR3... >gi_4753662_emb_CAA52779.2_ (X74767)

phosphoribosylglycinamide formyltransferase [Arabidopsis

thaliana]

Seq. No. 410772

Seq. ID uC-osflcyp051d04b1

Method BLASTX
NCBI GI g1657621
BLAST score 416
E value 5.0e-41
Match length 102
% identity 78

NCBI Description (U72505) G6p [Arabidopsis thaliana] >gi_3068711 (AF049236)

putative acyl-coA dehydrogenase [Arabidopsis thaliana]

>gi_5478795_dbj_BAA82478.1_ (AB017643) Short-chain acyl CoA

oxidase [Arabidopsis thaliana]

Seq. No. 410773

Seq. ID uC-osflcyp051d05b1

Method BLASTX
NCBI GI g1171008
BLAST score 531
E value 3.0e-54
Match length 120
% identity 73

NCBI Description POLLEN ALLERGEN PHL P 1 PRECURSOR (PHL P I)

>gi_629812_pir__S44182 allergen Phl p I - common timothy
>gi_473360 emb CAA55390 (X78813) Phl p I allergen [Phleum

pratense]

Seq. No. 410774

Seq. ID uC-osflcyp051d06b1

Method BLASTX
NCBI GI g4490299
BLAST score 147
E value 7.0e-10



Match length 42 % identity

NCBI Description (AL035678) hypothetical protein [Arabidopsis thaliana]

Seq. No. 410775

uC-osflcyp051d07b1 Seq. ID

Method BLASTX NCBI GI g2662343 BLAST score 168 E value 2.0e-12 41 Match length 80 % identity

NCBI Description (D63581) EF-1 alpha [Oryza sativa]

410776 Seq. No.

Seq. ID uC-osflcyp051d10b1

Method BLASTX NCBI GI g132105 BLAST score 588 E value 6.0e-61 Match length 130 % identity 85

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR

(RUBISCO SMALL SUBUNIT C) >gi_68094_pir__RKRZS9

ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_ (D00643) small subunit of ribulose-1,5-bisphosphate

carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa] >gi 226375 prf 1508256A ribulose bisphosphate

carboxylase S [Oryza sativa]

Seq. No. 410777

uC-osflcyp051d11b1 Seq. ID

Method BLASTX NCBI GI q266567 BLAST score 555 E value 4.0e-57 Match length 146 % identity 72

NCBI Description MITOCHONDRIAL PROCESSING PEPTIDASE ALPHA SUBUNIT PRECURSOR

(ALPHA-MPP) (UBIQUINOL-CYTOCHROME C REDUCTASE SUBUNIT II) >gi_421956_pir__S23558 mitochondrial processing peptidase
(EC 3.4.99.41) alpha chain precursor - potato

>gi_21493_emb_CAA46990_ (X66284) mitochondrial processing

peptidase [Solanum tuberosum]

Seq. No. 410778

Seq. ID uC-osflcyp051d12b1

Method BLASTX NCBI GI q430947 BLAST score 530 E value 3.0e-54Match length 130 75 % identity

NCBI Description (U01103) PSI type III chlorophyll a/b-binding protein

[Arabidopsis thaliana]

Seq. No.

410784

```
410779
Seq. No.
Seq. ID
                   uC-osflcyp051e03b1
Method
                   BLASTX
NCBI GI
                  g6063542
BLAST score
                   419
E value
                   2.0e-41
Match length
                   90
% identity
                   96
                   (AP000615) EST C74302(E30840) corresponds to a region of
NCBI Description
                   the predicted gene.; similar to glyceraldehyde-3-phosphate
                  dehydrogenase. (M64118) [Oryza sativa]
                   410780
Seq. No.
Seq. ID
                  uC-osflcyp051e06b1
Method
                  BLASTX
NCBI GI
                   q5912299
BLAST score
                   226
                   2.0e-18
E value
Match length
                   56
                   75
% identity
NCBI Description (AJ133787) gigantea homologue [Oryza sativa]
Seq. No.
                   410781
                  uC-osflcyp051e07b1
Seq. ID
Method
                  BLASTX
NCBI GI
                   g133867
BLAST score
                   372
E value
                   8.0e-36
Match length
                   98
% identity
                   76
NCBI Description
                  40S RIBOSOMAL PROTEIN S11 >gi_82722_pir__S16577 ribosomal
                   protein S11 - maize >gi_22470_emb_CAA39438_ (X55967)
                  ribosomal protein S11 [Zea mays]
Seq. No.
                   410782
Seq. ID
                   uC-osflcyp051e09a1
Method
                  BLASTN
NCBI GI
                   g600766
BLAST score
                   224
E value
                   1.0e-123
                   280
Match length
                   95
% identity
NCBI Description Oryza sativa cyclophilin 2 (Cyp2) gene, complete cds
Seq. No.
                   410783
Seq. ID
                  uC-osflcyp051e09b1
Method
                  BLASTN
NCBI GI
                   g2407274
BLAST score
                  111
E value
                  1.0e-55
Match length
                  143
                   94
% identity
                  Oryza sativa lipid transfer protein LPT III mRNA, complete
NCBI Description
                  cds
```

Match length

```
Seq. ID
                  uC-osflcyp051e10b1
Method
                  BLASTX
NCBI GI
                  q4835767
BLAST score
                  168
                  3.0e-12
E value
Match length
                  48
% identity
                  60
NCBI Description (AC007202) T8K14.16 [Arabidopsis thaliana]
                  410785
Seq. No.
                  uC-osflcyp051e11b1
Seq. ID
Method
                  BLASTX
                  g4886756
NCBI GI
BLAST score
                  257
                  2.0e-22
E value
Match length
                  62
                  73
% identity
                  (AF088917) cellulose synthase catalytic subunit
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                  410786
                  uC-osflcyp051e12b1
Seq. ID
Method
                  BLASTX
                  g5912299
NCBI GI
BLAST score
                  365
E value
                  8.0e-35
Match length
                  88
                  83
% identity
NCBI Description (AJ133787) gigantea homologue [Oryza sativa]
                  410787
Seq. No.
                  uC-osflcyp051f05a1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g6006355
BLAST score
                  39
E value
                  2.0e-12
Match length
                  87
                  86
% identity
NCBI Description Oryza sativa genomic DNA, chromosome 6, clone:P0493C11
Seq. No.
                   410788
                  uC-osflcyp051f06b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3126854
BLAST score
                  387
E value
                  1.0e-37
Match length
                  78
% identity
NCBI Description (AF061577) chlorophyll a/b binding protein [Oryza sativa]
Seq. No.
                   410789
Seq. ID
                  uC-osflcyp051f07a1
Method
                  BLASTX
NCBI GI
                  g6006879
BLAST score
                  197
E value
                  3.0e-15
                  67
```

```
% identity
                  61
                   (AC008153) putative eukaryotic translation initiation
NCBI Description
                  factor 3 subunit [Arabidopsis thaliana]
Seq. No.
                  410790
                  uC-osflcyp051f10b1
Seq. ID
                  BLASTX
Method
NCBI GI
                  g1814403
                  290
BLAST score
E value
                  2.0e-26
                  62
Match length
                  89
% identity
                  (U84889) methionine synthase [Mesembryanthemum
NCBI Description
                  crystallinum]
                  410791
Seq. No.
                  uC-osflcyp051f11b1
Seq. ID
                  BLASTX
Method
                  g4538911
NCBI GI
BLAST score
                  271
E value
                  8.0e-24
                  125
Match length
                   45
% identity
                  (AL049482) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  410792
Seq. ID
                  uC-osflcyp051g04b1
Method
                  BLASTX
                  q3650033
NCBI GI
                   224
BLAST score
                   6.0e-19
E value
Match length
                   69
                   67
% identity
NCBI Description (AC005396) unknown protein [Arabidopsis thaliana]
Seq. No.
                   410793
Seq. ID
                  uC-osflcyp051g10b1
Method
                   BLASTN
NCBI GI
                   q414704
BLAST score
                   73
E value
                   3.0e - 33
Match length
                   109
                   92
% identity
NCBI Description O.sativa mRNA for cytochrome b5
                   410794
Seq. No.
Seq. ID
                   uC-osflcyp051h07b1
Method
                   BLASTX
NCBI GI
                   q3869088
BLAST score
                   174
E value
                   5.0e-13
Match length
                   43
                   79
% identity
NCBI Description (AB019427) elongation factor-1 alpha [Nicotiana paniculata]
                   410795
Seq. No.
Seq. ID
                   uC-osflcyp051h12b1
```

```
BLASTX
Method
NCBI GI
                  g82496
                   296
BLAST score
E value
                   4.0e-27
                   62
Match length
                   95
% identity
NCBI Description phenylalanine ammonia-lyase (EC 4.3.1.5) - rice
                   410796
Seq. No.
Seq. ID
                   uC-osflcyp052a01b1
Method
                  BLASTN
                   g1136121
NCBI GI
                   70
BLAST score
                   2.0e-31
E value
                   146
Match length
% identity
                   87
NCBI Description O.sativa mRNA for alpha-tubulin (clone OSTA-136)
                   410797
Seq. No.
                  uC-osflcyp052a02b1
Seq. ID
Method
                   BLASTX
                   g4539006
NCBI GI
BLAST score
                   309
E value
                   2.0e-28
                   107
Match length
                   58
% identity
NCBI Description (AL049481) putative protein [Arabidopsis thaliana]
                   410798
Seq. No.
                   uC-osflcyp052a03b1
Seq. ID
Method
                  BLASTX
NCBI GI
                   g398849
BLAST score
                   643
E value
                   2.0e-67
Match length
                   128
% identity
NCBI Description (X74656) beta-5 tubulin [Zea mays]
Seq. No.
                   410799
Seq. ID
                   uC-osflcyp052a07b1
Method
                   BLASTX
NCBI GI
                   g5679684
BLAST score
                   756
E value
                   1.0e-80
Match length
                   156
% identity
                   25
NCBI Description
                   (AJ243828) phosphatase 2A regulatory A subunit [Oryza
                   sativa] >gi_5679686_emb_CAB51804.1_ (AJ243829) protein
                   phosphatase 2A A subunit [Oryza sativa]
Seq. No.
                   410800
Seq. ID
                   uC-osflcyp052a11a1
```

Method BLASTX
NCBI GI g600769
BLAST score 318
E value 3.0e-29
Match length 62

```
% identity
                    97
 NCBI Description (L29470) cyclophilin 2 [Oryza sativa]
                   410801
 Seq. No.
 Seq. ID
                   uC-osflcyp052a11b1
 Method
                   BLASTX
                   g1084455
 NCBI GI
 BLAST score
                   255
 E value
                   2.0e-22
 Match length
                   50
                   98
 % identity
 NCBI Description
                   peptidylprolyl isomerase (EC 5.2.1.8) Cyp2 - rice
                   >gi_600767 (L29469) cyclophilin 2 [Oryza sativa]
 Seq. No.
                   410802
 Seq. ID
                   uC-osflcyp052b01b1
 Method
                   BLASTX
 NCBI GI
                   q3024432
 BLAST score
                   502
 E value
                   1.0e-53
Match length
                   115
                   97
 % identity
 NCBI Description
                   PROTEASOME ALPHA SUBUNIT (MULTICATALYTIC ENDOPEPTIDASE
                   COMPLEX ALPHA SUBUNIT) >gi 1930070 (U92540) proteasome
                   alpha subunit [Oryza sativa]
 Seq. No.
                   410803
 Seq. ID
                   uC-osflcyp052b02b1
 Method
                   BLASTX
 NCBI GI
                   g4127348
 BLAST score
                   311
                   2.0e-28
 E value
Match length
                   89
                   63
 % identity
 NCBI Description
                  (AJ010449) glutathione transferase [Alopecurus myosuroides]
 Seq. No.
                   410804
 Seq. ID
                   uC-osflcyp052b03b1
Method
                   BLASTX
NCBI GI
                   q1421730
 BLAST score
                   251
E value
                   2.0e-21
Match length
                   68
 % identity
NCBI Description
                  (U43082) RF2 [Zea mays]
 Seq. No.
                   410805
Seq. ID
                   uC-osflcyp052b04b1
Method
                   BLASTX
NCBI GI
                   g2981620
BLAST score
                   218
E value
                   1.0e-17
Match length
                   87
~% identity
                   52
NCBI Description
                   (AB008856) mutated 3-ketoacyl-CoA thiolase [Arabidopsis
                   thaliana]
```

Seq. No. 410806 uC-osflcyp052b07b1 Seq. ID Method BLASTN NCBI GI g6041757 BLAST score 412 E value 0.0e+00Match length 432 99 % identity NCBI Description Genomic Sequence For Oryza sativa Clone 10P20, Lemont Strain, Complete Sequence, complete sequence 410807 Seq. No. uC-osflcyp052b08b1 Seq. ID Method BLASTX NCBI GI g2494116 BLAST score 270 E value 1.0e-23 56 Match length % identity 82 NCBI Description (AC002376) Similar to Synechocystis hypothetical protein (gb D90915). [Arabidopsis thaliana] 410808 Seq. No. uC-osflcyp052b10b1 Seq. ID Method BLASTN NCBI GI g459268 115 BLAST score E value 7.0e-58 Match length 303 84 % identity NCBI Description Z.mays mRNA Transcribed Sequence Seq. No. 410809 Seq. ID uC-osflcyp052b12b1 Method BLASTX NCBI GI q4218120 BLAST score 154 E value 3.0e-10 Match length 61 % identity 54 NCBI Description (AL035353) Proline-rich APG-like protein [Arabidopsis thaliana] 410810 Seq. No.

Seq. ID uC-osflcyp052c01b1

Method BLASTX
NCBI GI g1084427
BLAST score 315
E value 6.0e-29
Match length 65
% identity 74

NCBI Description gip1 protein - garden petunia >gi_825524_emb_CAA60677_

(X87225) gip1 [Petunia x hybrida]

Seq. No. 410811

Seq. ID uC-osflcyp052c03a1

Method BLASTX

```
NCBI GI
                   q1684855
BLAST score
                   420
E value
                   4.0e-41
Match length
                   84
% identity
                   25
NCBI Description (U77939) ubiquitin-like protein [Phaseolus vulgaris]
                   410812
Seq. No.
                  uC-osflcyp052c03b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1332579
BLAST score
                   680
E value
                   9.0e-72
Match length
                   139
% identity
                   10
NCBI Description (X98063) polyubiquitin [Pinus sylvestris]
                   410813
Seq. No.
Seq. ID
                  uC-osflcyp052c04b1
Method
                  BLASTX
NCBI GI
                  g2286153
BLAST score
                   329
E value
                   1.0e-30
Match length
                   76
% identity
                   84
NCBI Description (AF007581) cytoplasmic malate dehydrogenase [Zea mays]
Seq. No.
                   410814
Seq. ID
                  uC-osflcyp052c05b1
                  BLASTN
Method
NCBI GI
                  g2239261
BLAST score
                   191
E value
                   1.0e-103
Match length
                   467
% identity
                   86
NCBI Description Zea Mays mRNA for pectin methylesterase-like protein
                   410815
Seq. No.
Seq. ID
                  uC-osflcyp052c07b1
Method
                  BLASTX
NCBI GI
                   g1170937
BLAST score
                   569
E value
                   9.0e-62
Match length
                   120
% identity
                   98
NCBI Description
                  S-ADENOSYLMETHIONINE SYNTHETASE 1 (METHIONINE
                  ADENOSYLTRANSFERASE 1) (ADOMET SYNTHETASE 1)
                  >gi_450549_emb_CAA81481_ (Z26867) S-adenosyl methionine
                  synthetase [Oryza sativa]
Seq. No.
                   410816
Seq. ID
                  uC-osflcyp052c09b1
Method
                  BLASTX
NCBI GI
                  g3599491
BLAST score
                  522
E value
                  3.0e-53
Match length
                  145
```

% identity NCBI Description (AF085149) putative aminotransferase [Capsicum chinense] 410817 Seq. No. Seq. ID uC-osflcyp052c12b1 Method BLASTX NCBI GI q4758356 BLAST score 346 E value 1.0e-32 Match length 100 % identity 69 NCBI Description flap structure-specific endonuclease 1; MATURATION FACTOR 1 (MF1); DNase IV; RAD2_HUMAN >gi_729475_sp_P39748_FEN1_HUMAN FLAP ENDONUCLEASE-1 (MATURATION FACTOR 1) (MF1) >gi_1362788_pir__A56531 DNA structure-specific endonuclease FENT - human >gi_704377_bbs_157592 DNase IV=nuclear 42 kda 5' -> 3' exonuclease [human, HeLa cells, Peptide, 380 aa] >gi 642090 (L37374) endonuclease [Homo sapiens] >gi 3169155 (ACOO4770) FEN1 HUMAN; MATURATION FACTOR 1 (MF1); DNase IV; RAD2_HUMAN [Homo sapiens] >gi_3980293_emb_CAA54166_ (X76771) flap endonuclease-1 [Homo sapiens] 410818 Seq. No. Seq. ID uC-osflcyp052d01b1 Method BLASTX NCBI GI q671740 BLAST score 196 E value 4.0e-15 78 Match length % identity 53 NCBI Description (X84730) ribulose-bisphosphate carboxylase [synthetic construct] Seq. No. 410819 Seq. ID uC-osflcyp052d04b1 Method BLASTX NCBI GI q322854 BLAST score 586 E value 2.0e-60 Match length 124 % identity 98 NCBI Description pollen-specific protein - rice >qi 20310 emb CAA78897 (Z16402) pollen specific gene [Oryza satīva] 410820 Seq. No. Seq. ID uC-osflcyp052d05b1 Method BLASTX NCBI GI q3789954 BLAST score 835 E value 7.0e-90 Match length 156 % identity 100 NCBI Description (AF094776) chlorophyll a/b-binding protein precursor [Oryza sativa] Seq. No. 410821 Seq. ID uC-osflcyp052d06b1



Method BLASTN
NCBI GI 94097337
BLAST score 286
E value 1.0e-160
Match length 395
% identity 99

NCBI Description Oryza sativa metallothionein-like protein mRNA, complete

cds

Seq. No. 410822

Seq. ID uC-osflcyp052d10b1

Method BLASTX
NCBI GI g3915008
BLAST score 372
E value 1.0e-35
Match length 109
% identity 69

NCBI Description SUPEROXIDE DISMUTASE [CU-ZN], CHLOROPLAST PRECURSOR

>gi 1805502 dbj BAA12745.1 (D85239) superoxide dismutase

precusor [Oryza sativa]

Seq. No. 410823

Seq. ID uC-osflcyp052e02b1

Method BLASTX
NCBI GI g283008
BLAST score 682
E value 5.0e-72
Match length 131
% identity 99

NCBI Description sucrose synthase (EC 2.4.1.13) - rice

>gi 20366 emb CAA46017 (X64770) sucrose synthase [Oryza

sativa]

Seq. No. 410824

Seq. ID uC-osflcyp052e05b1

Method BLASTX
NCBI GI g1172969
BLAST score 344
E value 1.0e-32
Match length 73
% identity 96

NCBI Description 60S RIBOSOMAL PROTEIN L11 (L16) >gi 629552 pir S49033

ribosomal protein L11.e - Arabidopsis thaliana

>gi_550544_emb_CAA57394_ (X81798) ribosomal protein L16

[Arabidopsis thaliana]

Seq. No. 410825

Seq. ID uC-osflcyp052e08b1

Method BLASTX
NCBI GI g4512667
BLAST score 154
E value 7.0e-17
Match length 114
% identity 49

NCBI Description (AC006931) putative MAP kinase [Arabidopsis thaliana]

Seq. No. 410826

Seq. ID Method

NCBI GI

uC-osflcyp052f02b1 Seq. ID Method BLASTX NCBI GI g2982463 BLAST score 308 E value 4.0e-28 96 Match length 66 % identity (AL022223) putative protein [Arabidopsis thaliana] NCBI Description 410827 Seq. No. uC-osflcyp052f03b1 Seq. ID Method BLASTX g6041792 NCBI GI BLAST score 673 E value 7.0e-71Match length 154 79 % identity (AC009755) unknown protein [Arabidopsis thaliana] NCBI Description Seq. No. 410828 uC-osflcyp052f05b1 Seq. ID Method BLASTX NCBI GI g5734720 BLAST score 152 E value 7.0e-10 70 Match length % identity 36 (AC008075) Contains PF 01426 BAH (bromo-adjacent homology) NCBI Description domain. ESTs gb_N96349, gb_T42710, gb_H77084, gb_AA395147 and gb AA605500 come from this gene. [Arabidopsis thaliana] Seq. No. 410829 uC-osflcyp052f07b1 Seq. ID Method BLASTX NCBI GI q3193324 BLAST score 519 E value 7.0e-53 Match length 143 71 % identity (AF069299) contains similarity to WD domains, G-beta NCBI Description repeats (Pfam: G-beta.hmm, score: 22.80 and 35.84) [Arabidopsis thaliana] 410830 Seq. No. Seq. ID uC-osflcyp052f09b1 Method BLASTX NCBI GI g2914706 BLAST score 523 E value 3.0e-53 Match length 111 % identity NCBI Description (AC003974) putative homeobox protein [Arabidopsis thaliana] Seq. No. 410831

53341

uC-osflcyp052f10b1

BLASTX

g3377844

```
298
BLAST score
                  6.0e-27
E value
                  112
Match length
                  55
% identity
                  (AF076274) contains similarity to DNA
NCBI Description
                  (cytosine-5-)-methyltransferases [Arabidopsis thaliana]
                  410832
Seq. No.
                  uC-osflcyp052f11b1
Seq. ID
                  BLASTX
Method
                  q4678386
NCBI GI
BLAST score
                  234
                  2.0e-19
E value
                  79
Match length
% identity
                  54
NCBI Description (AL049656) putative protein [Arabidopsis thaliana]
                  410833
Seq. No.
                  uC-osflcyp052f12b1
Seq. ID
                  BLASTX
Method
NCBI GI
                  g1169528
                  739
BLAST score
                  1.0e-78
E value
                  150
Match length
                  96
% identity
NCBI Description ENOLASE 2 (2-PHOSPHOGLYCERATE DEHYDRATASE 2)
                   (2-PHOSPHO-D-GLYCERATE HYDRO-LYASE 2) >gi_602253 (U17973)
                  enolase [Zea mays]
Seq. No.
                   410834
                  uC-osflcyp052g03b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3695019
BLAST score
                   446
E value
                   3.0e-44
Match length
                  161
% identity
NCBI Description (AF055848) subtilisin-like protease [Arabidopsis thaliana]
Seq. No.
                   410835
                   uC-osflcyp052g05b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   q3868780
BLAST score
                   171
E value
                   5.0e-12
Match length
                   114
% identity
                   35
NCBI Description (AB008807) glutathione-dependent dehydroascorbate reductase
                   [Rattus rattus]
Seq. No.
                   410836
Seq. ID
                   uC-osflcyp052g06b1
Method
                   BLASTX
NCBI GI
                   g2501189
BLAST score
                   217
                   1.0e-17
E value
Match length
                   70
```



% identity 66

NCBI Description THIAMINE BIOSYNTHETIC ENZYME 1-1 PRECURSOR

>gi_2130146_pir__S61419 thiamine biosynthetic enzyme thi1-1
- maize >gi_596078 (U17350) thiamine biosynthetic enzyme

[Zea mays]

Seq. No. 410837

Seq. ID uC-osflcyp052g09b1

Method BLASTX
NCBI GI g2662341
BLAST score 841
E value 2.0e-90
Match length 165
% identity 98

NCBI Description (D63580) EF-1 alpha [Oryza sativa]

>gi_2662345_dbj_BAA23659_ (D63582) EF-1 alpha [Oryza sativa] >gi_2662347 dbj_BAA23660 (D63583) EF-1 alpha

[Oryza sativa]

Seq. No. 410838

Seq. ID uC-osflcyp052g10b1

Method BLASTX
NCBI GI g6006862
BLAST score 210
E value 2.0e-28
Match length 116
% identity 53

NCBI Description (AC009540) unknown protein [Arabidopsis thaliana]

Seq. No. 410839

Seq. ID uC-osflcyp052g11a1

Method BLASTX
NCBI GI g1332579
BLAST score 444
E value 6.0e-44
Match length 89
% identity 10

NCBI Description (X98063) polyubiquitin [Pinus sylvestris]

Seq. No. 410840

Seq. ID uC-osflcyp052g11b1

Method BLASTX
NCBI GI g2760349
BLAST score 779
E value 3.0e-83
Match length 158
% identity 22

NCBI Description (U84969) ubiquitin [Arabidopsis thaliana]

Seq. No. 410841

Seq. ID uC-osflcyp052g12b1

Method BLASTX
NCBI GI 94454032
BLAST score 162
E value 6.0e-12
Match length 65
% identity 52

```
NCBI Description (AL035394) putative protein [Arabidopsis thaliana]
                   410842
Seq. No.
Seq. ID
                   uC-osflcyp052h05b1
Method
                  BLASTN
NCBI GI
                   q6063530
BLAST score
                   37
E value
                   2.0e-11
Match length
                   49
                   94
% identity
NCBI Description Oryza sativa genomic DNA, chromosome 3, clone:P0043E01
                   410843
Seq. No.
Seq. ID
                  uC-osflcyp052h07b1
Method
                  BLASTX
NCBI GI
                  g3935147
BLAST score
                   240
E value
                   3.0e-20
Match length
                  117
% identity
                   46
                  (AC005106) T25N20.11 [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   410844
Seq. ID
                  uC-osflcyp052h08b1
Method
                  BLASTX
NCBI GI
                   q3885888
BLAST score
                   255
E value
                   3.0e-22
Match length
                   51
                   98
% identity
NCBI Description (AF093632) high mobility group protein [Oryza sativa]
Seq. No.
                   410845
Seq. ID
                  uC-osflcyp052h10b1
Method
                  BLASTX
NCBI GI
                   q4589965
BLAST score
                   554
E value
                   6.0e-57
Match length
                  137
                   73
% identity
NCBI Description
                  (AC007169) putative glyoxalase II [Arabidopsis thaliana]
Seq. No.
                   410846
Seq. ID
                  uC-osflcyp052h11b1
Method
                  BLASTN
NCBI GI
                  g3777597
BLAST score
                  207
E value
                   1.0e-113
                  207
Match length
% identity
                   100
NCBI Description
                  Oryza sativa clone LS273 30S ribosomal protein S17 (rps17)
                  mRNA, nuclear gene encoding chloroplast protein, complete
                  cds
                   410847
Seq. No.
Seq. ID
                  uC-osflcyp053a01b1
Method
                  BLASTX
```

Ţ



```
NCBI GI
                  g3482977
BLAST score
                  164
                  3.0e-11
E value
Match length
                  38
                  84
% identity
NCBI Description (AL031369) putative protein [Arabidopsis thaliana]
                  410848
Seq. No.
                  uC-osflcyp053a02b1
Seq. ID
Method
                  BLASTX
                  g4587566
NCBI GI
BLAST score
                  358
                  8.0e-34
E value
Match length
                  112
% identity
                  61
```

NCBI Description (AC006550) Contains 2 PF_00400 WD40, G-beta repeats.

[Arabidopsis thaliana]

Seq. No. 410849
Seq. ID uC-osflcyp053a07b1
Method BLASTX
NCBI GI g3451075
BLAST score 199
E value 2.0e-15

E value 2.0e Match length 55 % identity 65

NCBI Description (AL031326) putative protein [Arabidopsis thaliana]

Seq. No. 410850

Seq. ID uC-osflcyp053a08b1

Method BLASTX
NCBI GI g3075488
BLAST score 191
E value 8.0e-15
Match length 71
% identity 55

NCBI Description (AF058796) chlorophyll a/b-binding protein [Oryza sativa]

Seq. No. 410851

Seq. ID uC-osflcyp053a09b1

Method BLASTX
NCBI GI g3297809
BLAST score 153
E value 6.0e-10
Match length 112
% identity 33

NCBI Description (AL031032) putative protein [Arabidopsis thaliana]

Seq. No. 410852

Seq. ID uC-osflcyp053b01b1

Method BLASTX
NCBI GI g3868754
BLAST score 376
E value 5.0e-36
Match length 75
% identity 96

NCBI Description (D64013) catalase [Oryza sativa]

BLAST score

428

```
410853
Seq. No.
                  uC-osflcyp053b02b1
Seq. ID
                  BLASTX
Method
                  g3789948
NCBI GI
BLAST score
                  680
                  1.0e-71
E value
Match length
                  140
                  91
% identity
NCBI Description (AF094773) translation initiation factor 5A [Oryza sativa]
                  410854
Seq. No.
                  uC-osflcyp053b06b1
Seq. ID
                  BLASTX
Method
NCBI GI
                  g2832641
BLAST score
                  182
                  1.0e-13
E value
Match length
                  61
                  54
% identity
NCBI Description
                  (AL021710) glycolate oxidase - like protein [Arabidopsis
                  thaliana]
                  410855
Seq. No.
                  uC-osflcyp053c01b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2464901
                  517
BLAST score
                  2.0e-52
E value
                  138
Match length
% identity
NCBI Description (Z99708) putative protein [Arabidopsis thaliana]
                   410856
Seq. No.
                  uC-osflcyp053c02b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4126809
BLAST score
                  843
E value
                  2.0e-93
Match length
                  181
% identity
                   60
NCBI Description (AB017042) glyoxalase I [Oryza sativa]
Seq. No.
                   410857
                  uC-osflcyp053c03a1
Seq. ID
Method
                  BLASTX
NCBI GI
                   g4126809
BLAST score
                  254
                   7.0e-22
E value
                  50
Match length
% identity
NCBI Description (AB017042) glyoxalase I [Oryza sativa]
Seq. No.
                   410858
                   uC-osflcyp053c03b1
Seq. ID
                  BLASTX
Method
NCBI GI
                   g730580
```

E value Match length

% identity

132 84

```
E value
                   4.0e-49
                  113
Match length
                  96
% identity
                  60S ACIDIC RIBOSOMAL PROTEIN PO >gi 455401 dbj BAA04668_
NCBI Description
                   (D21130) acidic ribosomal protein PO [Oryza sativa]
                   410859
Seq. No.
                  uC-osflcyp053c06b1
Seq. ID
                  BLASTX
Method
                  g1491710
NCBI GI
BLAST score
                   163
                   2.0e-11
E value
                  73
Match length
                   44
% identity
                  (X96506) alpha subunit; forms heterodimer with NC2
NCBI Description
                   alpha/Dr1 [Homo sapiens]
Seq. No.
                   410860
                   uC-osflcyp053c11b1
Seq. ID
Method
                   BLASTX
                   g3868758
NCBI GI
BLAST score
                   645
E value
                   1.0e-67
Match length
                   164
% identity
                   74
NCBI Description (D89802) elongation factor 1B gamma [Oryza sativa]
Seq. No.
                   410861
                   uC-osflcyp053c12b1
Seq. ID
                   BLASTX
Method
                   q4191782
NCBI GI
                   372
BLAST score
                   1.0e-37
E value
                   102
Match length
                   76
% identity
NCBI Description (AC005917) WD-40 repeat protein [Arabidopsis thaliana]
Seq. No.
                   410862
                   uC-osflcyp053d03b1
Seq. ID
                   BLASTX
Method
                   g1710841
NCBI GI
                   494
BLAST score
E value
                   5.0e-50
                   108
Match length
                   93
% identity
                   ADENOSYLHOMOCYSTEINASE (S-ADENOSYL-L-HOMOCYSTEINE
NCBI Description
                   HYDROLASE) (ADOHCYASE) >gi_758247_emb_CAA56278_ (X79905)
                   S-adenosylhomocysteine hydrolase [Phalaenopsis sp.]
Seq. No.
                   410863
Seq. ID
                   uC-osflcyp053d06b1
Method
                   BLASTX
NCBI GI
                   q3107931
                   480
BLAST score
                   1.0e-53
```

```
(AB013353) UDP-glucose pyrophosphorylase [Pyrus pyrifolia]
NCBI Description
                  410864
Seq. No.
                  uC-osflcyp053d12b1
Seq. ID
                  BLASTX
Method
                  g4455335
NCBI GI
                  246
BLAST score
                  3.0e-29
E value
                  153
Match length
                   47
% identity
                  (AL035525) putative protein [Arabidopsis thaliana]
NCBI Description
                   410865
Seq. No.
                  uC-osflcyp053e03b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g5902360
                  538
BLAST score
                  7.0e-55
E value
                  147
Match length
                   69
% identity
NCBI Description (AC009322) Hypothetical protein [Arabidopsis thaliana]
                   410866
Seq. No.
                   uC-osflcyp053f02b1
Seq. ID
Method
                   BLASTX
                   g4321401
NCBI GI
BLAST score
                   339
                   1.0e-31
E value
                   92
Match length
                   33
% identity
NCBI Description (AF047353) LIM domain protein PLIM-2 [Helianthus annuus]
                   410867
Seq. No.
                   uC-osflcyp053f03b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2073375
BLAST score
                   505
E value
                   4.0e-51
                   158
Match length
% identity
                   61
                   (D85317) farnesyl pyrophosphate synthase [Oryza sativa]
NCBI Description
                   >gi 4063829 dbj BAA36276_ (AB021747) farnesyl diphosphate
                   synthase [Oryza sativa]
                   410868
Seq. No.
                   uC-osflcyp053f04b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   q4262174
BLAST score
                   150
E value
                   3.0e-10
Match length
                   50
% identity
NCBI Description (AC005508) 9058 [Arabidopsis thaliana]
Seq. No.
                   410869
                   uC-osflcyp053f06b1
Seq. ID
Method
                   BLASTX
```

NCBI GI g232031 BLAST score 335 E value 1.0e-31 Match length 72 % identity 93

NCBI Description ELONGATION FACTOR 1-BETA' (EF-1-BETA')

>gi 322851 pir S29224 translation elongation factor eEF-1

beta' chain - rice >gi 218161 dbj BAA02253 (D12821)

elongation factor 1 beta' [Oryza sativa]

Seq. No. 410870

Seq. ID uC-osflcyp053f07a1

Method BLASTN
NCBI GI g5091496
BLAST score 82
E value 3.0e-38
Match length 230
% identity 88

NCBI Description Oryza sativa genomic DNA, chromosome 6, clone P0680A03,

complete sequence

Seq. No. 410871

Seq. ID uC-osflcyp053f09b1

Method BLASTX
NCBI GI g1350986
BLAST score 611
E value 2.0e-63
Match length 151
% identity 81

NCBI Description 40S RIBOSOMAL PROTEIN S3A (CYC07 PROTEIN)

>gi 483431 dbj BAA05059 (D26060) cyc07 [Oryza sativa]

Seq. No. 410872

Seq. ID uC-osflcyp053g03b1

Method BLASTX
NCBI GI g5091529
BLAST score 515
E value 2.0e-52
Match length 126
% identity 79

NCBI Description (AB023482) ESTs C98382(C2985), D22444(C11129) correspond to

a region of the predicted gene.; Similar to Arabidopsis thaliana APK1 gene for protein tyrosine-serine-threonine

kinase.(D12522) [Oryza sativa]

Seq. No. 410873

Seq. ID uC-osflcyp053g06b1

Method BLASTN
NCBI GI g474006
BLAST score 65
E value 3.0e-28
Match length 168
% identity 86

NCBI Description Rice mRNA, partial homologous to ribosomal protein S11 gene

Seq. No. 410874

Seq. ID uC-osflcyp053g07b1

```
Method
                  BLASTX
NCBI GI
                  g320618
                  463
BLAST score
                  2.0e-46
E value
Match length
                  98
                  89
% identity
NCBI Description
                  chlorophyll a/b-binding protein I precursor - rice
                  >gi_218172_dbj_BAA00536_ (D00641) type I light-harvesting
                  chlorophyll a/b-binding protein [Oryza sativa]
                  >gi 227611 prf 1707316A chlorophyll a/b binding protein 1
                   [Oryza sativa]
Seq. No.
                  410875
                  uC-osflcyp053g10b1
Seq. ID
Method
                  BLASTX
                  g3925225
NCBI GI
BLAST score
                  202
                  7.0e-20
E value
Match length
                  102
                  59
% identity
NCBI Description
                  (AF037030) 6-phosphogluconate dehydrogenase isoenzyme B
                  [Zea mays]
                  410876
Seq. No.
Seq. ID
                  uC-osflcyp053h01b1
Method
                  BLASTX
                  g3643607
NCBI GI
BLAST score
                  693
E value
                  3.0e-73
Match length
                  153
% identity
                  80
NCBI Description (AC005395) unknown protein [Arabidopsis thaliana]
Seq. No.
                  410877
                  uC-osflcyp053h08b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4680206
BLAST score
                  172
E value
                  2.0e-19
Match length
                  73
% identity
                  74
NCBI Description (AF114171) hypothetical protein [Sorghum bicolor]
                  410878
Seq. No.
Seq. ID
                  uC-osflcyp053h09b1
Method
                  BLASTX
NCBI GI
                  g2244734
BLAST score
                  355
                  3.0e-34
E value
                  74
Match length
                  92
% identity
NCBI Description (D88414) actin [Gossypium hirsutum]
                  410879
Seq. No.
Seq. ID
                  uC-osflcyp053h10b1
Method
                  BLASTX
NCBI GI
                  g2130073
```

BLAST score 434
E value 3.0e-62
Match length 146
% identity 88
NCBI Description fructos

ion fructose-bisphosphate aldolase (EC 4.1.2.13) isoenzyme C-1,
 cytosolic - rice >gi_786178_dbj_BAA08845_ (D50307) aldolase

C-1 [Oryza sativa] >gi 790970 dbj BAA08830_ (D50301)

aldolase C-1 [Oryza sativa]

Seq. No. 410880

Seq. ID uC-osflcyp053h11b1

Method BLASTX
NCBI GI g4263778
BLAST score 300
E value 4.0e-27
Match length 130
% identity 45

NCBI Description (AC006068) putative serine carboxypeptidase II [Arabidopsis

thaliana]

Seq. No. 410881

Seq. ID uC-osflcyp054c03b1

Method BLASTX
NCBI GI 94406775
BLAST score 145
E value 7.0e-09
Match length 104
% identity 30

NCBI Description (AC006836) unknown protein [Arabidopsis thaliana]

Seq. No. 410882

Seq. ID uC-osflcyp054d07b1

Method BLASTX
NCBI GI g3868780
BLAST score 166
E value 2.0e-11
Match length 114
% identity 35

NCBI Description (AB008807) glutathione-dependent dehydroascorbate reductase

[Rattus rattus]

Seq. No. 410883

Seq. ID uC-osflcyp054e03b1

Method BLASTX
NCBI GI g1173069
BLAST score 487
E value 4.0e-52
Match length 148
% identity 67

NCBI Description 50S RIBOSOMAL PROTEIN L9, CHLOROPLAST PRECURSOR (CL13)

>gi_20881_emb_CAA32184_ (X14019) CL9 ribosomal preprotein

(AA -34 to 160) [Pisum sativum]

Seq. No. 410884

Seq. ID uC-osflcyp054e09b1

Method BLASTN NCBI GI g4097337

```
BLAST score
                  345
                  0.0e + 00
E value
                  416
Match length
                  100
% identity
NCBI Description Oryza sativa metallothionein-like protein mRNA, complete
                  410885
Seq. No.
                  uC-osflcyp054h09b1
Seq. ID
Method
                  BLASTX
                  g1261917
NCBI GI
                  319
BLAST score
E value
                  2.0e-29
                  90
Match length
                  61
% identity
NCBI Description (X96979) lipid transfer protein 7a2b [Hordeum vulgare]
                  410886
Seq. No.
                  uC-osflcyp055a01b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g21695
BLAST score
                  238
                  7.0e-20
E value
                  98
Match length
% identity
                  51
NCBI Description (X66014) cathepsin B [Triticum aestivum]
                  410887
Seq. No.
                  uC-osflcyp055a12b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4894182
BLAST score
                   323
E value
                  6.0e-30
Match length
                  132
                   54
% identity
NCBI Description
                  (AJ242551) 12-oxophytodienoate reductase [Lycopersicon
                  esculentum]
Seq. No.
                   410888
                  uC-osflcyp055b02b1
Seq. ID
Method
                  BLASTN
NCBI GI
                   g1835730
BLAST score
                  33
                   4.0e-09
E value
                  88
Match length
% identity
                  87
NCBI Description
                  Oryza sativa photosystem II 10 kDa polypeptide mRNA,
                  complete cds
                   410889
Seq. No.
Seq. ID
                  uC-osflcyp055b03b1
Method
                  BLASTX
NCBI GI
                  g4895186
BLAST score
                  661
E value
                  2.0e-69
Match length
                  155
% identity
                  79
```

BLAST score

```
NCBI Description
                   (AC007661) putative growth regulator protein [Arabidopsis
                   thalianal
Seq. No.
                   410890
                   uC-osflcyp055b04b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   q133867
BLAST score
                   336
E value
                   1.0e-31
Match length
                   113
% identity
                   58
NCBI Description 40S RIBOSOMAL PROTEIN S11 >gi_82722_pir__S16577 ribosomal
                   protein S11 - maize >gi 22470 emb_CAA39438_ (X55967)
                   ribosomal protein S11 [Zea mays]
                   410891
Seq. No.
                   uC-osflcyp055b07b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   q322854
BLAST score
                   667
                   3.0e-70
E value
Match length
                   131
% identity
                   98
NCBI Description
                   pollen-specific protein - rice >gi 20310 emb CAA78897
                   (Z16402) pollen specific gene [Oryza sativa]
                   410892
Seq. No.
Seq. ID
                   uC-osflcyp055b08b1
Method
                   BLASTX
NCBI GI
                   g131400
BLAST score
                   218
E value
                   1.0e-31
Match length
                   108
% identity
                   62
NCBI Description
                   PHOTOSYSTEM II 10 KD POLYPEPTIDE PRECURSOR
                   >gi_81471_pir__S00409 photosystem II 10K protein precursor
- spinach >gi_170127 (J03887) 10kd polypeptide precursor
                   [Spinacia oleracea]
                   410893
Seq. No.
Seq. ID
                   uC-osflcyp055b09a1
Method
                   BLASTX
NCBI GI
                   g1170937
BLAST score
                   295
E value
                   1.0e-35
                   78
Match length
                   99
% identity
NCBI Description S-ADENOSYLMETHIONINE SYNTHETASE 1 (METHIONINE
                   ADENOSYLTRANSFERASE 1) (ADOMET SYNTHETASE 1)
                   >gi 450549 emb CAA81481 (Z26867) S-adenosyl methionine
                   synthetase [Oryza sativa]
Seq. No.
                   410894
Seq. ID
                   uC-osflcyp055b09b1
Method
                   BLASTX
NCBI GI
                   g1170937
```

```
1.0e-57
E value
                  114
Match length
                  92
% identity
                  S-ADENOSYLMETHIONINE SYNTHETASE 1 (METHIONINE
NCBI Description
                  ADENOSYLTRANSFERASE 1) (ADOMET SYNTHETASE 1)
                  >gi_450549_emb_CAA81481_ (Z26867) S-adenosyl methionine
                  synthetase [Oryza sativa]
                  410895
Seq. No.
                  uC-osflcyp055c01b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3559814
BLAST score
                  760
                   4.0e-81
E value
                  155
Match length
                  90
% identity
                 (Y15781) transketolase 1 [Capsicum annuum]
NCBI Description
Seq. No.
                  410896
                  uC-osflcyp055c02b1
Seq. ID
                  BLASTX
Method
NCBI GI
                  g2130069
                  205
BLAST score
                   5.0e-16
E value
                   64
Match length
                   62
% identity
NCBI Description
                  catalase (EC 1.11.1.6) catA - rice
                  >gi 1261858 dbj_BAA06232_ (D29966) catalase [Oryza sativa]
                   410897
Seq. No.
                   uC-osflcyp055c03b1
Seq. ID
Method
                   BLASTN
                   g1255684
NCBI GI
BLAST score
                   68
                   5.0e-30
E value
Match length
                   160
% identity
                   86
NCBI Description Rice mRNA for aspartic protease, complete cds
                   410898
Seq. No.
                   uC-osflcyp055c04b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g585338
BLAST score
                   514
E value
                   3.0e-52
Match length
                   114
% identity
                   89
                   ADENYLATE KINASE B (ATP-AMP TRANSPHOSPHORYLASE)
NCBI Description
                   >gi 391879 dbj BAA01181 (D10335) adenylate kinase-b [Oryza
                   sativa]
Seq. No.
                   410899
                   uC-osflcyp055c05a1
Seq. ID
Method
                   BLASTN
                   g2623812
NCBI GI
BLAST score
                   46
```

4.0e-17

E value

Match length 74 % identity 92 NCBI Description Or

NCBI Description Oryza sativa glucanase mRNA, complete cds

Seq. No.

410900

Seq. ID uC-osflcyp055c05b1

Method BLASTX
NCBI GI g131205
BLAST score 178
E value 5.0e-13
Match length 36
% identity 100

NCBI Description PHOTOSYSTEM I REACTION CENTRE SUBUNIT VIII (PSI-I)

>gi_72677_pir__AlRZI photosystem I protein psaI - rice
chloroplast >gi_11996_emb_CAA33957_ (X15901) ORF36 [Oryza
sativa] >qi_226617 prf__1603356AP photosystem I small

peptide [Oryza sativa]

Seq. No. 410901

Seq. ID uC-osflcyp055c07b1

Method BLASTX
NCBI GI g3929545
BLAST score 493
E value 6.0e-70
Match length 146
% identity 97

NCBI Description (AF067194) S-adenosylmethionine decarboxylase [Oryza

sativa]

Seq. No. 410902

Seq. ID uC-osflcyp055c08b1

Method BLASTX
NCBI GI g2407281
BLAST score 422
E value 2.0e-65
Match length 136
% identity 97

NCBI Description (AF017363) ribulose 1,5-bisphosphate carboxylase small

subunit [Oryza sativa]

Seq. No. 410903

Seq. ID uC-osflcyp055c10b1

Method BLASTX
NCBI GI g1181331
BLAST score 447
E value 2.0e-44
Match length 120
% identity 69

NCBI Description (X77569) calnexin [Zea mays]

Seq. No. 410904

Seq. ID uC-osflcyp055c11b1

Method BLASTX
NCBI GI g4884528
BLAST score 210
E value 7.0e-21
Match length 88

```
% identity
                  (AB027429) beta-1,3-glucanase [Oryza sativa]
NCBI Description
                  410905
Seq. No.
                  uC-osflcyp055d01a1
Seq. ID
Method
                  BLASTX
                  g4584548
NCBI GI
                  530
BLAST score
                  5.0e-54
E value
                  107
Match length
                  89
% identity
                  (AL049608) putative protein [Arabidopsis thaliana]
NCBI Description
                  410906
Seq. No.
                  uC-osflcyp055d03b1
Seq. ID
Method
                  BLASTX
                  g3023271
NCBI GI
BLAST score
                  166
                  7.0e-12
E value
                  69
Match length
                  52
% identity
                  GLUTATHIONE-DEPENDENT FORMALDEHYDE DEHYDROGENASE (FDH)
NCBI Description
                   (FALDH) (GSH-FDH) >gi_1675394 (U77637) class III ADH enzyme
                   [Oryza sativa]
                  410907
Seq. No.
                  uC-osflcyp055d04b1
Seq. ID
Method
                  BLASTX
                  g5007080
NCBI GI
                  260
BLAST score
                  5.0e-23
E value
Match length
                  60
                  88
% identity
NCBI Description (AF153689) poly(A)-binding protein [Oryza sativa]
                  410908
Seq. No.
                  uC-osflcyp055d06b1
Seq. ID
Method
                  BLASTX
                  g100490
NCBI GI
BLAST score
                   621
                   8.0e-65
E value
                  127
Match length
                   28
% identity
                  polyubiquitin - garden snapdragon (fragment)
NCBI Description
                   >gi_16071_emb_CAA48140_ (X67957) ubiquitin [Antirrhinum
                  majus]
Seq. No.
                   410909
Seq. ID
                   uC-osflcyp055d08b1
Method
                   BLASTX
                   q3023271
NCBI GI
                   641
BLAST score
E value
                   3.0e-67
Match length
                   118
                   99
% identity
NCBI Description GLUTATHIONE-DEPENDENT FORMALDEHYDE DEHYDROGENASE (FDH)
                   (FALDH) (GSH-FDH) >gi 1675394 (U77637) class III ADH enzyme
```

Seq. No.

410915

```
[Oryza sativa]
                  410910
Seq. No.
                  uC-osflcyp055d10b1
Seq. ID
                  BLASTX
Method
                  q2130069
NCBI GI
                  262
BLAST score
                  9.0e-23
E value
                  59
Match length
                  88
% identity
                  catalase (EC 1.11.1.6) catA - rice
NCBI Description
                  >gi_1261858_dbj_BAA06232_ (D29966) catalase [Oryza sativa]
Seq. No.
                  410911
                  uC-osflcyp055d11b1
Seq. ID
                  BLASTX
Method
                  g4205079
NCBI GI
                  142
BLAST score
                  8.0e-09
E value
                  41
Match length
                  66
% identity
                  (U70425) ankyrin repeat-containing protein 2 [Arabidopsis
NCBI Description
                  thaliana]
                  410912
Seq. No.
                  uC-osflcyp055e01b1
Seq. ID
                  BLASTX
Method
NCBI GI
                  g3646373
                  599
BLAST score
                  3.0e-62
E value
                  119
Match length
                   95
% identity
NCBI Description (AJ011078) RGP1 protein [Oryza sativa]
                   410913
Seq. No.
                  uC-osflcyp055e02b1
Seq. ID
Method
                  BLASTX
NCBI GI
                   g2384675
                   347
BLAST score
                   8.0e-33
E value
                   96
Match length
                   70
% identity
                  (AF012659) putative potassium transporter AtKT4p
NCBI Description
                   [Arabidopsis thaliana]
                   410914
Seq. No.
Seq. ID
                   uC-osflcyp055e04b1
Method
                   BLASTX
NCBI GI
                   g2407281
BLAST score
                   462
                   3.0e-69
E value
Match length
                   133
% identity
                   94
                  (AF017363) ribulose 1,5-bisphosphate carboxylase small
NCBI Description
                   subunit [Oryza sativa]
```

```
uC-osflcyp055e05b1
Seq. ID
Method
                  BLASTX
                   q400803
NCBI GI
BLAST score
                   477
E value
                   3.0e-52
                   115
Match length
                   90
% identity
                  2,3-BISPHOSPHOGLYCERATE-INDEPENDENT PHOSPHOGLYCERATE MUTASE
NCBI Description
                   (PHOSPHOGLYCEROMUTASE) (BPG-INDEPENDENT PGAM) (PGAM-I)
                   >gi_283033_pir__A42807 phosphoglycerate mutase (EC
                   5.4.2.1), \overline{2}, 3-\overline{b} isphosphoglycerate-independent - maize
                   >gi 168588 (M80912) 2,3-bisphosphoglycerate-independent
                   phosphoglycerate mutase [Zea mays]
                   410916
Seq. No.
                   uC-osflcyp055e06b1
Seq. ID
Method
                   BLASTX
                   q4559398
NCBI GI
                   373
BLAST score
                   8.0e-36
E value
                   95
Match length
                   75
% identity
                  (AC006526) putative mitochondrial carrier protein
NCBI Description
                   [Arabidopsis thaliana]
                   410917
Seq. No.
Seq. ID
                   uC-osflcyp055e07b1
Method
                   BLASTX
                   g2384669
NCBI GI
                   151
BLAST score
                   5.0e-10
E value
Match length
                   46
                   59
% identity
NCBI Description (AF012656) putative potassium transporter AtKT1p
                   [Arabidopsis thaliana]
Seq. No.
                   410918
                   uC-osflcyp055e09b1
Seq. ID
Method
                   BLASTN
NCBI GI
                   q508974
BLAST score
                   59
E value
                   1.0e-24
Match length
                   83
                   93
% identity
                   Triticum aestivum Chinese spring protein disulfide
NCBI Description
                   isomerase (PDI) mRNA, complete cds
Seq. No.
                   410919
                   uC-osflcyp055f01a1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g585551
BLAST score
                   519
E value
                   1.0e-52
                   97
Match length
% identity
                   99
NCBI Description NUCLEOSIDE DIPHOSPHATE KINASE I (NDK I) (NDP KINASE I)
                   >qi 629798 pir S43330 nucleoside-diphosphate kinase (EC
```

2.7.4.6) - rice >gi_303849_dbj_BAA03798_ (D16292) nucleoside diphosphate kinase [Oryza sativa]

Seq. No. 410920

Seq. ID uC-osflcyp055f01b1

Method BLASTX
NCBI GI g585551
BLAST score 477
E value 6.0e-48
Match length 105
% identity 89

NCBI Description NUCLEOSIDE DIPHOSPHATE KINASE I (NDK I) (NDP KINASE I)

>gi_629798_pir__S43330 nucleoside-diphosphate kinase (EC

2.7.4.6) - rice >gi_303849_dbj_BAA03798_ (D16292) nucleoside diphosphate kinase [Oryza sativa]

Seq. No. 410921

Seq. ID uC-osflcyp055f03b1

Method BLASTX
NCBI GI g5802606
BLAST score 397
E value 2.0e-38
Match length 83
% identity 84

NCBI Description (AF174486) methylenetetrahydrofolate reductase [Zea mays]

Seq. No. 410922

Seq. ID uC-osflcyp055f04b1

Method BLASTX
NCBI GI g3746581
BLAST score 695
E value 2.0e-73
Match length 129
% identity 100

NCBI Description (AF062403) glutathione S-transferase II [Oryza sativa]

Seq. No. 410923

Seq. ID uC-osflcyp055f10b1

Method BLASTX
NCBI GI g2501449
BLAST score 289
E value 3.0e-26
Match length 54
% identity 100

NCBI Description UBIQUITIN-LIKE PROTEIN SMT3 >gi 1668773 emb CAA67922_

(X99608) ubiquitin-like protein [Oryza sativa]

Seq. No. 410924

Seq. ID uC-osflcyp055g01b1

Method BLASTX
NCBI GI g1709619
BLAST score 281
E value 9.0e-30
Match length 73
% identity 83

NCBI Description PROTEIN DISULFIDE ISOMERASE PRECURSOR (PDI)

>gi 2146814 pir S69181 protein disulfide isomerase (EC

5.3.4.1) precursor - maize >gi_625148 (L39014) protein disulfide isomerase [Zea mays]

Seq. No. 410925

Seq. ID uC-osflcyp055g02b1

Method BLASTX
NCBI GI g68592
BLAST score 655
E value 7.0e-69
Match length 127
% identity 97

NCBI Description glutamate--ammonia ligase (EC 6.3.1.2) gamma, cytosolic -

rice

Seq. No. 410926

Seq. ID uC-osflcyp055g05b1

Method BLASTX
NCBI GI 94432839
BLAST score 189
E value 4.0e-14
Match length 99
% identity 41

NCBI Description (AC006283) unknown protein [Arabidopsis thaliana]

Seq. No. 410927

Seq. ID uC-osflcyp055g06b1

Method BLASTX
NCBI GI g4206122
BLAST score 513
E value 1.0e-60
Match length 151
% identity 76

NCBI Description (AF097667) protein phosphatase 2C homolog [Mesembryanthemum

crystallinum]

Seq. No. 410928

Seq. ID uC-osflcyp055g07b1

Method BLASTX
NCBI GI g1170121
BLAST score 197
E value 2.0e-15
Match length 100
% identity 45

NCBI Description GLUTATHIONE S-TRANSFERASE 103-1A >gi 2129602 pir S66354

glutathione transferase (EC 2.5.1.18), auxin-inducible - Arabidopsis thaliana >gi_895700_emb_CAA61504_ (X89216) glutathione transferase [Arabidopsis thaliana] >gi_929957 (U30489) glutathione S-transferase [Arabidopsis thaliana] >gi_940381_dbj_BAA07917_ (D44465) Glutathione S-Transferase [Arabidopsis thaliana] >gi_3980390 (AC004561) glutathione

S-transferase [Arabidopsis thaliana]

>gi_4973229_gb_AAD34992.1_AF144382_1 (AF144382) glutathione

S-transferase [Arabidopsis thaliana]

Seq. No. 410929

Seq. ID uC-osflcyp055g08b1

Method BLASTN

NCBI GI

g82496

```
NCBI GI
                  q4105602
BLAST score
                  88
                  8.0e-42
E value
Match length
                  172
% identity
                  97
                  Oryza sativa metallothionein (MTe) gene, complete cds
NCBI Description
Seq. No.
                  410930
                  uC-osflcyp055g11b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4582436
BLAST score
                  436
E value
                  3.0e-43
Match length
                  121
% identity
                  73
NCBI Description
                  (AC007196) unknown protein [Arabidopsis thaliana]
Seq. No.
                  410931
                  uC-osflcyp055h03b1
Seq. ID
Method
                  BLASTX
                  g1877279
NCBI GI
BLAST score
                  470
E value
                  4.0e-47
Match length
                  142
% identity
                  65
                  (Z92770) fadE2 [Mycobacterium tuberculosis]
NCBI Description
Seq. No.
                  410932
                  uC-osflcyp055h08b1
Seq. ID
                  BLASTX
Method
NCBI GI
                  g2642213
BLAST score
                  162
                  4.0e-11
E value
                  68
Match length
                  49
% identity
                  (AF030385) nitrate-induced NOI protein [Zea mays]
NCBI Description
                  >gi_2895781 (AF045033) nitrate-induced NOI protein [Zea
                  mays]
                   410933
Seq. No.
                  uC-osflcyp055h11b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2130082
BLAST score
                  280
                  8.0e-25
E value
Match length
                  153
% identity
NCBI Description
                  protein kinase Xa21 (EC 2.7.1.-) - rice >gi 1122443
                   (U37133) receptor kinase-like protein [Oryza sativa]
                  >gi 2586085 (U72723) receptor kinase-like protein [Oryza
                   longistaminata] >gi_1586408_prf__2203451A receptor
                   kinase-like protein [Oryza sativa]
Seq. No.
                   410934
                  uC-osflcyp057a02b1
Seq. ID
Method
                  BLASTX
```

```
296
BLAST score
                  4.0e-27
E value
                  61
Match length
                  95
% identity
NCBI Description phenylalanine ammonia-lyase (EC 4.3.1.5) - rice
                  410935
Seq. No.
                  uC-osflcyp057a06b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4914332
BLAST score
                  153
                  1.0e-10
E value
                  50
Match length
% identity
                   60
                  (AC005489) F14N23.18 [Arabidopsis thaliana]
NCBI Description
                  410936
Seq. No.
                  uC-osflcyp057b01b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4567231
BLAST score
                  188
E value
                  1.0e-14
Match length
                   44
                   77
% identity
                  (AC007119) putative glucose-1-phosphate adenylyltransferase
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                   410937
                  uC-osflcyp057b03b1
Seq. ID
Method
                  BLASTX
NCBI GI
                   q3386621
BLAST score
                   553
                   9.0e-57
E value
Match length
                   160
                   67
% identity
NCBI Description (AC004665) unknown protein [Arabidopsis thaliana]
Seq. No.
                   410938
                   uC-osflcyp057b05b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2429343
BLAST score
                   211
E value
                   2.0e-17
                  72
Match length
                   58
% identity
NCBI Description (AF019376) calreticulin [Brassica napus]
                   410939
Seq. No.
                   uC-osflcyp057b09b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   q4972070
BLAST score
                   286
E value
                   5.0e-26
                  65
Match length
                   74
% identity
NCBI Description (AL078467) putative protein [Arabidopsis thaliana]
```

410940 Seq. No. uC-osflcyp057c01b1 Seq. ID Method BLASTX NCBI GI q4538939 BLAST score 743 5.0e-79 E value 155 Match length 87 % identity (AL049483) Col-O casein kinase I-like protein [Arabidopsis NCBI Description thaliana] 410941 Seq. No. uC-osflcyp057c03b1 Seq. ID BLASTX Method NCBI GI g2055230 BLAST score 200 2.0e-15E value Match length 121 40 % identity (AB000130) SRC2 [Glycine max] NCBI Description 410942 Seq. No. uC-osflcyp057c04b1 Seq. ID Method BLASTX NCBI GI q5051769 BLAST score 455 E value 3.0e-45Match length 151 58 % identity NCBI Description (AL078637) putative protein [Arabidopsis thaliana] 410943 Seq. No. uC-osflcyp057c05b1 Seq. ID Method BLASTN NCBI GI g454880 BLAST score 219 E value 1.0e-120 Match length 247 % identity 97 Rice mRNA for WSI724 protein induced by water stress, NCBI Description complete cds Seq. No. 410944 uC-osflcyp057c06b1 Seq. ID Method BLASTN NCBI GI g20177 BLAST score 166 E value 2.0e-88 190 Match length

97 % identity

Rice cab1R gene for light harvesting chlorophyll NCBI Description

a/b-binding protein

410945 Seq. No.

uC-osflcyp057c07b1 Seq. ID

BLASTX Method NCBI GI g100638

BLAST score 367 5.0e-35 E value Match length 111 % identity 58 pollen allergen Lol p I precursor (clone 5A) - perennial NCBI Description ryegrass >gi 168316 (M57474) pollen allergen [Lolium perenne] Seq. No. 410946 Seq. ID

uC-osflcyp057c08b1

Method BLASTX q2055230 NCBI GI 194 BLAST score 1.0e-14 E value Match length 121 % identity 40

(AB000130) SRC2 [Glycine max] NCBI Description

410947 Seq. No.

Seq. ID uC-osflcyp057c10b1

Method BLASTX NCBI GI g4235430 BLAST score 525 E value 2.0e-53 131 Match length % identity 73

NCBI Description (AF098458) latex-abundant protein [Hevea brasiliensis]

410948 Seq. No.

uC-osflcyp057d03b1 Seq. ID

Method BLASTN NCBI GI g5912298 BLAST score 157 E value 6.0e-83 Match length 205 % identity 95

NCBI Description Oryza sativa mRNA for gigantea homologue, partial

410949 Seq. No.

uC-osflcyp057d04b1 Seq. ID

Method BLASTX NCBI GI g3366930 BLAST score 282 E value 2.0e-25 Match length 80 % identity

(AF068745) putative phosphatidylinositol 4-kinase [Solanum NCBI Description

tuberosum]

410950 Seq. No.

Seq. ID uC-osflcyp057d05b1

Method BLASTN NCBI GI g758354 51 BLAST score E value 5.0e-20 Match length 75 92 % identity

NCBI GI

NCBI Description Z.mays mRNA for plasma membrane H+ ATPase Seq. No. 410951 Seq. ID uC-osflcyp057d06b1 Method BLASTX NCBI GI g5051789 219 BLAST score 7.0e-18 E value Match length 82 55 % identity NCBI Description (AL078637) putative protein [Arabidopsis thaliana] Seq. No. 410952 uC-osflcyp057d08b1 Seq. ID Method BLASTX NCBI GI q2980794 BLAST score 423 E value 1.0e-41 102 Match length 70 % identity NCBI Description (AL022197) myb-like protein [Arabidopsis thaliana] 410953 Seq. No. Seq. ID uC-osflcyp057d09a1 Method BLASTN NCBI GI q1041709 195 BLAST score E value 1.0e-105 358 Match length % identity 98 NCBI Description Oryza sativa expansin Os-EXP2 (Os-EXP2) mRNA, complete cds Seq. No. 410954 Seq. ID uC-osflcyp057d09b1 Method BLASTN NCBI GI g1041709 BLAST score 75 E value 2.0e-34 Match length 107 % identity 93 NCBI Description Oryza sativa expansin Os-EXP2 (Os-EXP2) mRNA, complete cds 410955 Seq. No. Seq. ID uC-osflcyp057d11b1 Method BLASTX NCBI GI g3660471 BLAST score 390 E value 8.0e-56 Match length 122 89 % identity (AJ001809) succinate dehydrogenase flavoprotein alpha NCBI Description subunit [Arabidopsis thaliana] 410956 Seq. No. Seq. ID uC-osflcyp057d12b1 Method BLASTX

53365

g1835731

```
BLAST score
                    316
                    5.0e-29
E value
Match length
                    71
% identity
                    85
                   (U86018) photosystem II 10 kDa polypeptide [Oryza sativa]
NCBI Description
                    410957
Seq. No.
Seq. ID
                    uC-osflcyp057e03b1
Method
                    BLASTX
NCBI GI
                    q1143864
BLAST score
                    257
                    1.0e-29
E value
                    88
Match length
                    78
% identity
NCBI Description (U28047) beta glucosidase [Oryza sativa]
                    410958
Seq. No.
                    uC-osflcyp057e05b1
Seq. ID
Method
                    BLASTN
NCBI GI
                    q600766
BLAST score
                    95
                    3.0e-46
E value
Match length
                    123
% identity
NCBI Description Oryza sativa cyclophilin 2 (Cyp2) gene, complete cds
                    410959
Seq. No.
Seq. ID
                    uC-osflcyp057e10b1
Method
                    BLASTX
NCBI GI
                    g4505235
BLAST score
                    159
E value
                    3.0e-11
                    53
Match length
% identity
                    57
NCBI Description mannose-6- phosphate isomerase >gi_462567_sp_P34949_MANA_HUMAN MANNOSE-6-PHOSPHATE ISOMERASE (PHOSPHOMANNOSE ISOMERASE) (PMI)
                    (PHOSPHOHEXOMUTASE) >gi_631328_pir__S41122 mannose-6-phosphate isomerase (EC 5.3.1.8) - human
                    >gi 416017 emb CAA53657 (X76057) phosphomannose isomerase
                    [Homo sapiens] >gi_740967_prf__2006245A phosphomannose
                    isomerase [Homo sapiens]
Seq. No.
                    410960
Seq. ID
                    uC-osflcyp057e11b1
Method
                    BLASTX
NCBI GI
                    g1173218
BLAST score
                    221
E value
                    7.0e-18
                    52
Match length
% identity
                    85
NCBI Description 40S RIBOSOMAL PROTEIN S15A >gi 440824 (L27461) ribosomal
                    protein S15 [Arabidopsis thaliana] >gi 2150130 (AF001412)
                    cytoplasmic ribosomal protein S15a [Arabidopsis thaliana]
Seq. No.
                    410961
Seq. ID
                    uC-osflcyp057f04b1
```

Method BLASTX
NCBI GI g2129549
BLAST score 235
E value 1.0e-19
Match length 69
% identity 61

NCBI Description calcium-dependent protein kinase (EC 2.7.1.-) CDPK19 -

Arabidopsis thaliana >gi_2129551_pir__S71778

calcium-dependent protein kinase 19 - Arabidopsis thaliana

>gi_836942 (U20624) calcium-dependent protein kinase

[Arabidopsis thaliana] >gi_836948 (U20627)

calcium-dependent protein kinase [Arabidopsis thaliana]

Seq. No. 410962

Seq. ID uC-osflcyp057f07b1

Method BLASTX
NCBI GI g2130073
BLAST score 466
E value 2.0e-60
Match length 131
% identity 98

NCBI Description fructose-bisphosphate aldolase (EC 4.1.2.13) isoenzyme C-1,

cytosolic - rice >gi_786178_dbj_BAA08845_ (D50307) aldolase

C-1 [Oryza sativa] >gi_790970_dbj_BAA08830_ (D50301)

aldolase C-1 [Oryza sativa]

Seq. No. 410963

Seq. ID uC-osflcyp057f09b1

Method BLASTX
NCBI GI g2352921
BLAST score 429
E value 1.0e-46
Match length 104
% identity 91

NCBI Description (AF012862) cytosolic glucose-6-phosphate dehydrogenase 1

[Petroselinum crispum]

Seq. No. 410964

Seq. ID uC-osflcyp057g03b1

Method BLASTX
NCBI GI g6006853
BLAST score 377
E value 3.0e-36
Match length 102
% identity 68

NCBI Description (AC009540) unknown protein [Arabidopsis thaliana]

Seq. No. 410965

Seq. ID uC-osflcyp057g04b1

Method BLASTN
NCBI GI g20181
BLAST score 73
E value 4.0e-33
Match length 149
% identity 87

NCBI Description Rice cab2R gene for light harvesting chlorophyll

a/b-binding protein

```
410966
Seq. No.
                  uC-osflcyp057g08b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4741844
BLAST score
                  318
                  6.0e-30
E value
                  66
Match length
                  94
% identity
                  (AF112964) small GTP-binding protein [Triticum aestivum]
NCBI Description
Seq. No.
                  410967
Seq. ID
                  uC-osflcyp057g12b1
Method
                  BLASTX
NCBI GI
                  q4415923
BLAST score
                  175
                   1.0e-12
E value
Match length
                  77
                   45
% identity
                  (AC006282) putative glucosyl transferase [Arabidopsis
NCBI Description
                  thaliana]
                   410968
Seq. No.
                  uC-osflcyp057h03b1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g5803242
BLAST score
                   274
                  1.0e-152
E value
                   477
Match length
                   98
% identity
NCBI Description Oryza sativa genomic DNA, chromosome 6, clone:P0535G04
                   410969
Seq. No.
Seq. ID
                   uC-osflcyp057h06b1
Method
                   BLASTX
NCBI GI
                   q4585987
BLAST score
                   453
E value
                   1.0e-53
Match length
                   154
% identity
                   69
NCBI Description
                  (AC005287) Similar to nucleolar protein [Arabidopsis
                   thaliana]
                   410970
Seq. No.
                   uC-osflcyp057h09b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g5733884
BLAST score
                   142
E value
                   3.0e-09
                   36
Match length
                   69
% identity
                   (AC007932) Similar to gb\_U28007 Pto kinase interactor 1
NCBI Description
                   (Ptil) from Lycopersicon esculentum and contains a PF 00069
                   Eukaryotic protein kinase domain. [Arabidopsis thaliana]
Seq. No.
                   410971
Seq. ID
                   uC-osflcyp058a01b1
```

Seq. ID

```
BLASTN
Method
NCBI GI
                  g21832
                  39
BLAST score
                  2.0e-12
E value
                  43
Match length
                  98
% identity
                  Wheat mRNA for chloroplast phosphoglycerate kinase (EC
NCBI Description
                  2.7.2.3)
                  410972
Seq. No.
                  uC-osflcyp058a05a1
Seq. ID
Method
                  BLASTX
                  g131194
NCBI GI
BLAST score
                  175
                  1.0e-12
E value
Match length
                  42
                  71
% identity
                  PHOTOSYSTEM I REACTION CENTRE SUBUNIT V PRECURSOR
NCBI Description
                   (PHOTOSYSTEM I 9 KD PROTEIN) (PSI-G) >gi_72686_pir__F1SP5
                  photosystem I chain V precursor - spinach
                  >gi_21299_emb_CAA31524_ (X13134) PSI subunit V preprotein
                   (AA -69 to 98) [Spinacia oleracea] >gi_226167_prf__1413236B
                  photosystem I reaction center V [Spinacia oleracea]
                   410973
Seq. No.
                  uC-osflcyp058a08b1
Seq. ID
                  BLASTX
Method
                   g3063698
NCBI GI
                   189
BLAST score
                   4.0e-14
E value
                   161
Match length
                   39
% identity
                 (AL022537) putative protein [Arabidopsis thaliana]
NCBI Description
                   410974
Seq. No.
                   uC-osflcyp058a11b1
Seq. ID
Method
                   BLASTN
NCBI GI
                   g2182028
                   254
BLAST score
                   1.0e-141
E value
                   274
Match length
                   99
% identity
NCBI Description Oryza sativa mRNA for shaggy-like kinase etha
                   410975
Seq. No.
Seq. ID
                   uC-osflcyp058b01a1
Method
                   BLASTX
NCBI GI
                   g2275202
BLAST score
                   528
                   1.0e-53
E value
                   169
Match length
% identity
                   (AC002337) acyl-CoA synthetase isolog [Arabidopsis
NCBI Description
                   thaliana]
                   410976
Seq. No.
```

53369

uC-osflcyp058b01b1

```
Method
                   BLASTX
                   g2275202
NCBI GI
                   394
BLAST score
                   4.0e-38
E value
                   120
Match length
                   56
% identity
                   (ACO02337) acyl-CoA synthetase isolog [Arabidopsis
NCBI Description
                   thaliana]
                   410977
Seq. No.
                   uC-osflcyp058b07b1
Seq. ID
Method
                   BLASTX
                   g1421730
NCBI GI
                   192
BLAST score
                   1.0e-14
E value
Match length
                   55
                   69
% identity
                   (U43082) RF2 [Zea mays]
NCBI Description
Seq. No.
                   410978
                   uC-osflcyp058b08a1
Seq. ID
                   BLASTX
Method
NCBI GI
                   g584892
                   143
BLAST score
                   9.0e-09
E value
                   116
Match length
                   27
% identity
                   SERINE CARBOXYPEPTIDASE I PRECURSOR (CARBOXYPEPTIDASE C)
NCBI Description
                   >gi_629805_pir__S43516 serine carboxypeptidase I - rice
                   >gi 409580 dbj BAA04510 (D17586) serine carboxypeptidase I
                   [Oryza sativa]
                   410979
Seq. No.
                   uC-osflcyp058b08b1
Seq. ID
                   BLASTX
Method
                   g3169173
NCBI GI
BLAST score
                    171
                    3.0e-12
E value
                    71
Match length
                    42
% identity
                   (AC004401) putative serine carboxypeptidase I [Arabidopsis
NCBI Description
                   thaliana] >gi_3445215_gb_AAC32445.1_ (AC004786) putative serine carboxypeptidase I [Arabidopsis thaliana]
                    410980
Seq. No.
                    uC-osflcyp058b10b1
Seq. ID
Method
                    BLASTX
                    g3929333
NCBI GI
BLAST score
                    185
                    6.0e-14
E value
                    63
Match length
                    59
% identity
NCBI Description CYTOCHROME P450 76B1 (7-ETHOXYCOUMARIN O-DEETHYLASE) (ECOD)
                    (PHENYLUREA DEALKYLASE) >gi_2370230_emb_CAA71054_ (Y09920)
                    7-ethoxycoumarin O-deethylase [Helianthus tuberosus]
```

410981

Seq. No.

uC-osflcyp058b11b1 Seq. ID BLASTX Method NCBI GI q115787 862 BLAST score 6.0e-93 E value Match length 172 94 % identity CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I NCBI Description CAB-2) (LHCP) >gi_82461_pir__S03706 chlorophyll a/b-binding protein 2R precursor - rice >gi 20182 emb CAA32109 (X13909) chlorophyll a/b-binding preprotein (AA -28 to 235) [Oryza sativa] 410982 Seq. No. uC-osflcyp058b12b1 Seq. ID Method BLASTX g115787 NCBI GI BLAST score 856 3.0e-92 E value 168 Match length 96 % identity CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I NCBI Description CAB-2) (LHCP) >gi_82461_pir__S03706 chlorophyll a/b-binding protein 2R precursor - rice >gi_20182_emb_CAA32109 (X13909) chlorophyll a/b-binding preprotein (AA -28 to 235) [Oryza sativa] Seq. No. 410983 uC-osflcyp058c03b1 Seq. ID BLASTX Method q4079800 NCBI GI 436 BLAST score 9.0e-52 E value 109 Match length 99 % identity (AF052503) S-phase-specific ribosomal protein [Oryza NCBI Description sativa] 410984 Seq. No. uC-osflcyp058c07b1 Seq. ID Method BLASTX NCBI GI q3402693 BLAST score 185 1.0e-13 E value 98 Match length 44 % identity NCBI Description (AC004697) unknown protein [Arabidopsis thaliana] 410985 Seq. No. uC-osflcyp058c11b1 Seq. ID Method BLASTX NCBI GI q417103 BLAST score 673 9.0e-71 E value 136 Match length 99 % identity NCBI Description HISTONE H3.2, MINOR >gi_282871_pir__S24346 histone

H3.3-like protein - Arabidopsis thaliana >gi_16324_emb_CAA42957_ (X60429) histone H3.3 like protein [Arabidopsis thaliana] >gi_404825_emb_CAA42958_ (X60429) histone H3.3 like protein [Arabidopsis thaliana] >gi 488563 (U09458) histone H3.2 [Medicago sativa] $>gi_488567$ ($\overline{U}09460$) histone H3.2 [Medicago sativa] >gi_488569 (U09461) histone H3.2 [Medicago sativa] >gi_488575 (U09464) histone H3.2 [Medicago sativa] $>gi_4885\overline{7}7$ (U09465) histone H3.2 H3 [Lolium temulentum] $>gi_1\overline{435157}$ _emb_CA $\overline{A}58445$ _ (X83422) histone H3 variant H3.3 [Lycopersicon esculentum] >gi 2558944 (AF024716) histone 3 [Gossypium hirsutum] >gi_3273350_dbj_BAA31218_ (AB015760) histone H3 [Nicotiana tabacum] >gi 3885890 (AFO93633) histone H3 [Oryza sativa] >gi_4038469_gb_AAC97380_ (AF109910) histone H3 [Porteresia coarctata] >gi_4490754_emb_CAB38916.1_ (AL035708) histone H3.3 [Arabidopsis thaliana] >gi_4490755_emb_CAB38917.1_ (AL035708) Histon H3 [Arabidopsis thaliana] >gi_6006364_dbj_BAA84794.1_ (AP000559) EST D15300(C0425) corresponds to a region of the predicted gene.; Similar to histone H3 (AB015760) [Oryza sativa]

Seq. No. 410986

Seq. ID uC-osflcyp058d05b1

Method BLASTX
NCBI GI g5051773
BLAST score 223
E value 5.0e-18
Match length 137
% identity 39

NCBI Description (AL078637) putative protein [Arabidopsis thaliana]

Seq. No. 410987

Seq. ID uC-osflcyp058d06b1

Method BLASTX
NCBI GI g3915866
BLAST score 257
E value 5.0e-22
Match length 79
% identity 67

NCBI Description GLUTAMINYL-TRNA SYNTHETASE (GLUTAMINE--TRNA LIGASE) (GLNRS)

>gi_2995455_emb_CAA62901_ (X91787) tRNA-glutamine

synthetase [Lupinus luteus]

Seq. No. 410988

Seq. ID uC-osflcyp058d10b1

Method BLASTX
NCBI GI g3688189
BLAST score 718
E value 4.0e-76
Match length 160
% identity 79

NCBI Description (AL031804) putative protein kinase [Arabidopsis thaliana]

Seq. No. 410989

Seq. ID uC-osflcyp058d11a1

Method BLASTX

% identity

```
NCBI GI
                  q136739
BLAST score
                  331
                  5.0e - 31
E value
Match length
                  89
% identity
                  82
                  UTP--GLUCOSE-1-PHOSPHATE URIDYLYLTRANSFERASE (UDP-GLUCOSE
NCBI Description
                  PYROPHOSPHORYLASE) (UDPGP) >gi 67061 pir XNPOU
                  UTP--glucose-1-phosphate uridylyltransferase (EC 2.7.7.9) -
                  potato >gi 218001 dbj BAA00570_ (D00667) UDP-glucose
                  pyrophosphorylase precursor [Solanum tuberosum]
Seq. No.
                  410990
                  uC-osflcyp058d11b1
Seq. ID
                  BLASTX
Method
NCBI GI
                   q2117937
BLAST score
                   584
                   2.0e-60
E value
Match length
                   159
                   72
% identity
                  UTP--glucose-1-phosphate uridylyltransferase (EC 2.7.7.9) -
NCBI Description
                  barley >gi 1212996 emb CAA62689 (X91347) UDP-glucose
                  pyrophosphorylase [Hordeum vulgare]
                   410991
Seq. No.
                   uC-osflcyp058d12b1
Seq. ID
                   BLASTX
Method
                   q3929545
NCBI GI
BLAST score
                   781
                   1.0e-83
E value
Match length
                   147
                   99
% identity
                   (AF067194) S-adenosylmethionine decarboxylase [Oryza
NCBI Description
                   sativa]
                   410992
Seq. No.
                   uC-osflcyp058e05b1
Seq. ID
                   BLASTX
Method
NCBI GI
                   q4587549
                   550
BLAST score
                   2.0e-56
E value
                   137
Match length
                   74
% identity
                   (AC006577) Similar to gb U55861 RNA binding protein
NCBI Description
                   nucleolysin (TIAR) from Mus musculus and contains several
                   PF_00076 RNA recognition motif domains. ESTs gb_T21032 and
                   gb T44127 come from this gene. [Arabidopsis t
Seq. No.
                   410993
Seq. ID
                   uC-osflcyp058e07a1
                   BLASTX
Method
                   q2764574
NCBI GI
                   202
BLAST score
E value
                   1.0e-15
                   74
Match length
                   50
```

NCBI Description (AJ001009) pore protein of 24 kD (OEP24) [Pisum sativum]

```
410994
Seq. No.
                  uC-osflcyp058e12b1
Seq. ID
                  BLASTN
Method
NCBI GI
                  q4574136
BLAST score
                  232
                  1.0e-128
E value
                  264
Match length
% identity
                  97
NCBI Description Oryza sativa cysteine synthase (rcs2) mRNA, complete cds
                  410995
Seq. No.
                  uC-osflcyp058f08b1
Seq. ID
                  BLASTX
Method
                  g4885026
NCBI GI
                   604
BLAST score
                  7.0e-63
E value
Match length
                  133
                   86
% identity
                  (AF147738) myosin VIII ZMM3 [Zea mays]
NCBI Description
                   410996
Seq. No.
                   uC-osflcyp058f09b1
Seq. ID
                   BLASTX
Method
NCBI GI
                   q4567245
                   260
BLAST score
                   2.0e-22
E value
                   75
Match length
                   73
% identity
                  (AC007070) unknown protein [Arabidopsis thaliana]
NCBI Description
                   410997
Seq. No.
                   uC-osflcyp058f11a1
Seq. ID
                   BLASTX
Method
NCBI GI
                   g3789942
                   462
BLAST score
                   4.0e-46
E value
                   93
Match length
                   21
% identity
                  (AF093505) polyubiquitin [Saccharum hybrid cultivar
NCBI Description
                   H32-8560]
                   410998
Seq. No.
                   uC-osflcyp058f11b1
Seq. ID
                   BLASTX
Method
                   g1332579
NCBI GI
                   241
BLAST score
                   5.0e-34
E value
                   90
Match length
                   10
% identity
NCBI Description (X98063) polyubiquitin [Pinus sylvestris]
                   410999
Seq. No.
                   uC-osflcyp058f12b1
Seq. ID
                   BLASTX
Method
                   q6056422
NCBI GI
                   265
BLAST score
                   2.0e-23
E value
```

```
Match length
                  94
                  53
% identity
                  (AC009525) Similar to pectinesterases [Arabidopsis
NCBI Description
                  thaliana]
                  411000
Seq. No.
                  uC-osflcyp058g03b1
Seq. ID
Method
                  BLASTX
                  g4567283
NCBI GI
BLAST score
                  326
                  3.0e-30
E value
Match length
                  90
                  71
% identity
                  (AC006841) unknown protein [Arabidopsis thaliana]
NCBI Description
                   411001
Seq. No.
Seq. ID
                   uC-osflcyp058g04b1
                  BLASTX
Method
                   g3413473
NCBI GI
BLAST score
                   357
                   9.0e - 34
E value
                   99
Match length
                   69
% identity
NCBI Description (AJ006308) tyrosine phosphatase 1 [Glycine max]
                   411002
Seq. No.
                   uC-osflcyp058g05b1
Seq. ID
                  BLASTX
Method
NCBI GI
                   q3421090
BLAST score
                   682
                   8.0e-72
E value
Match length
                   165
                   84
% identity
                  (AF043525) 20S proteasome subunit PAE2 [Arabidopsis
NCBI Description
                   thaliana]
                   411003
Seq. No.
                   uC-osflcyp058g06b1
Seq. ID
Method
                   BLASTX
                   g4588906
NCBI GI
                   568
BLAST score
                   1.0e-58
E value
                   126
Match length
% identity
NCBI Description (AF118149) ribosomal protein S7 [Secale cereale]
                   411004
Seq. No.
                   uC-osflcyp058g08b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2507281
                   526
BLAST score
                   4.0e-54
E value
                   105
Match length
                   98
% identity
```

NCBI Description GTP-BINDING NUCLEAR PROTEIN RAN-2 >gi_1668706_emb_CAA66048_ (X97380) atran2 [Arabidopsis thaliana]

Seq. ID

Method

NCBI GI

```
Seq. No.
                  411005
                  uC-osflcyp058g12b1
Seq. ID
                  BLASTN
Method
                  q6063530
NCBI GI
                  55
BLAST score
                  5.0e-22
E value
Match length
                  123
                  88
% identity
                  Oryza sativa genomic DNA, chromosome 3, clone:P0043E01
NCBI Description
                  411006
Seq. No.
                  uC-osflcyp061a01b1
Seq. ID
                  BLASTX
Method
                  q2443886
NCBI GI
BLAST score
                  616
                  3.0e-64
E value
Match length
                  152
                  78
% identity
                  (AC002294) Unknown protein [Arabidopsis thaliana]
NCBI Description
                   411007
Seq. No.
                  uC-osflcyp061a03b1
Seq. ID
                   BLASTX
Method
                   g5596468
NCBI GI
                   373
BLAST score
                   1.0e-35
E value
                   128
Match length
                   54
% identity
                  (AL096882) putative protein [Arabidopsis thaliana]
NCBI Description
                   411008
Seq. No.
                   uC-osflcyp061a04b1
Seq. ID
                   BLASTX
Method
                   g464981
NCBI GI
                   770
BLAST score
                   3.0e-82
E value
                   148
Match length
                   95
% identity
NCBI Description UBIQUITIN-CONJUGATING ENZYME E2-17 KD (UBIQUITIN-PROTEIN
                   LIGASE) (UBIQUITIN CARRIER PROTEIN) >gi_388207 (L23762)
                   ubiquitin carrier protein [Lycopersicon esculentum]
                   411009
Seq. No.
                   uC-osflcyp061a06b1
Seq. ID
                   BLASTX
Method
                   g3334320
NCBI GI
                   679
BLAST score
                   2.0e-71
E value
                   137
Match length
                   95
 % identity
NCBI Description 40S RIBOSOMAL PROTEIN SA (P40) >gi_2444420 (AF020553)
                   ribosome-associated protein p40 [GTycine max]
                   411010
 Seq. No.
```

53376

uC-osflcyp061a07b1

BLASTX

g2708744

BLAST score 182 6.0e-19 E value 119 Match length 47 % identity (AC003952) putative Bop-like zinc finger protein NCBI Description [Arabidopsis thaliana] 411011 Seq. No. uC-osflcyp061a09b1 Seq. ID Method BLASTX g3123264 NCBI GI BLAST score 573 4.0e-59 E value 136 Match length % identity 82 60S RIBOSOMAL PROTEIN L27 >gi 2244857 emb_CAB10279.1_ NCBI Description (Z97337) ribosomal protein [Arabidopsis thaliana] 411012 Seq. No. uC-osflcyp061a10b1 Seq. ID Method BLASTX g5903036 NCBI GI BLAST score 303 2.0e-27 E value Match length 94 % identity 60 (AC008016) F6D8.5 [Arabidopsis thaliana] NCBI Description Seq. No. 411013 uC-osflcyp061a11b1 Seq. ID BLASTX Method g1709620 NCBI GI BLAST score 292 3.0e-26 E value 124 Match length 52 % identity PROTEIN DISULFIDE ISOMERASE PRECURSOR (PDI) >gi_508975 NCBI Description (U11496) protein disulfide isomerase [Triticum aestivum] >gi 1094851_prf__2106410A protein disulfide isomerase [Triticum aestivum] 411014 Seq. No. uC-osflcyp061b01b1 Seq. ID BLASTN Method g4680189 NCBI GI BLAST score 36 E value 2.0e-10

Match length 60 90 % identity

Oryza sativa subsp. indica putative dnaJ-like protein, NCBI Description

putative myb-related protein, putative farnesyl

pyrophosphate synthase, and hypothetical protein genes,

complete cds

411015 Seq. No.

uC-osflcyp061b02b1 Seq. ID

Method BLASTX

```
g4200122
NCBI GI
BLAST score
                  158
                  2.0e-10
E value
Match length
                  40
                  72
% identity
                  (AJ009555) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                  411016
Seq. No.
                  uC-osflcyp061b03b1
Seq. ID
                  BLASTX
Method
                  g2982458
NCBI GI
BLAST score
                  277
                  2.0e-24
E value
                  74
Match length
                  74
% identity
                  (AL022223) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  411017
                  uC-osflcyp061b10b1
Seq. ID
                  BLASTX
Method
                  g4895189
NCBI GI
                  145
BLAST score
                   6.0e-09
E value
                  70
Match length
                   43
% identity
                  (AC007661) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   411018
                  uC-osflcyp061b11b1
Seq. ID
                  BLASTN
Method
                   q5042437
NCBI GI
                   41
BLAST score
                   1.0e-13
E value
                   65
Match length
                   91
% identity
NCBI Description Oryza sativa BAC T49B20 genomic sequence, complete sequence
Seq. No.
                   411019
                   uC-osflcyp061c03b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   q4204265
BLAST score
                   279
                   1.0e-24
E value
                   113
Match length
% identity
                   58
NCBI Description (AC005223) 45643 [Arabidopsis thaliana]
Seq. No.
                   411020
Seq. ID
                   uC-osflcyp061c04b1
                   BLASTX
Method
NCBI GI
                   q1632822
BLAST score
                   673
E value
                   6.0e-71
Match length
                   133
                   97
% identity
                  (Y08962) transmembrane protein [Oryza sativa] >gi_1667594
NCBI Description
                   (U77297) transmembrane protein [Oryza sativa]
```

```
Seq. No.
                  411021
                  uC-osflcyp061c05b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2641619
BLAST score
                  572
                  5.0e-59
E value
Match length
                  114
                  89
% identity
                  (AF032468) ubiquitin-conjugating enzyme protein E2 [Zea
NCBI Description
                  mays]
Seq. No.
                  411022
Seq. ID
                  uC-osflcyp061c06b1
                  BLASTX
Method
NCBI GI
                  q3914685
BLAST score
                  638
                  1.0e-66
E value
Match length
                  144
% identity
                  86
                  60S RIBOSOMAL PROTEIN L17 >gi 2668748 (AF034948) ribosomal
NCBI Description
                  protein L17 [Zea mays]
Seq. No.
                  411023
                  uC-osflcyp061c08b1
Seq. ID
                  BLASTX
Method
NCBI GI
                  g548493
BLAST score
                   408
E value
                  1.0e-39
Match length
                  157
                   52
% identity
NCBI Description EXOPOLYGALACTURONASE PRECURSOR (EXOPG) (PECTINASE)
                   (GALACTURAN 1,4-ALPHA-GALACTURONIDASE)
                   >gi 629854 pir S30067 polygalacturonase - maize
                   >gi 288612 emb CAA47052 (X66422) polygalacturonase [Zea
                  mays]
Seq. No.
                   411024
                   uC-osflcyp061c09b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g4732123
BLAST score
                   249
E value
                   4.0e-21
                   125
Match length
                   50
% identity
NCBI Description (AF129087) mitogen-activated protein kinase homologue
                   [Medicago sativa]
                   411025
Seq. No.
                   uC-osflcyp061c11b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g5903036
BLAST score
                   273
                   6.0e-24
E value
Match length
                   105
                   52
% identity
NCBI Description (AC008016) F6D8.5 [Arabidopsis thaliana]
```

```
411026
Seq. No.
                  uC-osflcyp061d04b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2623248
BLAST score
                   389
                   2.0e-37
E value
Match length
                  167
                   47
% identity
                  (AF030882) SU1 isoamylase [Zea mays]
NCBI Description
Seq. No.
                   411027
                   uC-osflcyp061d05b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g1136120
BLAST score
                   637
                   1.0e-66
E value
Match length
                   124
% identity
                   96
                  (X91806) alpha-tubulin [Oryza sativa]
NCBI Description
Seq. No.
                   411028
Seq. ID
                   uC-osflcyp061d09b1
Method
                   BLASTX
NCBI GI
                   g6093742
BLAST score
                   233
                   3.0e-19
E value
Match length
                   158
% identity
                   36
                   PECTINESTERASE PRECURSOR (PECTIN METHYLESTERASE) (PE) (P65)
NCBI Description
                   >qi 886130 (U28148) putative pectinesterase [Medicago
                   sativa]
                   411029
Seq. No.
                   uC-osflcyp061d10b1
Seq. ID
                   BLASTX
Method
                   g4165488
NCBI GI
BLAST score
                   679
E value
                   2.0e-71
                   170
Match length
% identity
                   81
                  (AJ132399) alpha-tubulin 3 [Hordeum vulgare]
NCBI Description
                   411030
Seq. No.
                   uC-osflcyp061e01b1
Seq. ID
                   BLASTX
Method
                   g5031281
NCBI GI
BLAST score
                   450
                   1.0e-44
E value
Match length
                   136
                   63
% identity
                  (AF139499) unknown [Prunus armeniaca]
NCBI Description
Seq. No.
                   411031
                   uC-osflcyp061e02b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2224915
```

```
BLAST score
                  437
E value
                   4.0e-43
                  92
Match length
                  79
% identity
                  (U95968) beta-expansin [Oryza sativa]
NCBI Description
Seq. No.
                  411032
                  uC-osflcyp061e03b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4115938
BLAST score
                  623
                  6.0e-65
E value
                  171
Match length
                  73
% identity
                  (AF118223) contains similarity several bacterial
NCBI Description
                   glutathione-regulated potassium efflux system proteins
                   [Arabidopsis thaliana]
                   411033
Seq. No.
                  uC-osflcyp061e04b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1769887
BLAST score
                  233
                  7.0e-30
E value
                  145
Match length
                   50
% identity
NCBI Description
                  (X95736) amino acid permease 6 [Arabidopsis thaliana]
                   411034
Seq. No.
                  uC-osflcyp061e09b1
Seq. ID
Method
                  BLASTX
NCBI GI
                   g4056568
BLAST score
                   554
                   7.0e-57
E value
Match length
                  164
                   48
% identity
NCBI Description
                  (U90944) PDI-like protein [Zea mays]
                   411035
Seq. No.
                   uC-osflcyp061e10b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   q1136122
                   735
BLAST score
                   4.0e-78
E value
                   137
Match length
                   99
% identity
NCBI Description
                  (X91807) alfa-tubulin [Oryza sativa]
Seq. No.
                   411036
                   uC-osflcyp061e11b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2498586
BLAST score
                   578
                   1.0e-59
E value
Match length
                   127
% identity
NCBI Description MAJOR POLLEN ALLERGEN ORY S 1 PRECURSOR (ORY S I)
```

```
>gi 1173557 (U31771) Ory s 1 [Oryza sativa]
                  411037
Seq. No.
                  uC-osflcyp061f02b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3805765
BLAST score
                  589
                  5.0e-61
E value
                  161
Match length
                  73
% identity
                  (AC005693) putative protein kinase [Arabidopsis thaliana]
NCBI Description
                  411038
Seq. No.
                  uC-osflcyp061f03b1
Seq. ID
                  BLASTX
Method
NCBI GI
                  q2688830
BLAST score
                  576
E value
                  2.0e-59
                  154
Match length
                  74
% identity
                  (AF000952) putative sugar transporter [Prunus armeniaca]
NCBI Description
                   411039
Seq. No.
                  uC-osflcyp061f05b1
Seq. ID
Method
                  BLASTX
                   q6006363
NCBI GI
                   299
BLAST score
                   5.0e-27
E value
                   59
Match length
                   97
% identity
                  (AP000559) ESTs AU078183(C62904), C73912(E21020) correspond
NCBI Description
                   to a region of the predicted gene.; Similar to water stress
                   inducible protein (U74296) [Oryza sativa]
                   411040
Seq. No.
Seq. ID
                   uC-osflcyp061f07b1
Method
                   BLASTX
NCBI GI
                   q5091608
BLAST score
                   188
                   6.0e-14
E value
Match length
                   39
% identity
                   97
                   (ACO07858) Identical to gb_D50317 ADP glucose
NCBI Description
                   pyrophosphorylase large subunit from Oryza sativa.
                   dbj D22125 and dbj D15718 come from
Seq. No.
                   411041
                   uC-osflcyp061f08b1
Seq. ID
Method
                   BLASTN
NCBI GI
                   g5410347
                   98
BLAST score
E value
                   2.0e-47
                   409
Match length
                   87
% identity
NCBI Description Sorghum bicolor BAC clone 110K5, partial sequence
```

411042

Seq. No.

```
uC-osflcyp061f09b1
Seq. ID
Method
                  BLASTX
                  g2832898
NCBI GI
                  333
BLAST score
E value
                  5.0e-31
                  84
Match length
                  71
% identity
                  (AJ000886) Tetrafunctional protein of glyoxysomal fatty
NCBI Description
                  acid beta-oxidation [Brassica napus]
Seq. No.
                  411043
                  uC-osflcyp061f10b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g122106
                  410
BLAST score
                  5.0e-40
E value
                  82
Match length
                  100
% identity
                  HISTONE H4 >gi_70771_pir__HSZM4 histone H4 - maize
NCBI Description
                  >qi 81642 pir S06904 histone H4 - Arabidopsis thaliana
                  >gi 2119028 pir S60475 histone H4 - garden pea
                  >gi 21795 emb CAA24924 (X00043) histone H4 [Triticum
                  aestivum] >gi_166740 (M17132) histone H4 [Arabidopsis
                  thaliana] >gi_166742 (M17133) histone H4 [Arabidopsis
                  thaliana] >gi 168499 (M36659) histone H4 (H4C13) [Zea mays]
                  >gi 168501 (M13370) histone H4 [Zea mays] >gi_168503
                   (M1\overline{3}377) histone H4 [Zea mays] >gi_498898 (U10042) histone
                  H4 homolog [Pisum sativum] >gi_1806285_emb_CAB01914_
                   (Z79638) histone H4 homologue [Sesbania rostrata]
                  >gi_3927823 (AC005727) histone H4 [Arabidopsis thaliana]
                  >gi 4580385 gb AAD24364.1 AC007184_4 (AC007184) histone H4
                   [Arabidopsis thaliana] >gi_6009915_dbj_BAA85120.1_
                   (AB018245) histone H4-like protein [Solanum melongena]
                  >gi_225838_prf__1314298A histone H4 [Arabidopsis thaliana]
                   411044
Seq. No.
Seq. ID
                  uC-osflcyp061f12b1
Method
                  BLASTX
NCBI GI
                   a4506469
                   271
BLAST score
                   5.0e-24
E value
Match length
                   91
                   66
% identity
                  RecQ protein-like (DNA helicase Q1-like)
NCBI Description
                   >gi_1172898_sp_P46063_RECQ_HUMAN ATP-DEPENDENT DNA HELICASE
                   Q1 >gi 619863 (L36140) DNA helicase [Homo sapiens]
Seq. No.
                   411045
Seq. ID
                   uC-osflcyp061g02b1
Method
                   BLASTX
NCBI GI
                   q2130078
BLAST score
                   446
E value
                   3.0e-44
Match length
                   103
                   84
% identity
NCBI Description MADS-box protein 3 - rice >gi_886405 (L37528) MADS box
                   protein [Oryza sativa]
```

411046 Seq. No. uC-osflcyp061g04b1 Seq. ID Method BLASTX q131205 NCBI GI 178 BLAST score 9.0e-13 E value Match length 36 100 % identity PHOTOSYSTEM I REACTION CENTRE SUBUNIT VIII (PSI-I) NCBI Description >gi 72677 pir A1RZI photosystem I protein psaI - rice chloroplast >gi_11996_emb_CAA33957_ (X15901) ORF36 [Oryza sativa] >gi 226617 prf 1603356AP photosystem I small peptide [Oryza sativa] 411047 Seq. No. Seq. ID uC-osflcyp061g06b1 BLASTX Method NCBI GI g2055230 BLAST score 200 2.0e-15 E value Match length 121 40 % identity NCBI Description (AB000130) SRC2 [Glycine max] 411048 Seq. No. uC-osflcyp061g07b1 Seq. ID BLASTX Method NCBI GI q6094049 557 BLAST score 3.0e-57 E value 111 Match length 97 % identity NCBI Description 60S RIBOSOMAL PROTEIN L30 >gi 2668750 (AF034949) ribosomal protein L30 [Zea mays] 411049 Seq. No. uC-osflcyp061g08b1 Seq. ID BLASTX Method g5042455 NCBI GI 866 BLAST score 2.0e-93 E value 169 Match length 96 % identity NCBI Description (AC007789) NADP-dependent isocitrate dehydrogenase [Oryza sativa] 411050 Seq. No. uC-osflcyp061g10b1 Seq. ID Method BLASTX g3075488 NCBI GI 674 BLAST score 6.0e-71 E value Match length 147 88 % identity NCBI Description (AF058796) chlorophyll a/b-binding protein [Oryza sativa]

BLAST score

201

```
Seq. No.
                  411051
                  uC-osflcyp061g11b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q476752
BLAST score
                  702
                  3.0e-74
E value
Match length
                  150
                  90
% identity
                  (L24073) rubisco large subunit [Oryza sativa]
NCBI Description
                  >gi 1583954 prf__2121489A
                  RuBisCO:SUBUNIT=large:ISOTYPE=truncated [Oryza sativa]
                  411052
Seq. No.
                  uC-osflcyp061g12b1
Seq. ID
Method
                  BLASTX
                  g4678935
NCBI GI
BLAST score
                  344
                  3.0e - 32
E value
                  90
Match length
                  67
% identity
                  (AL049711) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  411053
                  uC-osflcyp061h01b1
Seq. ID
Method
                  BLASTX
                  g1737492
NCBI GI
BLAST score
                  453
E value
                  5.0e-45
Match length
                  120
                  78
% identity
                 (U81318) poly(A)-binding protein [Triticum aestivum]
NCBI Description
                  411054
Seq. No.
                  uC-osflcyp061h02b1
Seq. ID
                  BLASTX
Method
                  g5499713
NCBI GI
BLAST score
                  231
E value
                   5.0e-19
                  126
Match length
                   47
% identity
NCBI Description (U78762) receptor-like kinase ARK1AS [Triticum aestivum]
Seq. No.
                   411055
                  uC-osflcyp061h03b1
Seq. ID
Method
                  BLASTX
                   q2072727
NCBI GI
BLAST score
                   530
E value
                   4.0e-54
Match length
                  104
% identity
                   100
NCBI Description (Y12595) Fd-GOGAT protein [Oryza sativa]
Seq. No.
                   411056
Seq. ID
                   uC-osflcyp061h05b1
Method
                   BLASTX
NCBI GI
                   g4006978
```

Match length

67

E value 2.0e-15 Match length 87 % identity 44 (AJ131335) pollen allergen (group II) [Cynodon dactylon] NCBI Description 411057 Seq. No. uC-osflcyp061h06b1 Seq. ID BLASTX Method g2407281 NCBI GI 731 BLAST score 1.0e-77 E value Match length 143 % identity 97 (AF017363) ribulose 1,5-bisphosphate carboxylase small NCBI Description subunit [Oryza sativa] 411058 Seq. No. uC-osflcyp061h07b1 Seq. ID Method BLASTX q6091734 NCBI GI BLAST score 172 4.0e-12 E value Match length 66 % identity 45 (AC010797) hypothetical protein [Arabidopsis thaliana] NCBI Description 411059 Seq. No. Seq. ID uC-osflcyp061h08b1 Method BLASTX g5042455 NCBI GI BLAST score 312 1.0e-28 E value Match length 142 51 % identity (AC007789) NADP-dependent isocitrate dehydrogenase [Oryza NCBI Description sativa] Seq. No. 411060 uC-osflcyp061h12b1 Seq. ID Method BLASTX NCBI GI q1709563 BLAST score 830 E value 3.0e-89 Match length 169 96 % identity PHENYLALANINE AMMONIA-LYASE >gi_2130081_pir__S66313 NCBI Description phenylalanine ammonia-lyase (EC 4.3.1.5) - rice >gi_871494_emb_CAA61198_ (X87946) phenylalanine ammonia-lyase [Oryza sativa] 411061 Seq. No. uC-osflcyp062a02a1 Seq. ID Method BLASTX NCBI GI g3123264 BLAST score 169 E value 9.0e-12

```
% identity
                  58
                  60S RIBOSOMAL PROTEIN L27 >gi 2244857 emb CAB10279.1
NCBI Description
                  (Z97337) ribosomal protein [Arabidopsis thaliana]
                  411062
Seq. No.
                  uC-osflcyp062b09a1
Seq. ID
Method
                  BLASTX
                  g2708744
NCBI GI
                  148
BLAST score
                  2.0e-09
E value
                  52
Match length
% identity
                  62
                  (AC003952) putative Bop-like zinc finger protein
NCBI Description
                  [Arabidopsis thaliana]
Seq. No.
                  411063
                  uC-osflcyp062b10a1
Seq. ID
Method
                  BLASTN
                  q5042437
NCBI GI
                  41
BLAST score
                  1.0e-13
E value
                  65
Match length
                  91
% identity
NCBI Description Oryza sativa BAC T49B20 genomic sequence, complete sequence
                  411064
Seq. No.
                  uC-osflcyp062c03a1
Seq. ID
Method
                  BLASTX
                  g4680190
NCBI GI
                  211
BLAST score
                  1.0e-16
E value
Match length
                  54
                  81
% identity
                  (AF111710) putative dnaJ-like protein [Oryza sativa subsp.
NCBI Description
                  indica]
Seq. No.
                  411065
                  uC-osflcyp062c04a1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2641619
BLAST score
                  371
E value
                   2.0e-35
Match length
                  86
% identity
                  81
                  (AF032468) ubiquitin-conjugating enzyme protein E2 [Zea
NCBI Description
                  mays]
Seq. No.
                   411066
Seq. ID
                  uC-osflcyp062c05a1
Method
                  BLASTX
NCBI GI
                   g3914685
BLAST score
                   426
E value
                   8.0e-42
Match length
                  101
% identity
                   83
NCBI Description 60S RIBOSOMAL PROTEIN L17 >gi 2668748 (AF034948) ribosomal
                  protein L17 [Zea mays]
```

```
411067
Seq. No.
                  uC-osflcyp062d04a1
Seq. ID
                  BLASTX
Method
NCBI GI
                  q4098272
                  298
BLAST score
                  1.0e-27
E value
                  68
Match length
                  99
% identity
                  (U76558) alpha-tubulin [Triticum aestivum]
NCBI Description
                  411068
Seq. No.
                  uC-osflcyp062d06a1
Seq. ID
                  BLASTX
Method
                  g4101703
NCBI GI
                  140
BLAST score
                   9.0e-09
E value
                   33
Match length
                   70
% identity
                  (AF006078) glucose acyltransferase [Solanum berthaultii]
NCBI Description
                   411069
Seq. No.
                   uC-osflcyp062e08a1
Seq. ID
                   BLASTX
Method
                   g4056568
NCBI GI
                   372
BLAST score
                   2.0e-35
E value
                   113
Match length
                   65
% identity
NCBI Description (U90944) PDI-like protein [Zea mays]
                   411070
Seq. No.
                   uC-osflcyp062e10a1
Seq. ID
                   BLASTX
Method
                   q1136122
NCBI GI
BLAST score
                   193
E value
                   1.0e-14
Match length
                   61
                   66
% identity
NCBI Description (X91807) alfa-tubulin [Oryza sativa]
Seq. No.
                   411071
                   uC-osflcyp062e12a1
Seq. ID
Method
                   BLASTN
NCBI GI
                   g1136121
BLAST score
                   203
E value
                   1.0e-110
                   371
Match length
                   89
% identity
NCBI Description O.sativa mRNA for alpha-tubulin (clone OSTA-136)
Seq. No.
                   411072
                   uC-osflcyp062f04a1
Seq. ID
                   BLASTN
Method
                   g6006355
NCBI GI
BLAST score
                   110
                   9.0e-55
E value
```

Match length 292 % identity 88 NCBI Description Oryza sativa genomic DNA, chromosome 6, clone:P0493C11 Seq. No. 411073 uC-osflcyp062f05a1 Seq. ID BLASTN Method NCBI GI q1296954 BLAST score 108 1.0e-53E value Match length 272 85 % identity NCBI Description O.sativa mRNA for novel protein, osr40c1 Seq. No. 411074 Seq. ID uC-osflcyp062f12a1 Method BLASTX NCBI GI g1136122 BLAST score 273 4.0e-32 E value Match length 84 % identity 90 NCBI Description (X91807) alfa-tubulin [Oryza sativa] Seq. No. 411075 uC-osflcyp062g01a1 Seq. ID Method BLASTX NCBI GI q4510383 BLAST score 311 1.0e-28 E value Match length 94 67 % identity NCBI Description (AC007017) unknown protein [Arabidopsis thaliana] 411076 Seq. No. uC-osflcyp062g07a1 Seq. ID Method BLASTN NCBI GI g5042437 BLAST score 414 E value 0.0e + 00Match length 507 99 % identity NCBI Description Oryza sativa BAC T49B20 genomic sequence, complete sequence 411077 Seq. No. uC-osflcyp062g09a1 Seq. ID Method BLASTN NCBI GI g5091597 BLAST score 50 6.0e-19 E value Match length 142 % identity NCBI Description Oryza sativa chromosome 1 BAC 10A19I, complete sequence

Seq. No. 411078

Seq. ID uC-osflcyp062g12a1

Method BLASTX

NCBI GI g1806283 BLAST score 302 E value 2.0e-27 Match length 61 % identity 98 NCBI Description (Z79637) Histone H4 homologue [Sesbania rostrata] Seq. No. 411079 Seq. ID uC-osflcyp062h01a1 Method BLASTX NCBI GI g1737492 BLAST score 263 E value 7.0e-23 Match length 64 % identity 88 NCBI Description (U81318) poly(A)-binding protein [Triticum aestivum] Seq. No. 411080 Seq. ID uC-osflcyp062h02a1 Method BLASTN NCBI GI g5042437 BLAST score 49 E value 2.0e-18 Match length 133 % identity 84 NCBI Description Oryza sativa BAC T49B20 genomic sequence, complete sequence

Seq. No. 411081

Seq. ID uC-osflcyp062h04a1

Method BLASTX NCBI GI q132105 BLAST score 676 E value 3.0e-71Match length 131 % identity 95

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR

(RUBISCO SMALL SUBUNIT C) >gi_68094_pir__RKRZS9

ribulose-bisphosphate carboxy \overline{l} ase ($\overline{E}C$ 4.1.1.39) small chain precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_

(D00643) small subunit of ribulose-1,5-bisphosphate

carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa] >gi_226375_prf__1508256A ribulose bisphosphate

carboxylase S [Oryza sativa]

Seq. No. 411082

Seq. ID uC-osflcyp062h06a1

Method BLASTN NCBI GI g11957 BLAST score 376 E value 0.0e+00Match length 464 % identity 96

NCBI Description Rice complete chloroplast genome

Seq. No. 411083

Seq. ID uC-osflcyp062h11a1

Method BLASTN g11957 NCBI GI BLAST score 319 E value 1.0e-179 Match length 471 98 % identity NCBI Description Rice complete chloroplast genome Seq. No. 411084 Seq. ID uC-osflcyp062h12a1 Method BLASTX NCBI GI g2326947 Ī55 BLAST score E value 3.0e-10 Match length 35 % identity 80 NCBI Description (Z50801) Chlorophyll a/b-binding protein CP29 precursor [Zea mays] Seq. No. 411085 Seq. ID uC-osflcyp064a02b1 Method BLASTX NCBI GI q5917803 BLAST score 344 E value 1.0e-50 Match length 157 % identity 75 NCBI Description (AF185635) S-adenosyl-L-homocysteinase [Lupinus luteus] Seq. No. 411086 Seq. ID uC-osflcyp064a04b1 Method BLASTX NCBI GI g2088647 BLAST score 541 E value 2.0e-55 Match length 151 % identity 69 NCBI Description (AF002109) hypothetical protein [Arabidopsis thaliana] >gi_3158394 (AF036340) LRR-containing F-box protein [Arabidopsis thaliana] Seq. No. 411087 Seq. ID uC-osflcyp064a05b1 Method BLASTX NCBI GI g4406775 BLAST score 158 E value 1.0e-10

Match length 113 % identity

NCBI Description (AC006836) unknown protein [Arabidopsis thaliana]

Seq. No. 411088

Seq. ID uC-osflcyp064a06b1

Method BLASTX NCBI GI g1209251 BLAST score 180 E value 4.0e-13

```
Match length
                   114
% identity
                   38
NCBI Description (L36883) thionin [Hordeum vulgare]
Seq. No.
                   411089
Seq. ID
                   uC-osflcyp064a08b1
Method
                   BLASTX
NCBI GI
                   q4490728
BLAST score
                   290
E value
                   7.0e-26
Match length
                   65
% identity
                   75
NCBI Description (AL035709) putative protein [Arabidopsis thaliana]
Seq. No.
                   411090
Seq. ID
                   uC-osflcyp064a09b1
Method
                   BLASTX
NCBI GI
                   g5596484
BLAST score
                   635
E value
                   2.0e-66
Match length
                   161
                   80
% identity
NCBI Description (AL096882) beta-adaptin-like protein [Arabidopsis thaliana]
Seq. No.
                   411091
Seq. ID
                  uC-osflcyp064a10b1
Method
                  BLASTX
NCBI GI
                   q4337175
BLAST score
                  230
E value
                   6.0e-19
Match length
                  129
% identity
                   41
NCBI Description
                   (AC006416) ESTs gb_T20589, gb_T04648, gb_AA597906,
                   gb_T04111, gb_R84180, gb_R65428, gb_T44439, gb T76570,
                  gb_R90004, gb_T45020, gb_T42457, gb_T20921, gb_AA042762 and
                  gb_AA720210 come from this gene. [Arabidopsis thaliana]
Seq. No.
                   411092
Seq. ID
                  uC-osflcyp064a11b1
Method
                  BLASTX
NCBI GI
                  g5669871
BLAST score
                  323
E value
                  3.0e-30
Match length
                  75
% identity
                  80
NCBI Description (AF135014) dihydrolipoamide S-acetyltransferase [Zea mays]
Seq. No.
                  411093
Seq. ID
                  uC-osflcyp064a12b1
Method
                  BLASTX
NCBI GI
                  q1076746
BLAST score
                  338
E value
                  6.0e-32
Match length
                  93
% identity
                  74
NCBI Description
                  heat shock protein 70 - rice (fragment)
                  >gi_763160_emb_CAA47948_ (X67711) heat shock protein 70
```

```
[Oryza sativa]
                   411094
Seq. No.
Seq. ID
                   uC-osflcyp064b03b1
Method
                   BLASTX
NCBI GI
                   g3559805
BLAST score
                   435
E value
                   1.0e-48
Match length
                   145
% identity
                   60
NCBI Description
                   (AJ006787) putative phytochelatin synthetase [Arabidopsis
                   thaliana]
                   411095
Seq. No.
Seq. ID
                   uC-osflcyp064b04b1
Method
                   BLASTX
NCBI GI
                   q3413700
BLAST score
                   485
E value
                   6.0e-49
Match length
                   126
% identity
                   78
NCBI Description (AC004747) putative YME1 protein [Arabidopsis thaliana]
                   411096
Seq. No.
                   uC-osflcyp064b07b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   a115787
BLAST score
                   406
E value
                   1.0e-39
Match length
                   79
% identity
                   96
NCBI Description
                   CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I
                   CAB-2) (LHCP) >gi_82461_pir__S03706 chlorophyll a/b-binding protein 2R precursor - rice >gi_20182_emb_CAA32109_
                   (X13909) chlorophyll a/b-binding preprotein (AA -28 to 235)
                   [Oryza sativa]
                   411097
Seq. No.
Seq. ID
                   uC-osflcyp064b08b1
Method
                   BLASTX
NCBI GI
                   g2832641
BLAST score
                   482
E value
                   2.0e-48
Match length
                   155
                   59
% identity
NCBI Description
                   (AL021710) glycolate oxidase - like protein [Arabidopsis
                   thaliana]
Seq. No.
                   411098
Seq. ID
                   uC-osflcyp064b09b1
Method
                   BLASTX
NCBI GI
                   g2119278
BLAST score
                   740
E value
                   9.0e-90
Match length
                   177
% identity
                   89
```

NCBI Description tubulin beta-1 chain - rice

```
411099
Seq. No.
                                                                            15h. .
                  uC-osflcyp064b10b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1084455
                   634
BLAST score
                   3.0e-66
E value
Match length
                  132
                   90
% identity
NCBI Description
                  peptidylprolyl isomerase (EC 5.2.1.8) Cyp2 - rice
                  >gi_600767 (L29469) cyclophilin 2 [Oryza sativa]
Seq. No.
                   411100
                  uC-osflcyp064b11b1
Seq. ID
Method
                  BLASTX
                  g2244847
NCBI GI
BLAST score
                   169
E value
                   1.0e-11
Match length
                   124
                   39
% identity
NCBI Description
                  (Z97337) hydroxyproline-rich glycoprotein homolog
                   [Arabidopsis thaliana]
                   411101
Seq. No.
Seq. ID
                  uC-osflcyp064b12b1
Method
                  BLASTX
NCBI GI
                   q100598
                   529
BLAST score
                   7.0e-54
E value
Match length
                  141
% identity
                   77
NCBI Description ubiquitin / ribosomal protein S27a-1 - barley >gi 167073
                   (M60175) ubiquitin [Hordeum vulgare]
Seq. No.
                   411102
Seq. ID
                  uC-osflcyp064c03b1
Method
                  BLASTX
NCBI GI
                   g5007084
BLAST score
                   488
E value
                   3.0e-49
Match length
                   95
% identity
                   99
                  (AF155333) NADP-specific isocitrate dehydrogenase [Oryza
NCBI Description
                   sativa]
Seq. No.
                   411103
Seq. ID
                  uC-osflcyp064c04b1
Method
                  BLASTX
NCBI GI
                   g1399510
BLAST score
                   387
E value
                  2.0e-54
Match length
                  147
                   78
% identity
NCBI Description (U50064) type A-like cyclin [Zea mays]
Seq. No.
                   411104
                  uC-osflcyp064c06b1
Seq. ID
```

```
BLASTX
Method
                   q417154
NCBI GI
BLAST score
                   655
E value
                   7.0e-69
Match length
                   133
                   98
% identity
NCBI Description
                  HEAT SHOCK PROTEIN 82 >gi_100685_pir__S25541 heat shock
                   protein 82 - rice (strain Taichung Native One)
                   >gi_20256_emb_CAA77978_ (Z11920) heat shock protein 82
                   (HSP82) [Oryza sativa]
                   411105
Seq. No.
Seq. ID
                   uC-osflcyp064c07b1
Method
                   BLASTX
NCBI GI
                   g2688824
BLAST score
                   254
                   1.0e-21
E value
Match length
                   121
                   49
% identity
NCBI Description
                   (U93273) putative auxin-repressed protein [Prunus
                   armeniaca]
                   411106
Seq. No.
Seq. ID
                   uC-osflcyp064c11b1
Method
                   BLASTX
NCBI GI
                   g2493318
BLAST score
                   147
E value
                   3.0e-09
Match length
                   55
                   55
% identity
NCBI Description BLUE COPPER PROTEIN PRECURSOR >gi_562779_emb_CAA80963_
                   (Z25471) blue copper protein [Pisum sativum]
                   >gi 1098264 prf 2115352A blue Cu protein [Pisum sativum]
                   411107
Seq. No.
Seq. ID
                   uC-osflcyp064c12b1
Method
                   BLASTX
NCBI GI
                   q5881940
BLAST score
                   187
E value
                   1.0e-22
Match length
                   148
% identity
NCBI Description
                   (AL117387) putative secreted protein [Streptomyces
                   coelicolor A3(2)]
Seq. No.
                   411108
Seq. ID
                   uC-osflcyp064d01b1
Method
                   BLASTX
NCBI GI
                   g2293480
BLAST score
                   449
E value
                   1.0e-44
Match length
                  89
% identity
                   98
NCBI Description
                  (AF011331) glycine-rich protein [Oryza sativa]
Seq. No.
                   411109
Seq. ID
                  uC-osflcyp064d04b1
```

Method BLASTX NCBI GI a3646373 BLAST score 835 E value 8.0e-90 Match length 156 99 % identity NCBI Description (AJ011078) RGP1 protein [Oryza sativa] Seq. No. 411110 Seq. ID uC-osflcyp064d05b1 Method BLASTX NCBI GI g3549667 BLAST score 518 E value 9.0e-53 Match length 147 % identity 69 (AL031394) Arabidopsis dynamin-like protein ADL2 NCBI Description [Arabidopsis thaliana] Seq. No. 411111 uC-osflcyp064d10b1 Seq. ID Method BLASTX g3860264 NCBI GI BLAST score 395 E value 3.0e-38 Match length 116 % identity 66 NCBI Description (AC005824) unknown protein [Arabidopsis thaliana] 411112 Seq. No. Seq. ID uC-osflcyp064d12b1 Method BLASTX NCBI GI q4836509 BLAST score 209 E value 2.0e-16 Match length 85 % identity 48 NCBI Description (AF124785) NADH-ubiquinone oxidoreductase 18 kDa IP subunit [Mus musculus] Seq. No. 411113 Seq. ID uC-osflcyp064e01b1 Method BLASTX NCBI GI g2662343 BLAST score 792 E value 9.0e-85 Match length 154 98 % identity NCBI Description (D63581) EF-1 alpha [Oryza sativa] Seq. No. 411114

Seq. ID uC-osflcyp064e02b1

Method BLASTX NCBI GI g730547 BLAST score 345 E value 8.0e-33 Match length 85

% identity 78 NCBI Description 60S RIBOSOMAL PROTEIN L27 >gi 6010292 emb CAB57298.1 (Z30162) 60S ribosomal protein L27 [Solanum tuberosum] 411115 Seq. No. uC-osflcyp064e05b1 Seq. ID Method BLASTX NCBI GI g2662341 851 BLAST score E value 1.0e-91 Match length 161 100 % identity (D63580) EF-1 alpha [Oryza sativa] NCBI Description >gi_2662345_dbj_BAA23659_ (D63582) EF-1 alpha [Oryza satīva] >gi_2662347_dbj_BAA23660_ (D63583) EF-1 alpha [Oryza sativa] 411116 Seq. No. uC-osflcyp064e07a1 Seq. ID Method BLASTX NCBI GI g3212879 BLAST score 281 5.0e-25 E value 75 Match length 67 % identity (AC004005) putative ribosomal protein L7 [Arabidopsis NCBI Description thaliana] 411117 Seq. No. uC-osflcyp064e07b1 Seq. ID Method

Method BLASTX
NCBI GI g445613
BLAST score 645
E value 2.0e-67
Match length 177
% identity 68

NCBI Description ribosomal protein L7 [Solanum tuberosum]

Seq. No. 411118

Seq. ID uC-osflcyp064e08b1

Method BLASTN
NCBI GI g4680189
BLAST score 35
E value 6.0e-10
Match length 51
% identity 92

NCBI Description Oryza sativa subsp. indica putative dnaJ-like protein,

putative myb-related protein, putative farnesyl

pyrophosphate synthase, and hypothetical protein genes,

complete cds

Seq. No. 411119

Seq. ID uC-osflcyp064e09b1

Method BLASTX
NCBI GI g4582436
BLAST score 686
E value 3.0e-72

% identity

NCBI Description



```
Match length
                   175
% identity
                   76
NCBI Description (AC007196) unknown protein [Arabidopsis thaliana]
Seq. No.
                   411120
Seq. ID
                   uC-osflcyp064e11b1
Method
                   BLASTX
NCBI GI
                   g3004565
BLAST score
                   497
E value
                   4.0e-50
Match length
                   175
% identity
                   57
NCBI Description (AC003673) putative protein kinase [Arabidopsis thaliana]
Seq. No.
                   411121
Seq. ID
                   uC-osflcyp064e12b1
Method
                   BLASTX
NCBI GI
                   g1076809
BLAST score
                   862
E value
                   6.0e-93
Match length
                   179
% identity
                   94
                  H+-transporting ATPase (EC 3.6.1.35) - maize
NCBI Description
                   >gi_758355_emb_CAA59800_ (X85805) H(+)-transporting ATPase
                   [Zea mays]
Seq. No.
                   411122
Seq. ID
                   uC-osflcyp064f01b1
Method
                  BLASTX
NCBI GI
                   g4490316
BLAST score
                   392
E value
                   7.0e-38
Match length
                  172
% identity
                   48
NCBI Description (AL035678) nucellin-like protein [Arabidopsis thaliana]
Seq. No.
                   411123
Seq. ID
                  uC-osflcyp064f03b1
Method
                  BLASTX
NCBI GI
                  g401190
BLAST score
                  629
E value
                  1.0e-65
Match length
                  137
% identity
                  83
NCBI Description
                  THAUMATIN-LIKE PROTEIN PRECURSOR >gi 100715 pir S25551
                  thaumatin-like protein - rice >gi 20376 emb CAA48278
                  (X68197) thaumatin-like protein [Oryza sativa]
Seq. No.
                  411124
Seq. ID
                  uC-osflcyp064f05b1
Method
                  BLASTX
NCBI GI
                  g2791900
BLAST score
                  210
E value
                  1.0e-16
Match length
                  86
```

(AJ000057) PP7 [Arabidopsis thaliana]

Seq. No. 411125 Seq. ID uC-osflcyp064f09b1 Method BLASTX NCBI GI q4200249 BLAST score 153 E value 7.0e-10Match length 105 % identity 32 NCBI Description (AL035297) hypothetical protein [Homo sapiens] Seq. No. 411126 Seq. ID uC-osflcyp064f12b1 Method BLASTX NCBI GI q131192 BLAST score 512 6.0e-52 E value Match length 142 % identity 72 NCBI Description PHOTOSYSTEM I REACTION CENTRE SUBUNIT V PRECURSOR (PHOTOSYSTEM I 9 KD PROTEIN) (PSI-G) >gi_100606_pir__S20937 photosystem I chain V precursor - barley >gi_19091_emb_CAA42727_ (X60158) photosystem I polypeptide PSI-G precursor [Hordeum vulgare] Seq. No. 411127 Seq. ID uC-osflcyp064g02b1 Method BLASTN NCBI GI q12413 BLAST score 64 E value 3.0e-27 Match length 91 % identity 93 Maize chloroplast clpP (3'end), rps12 (exon 1) and rp120 NCBI Description genes for ATP-dependent protease and ribosomal proteins S12/L20 Seq. No. 411128 Seq. ID uC-osflcyp064g03b1 Method BLASTX NCBI GI g5688947 BLAST score 201 E value 1.0e-15 Match length 44 % identity NCBI Description (AB017428) succinate dehydrogenase iron-protein subunit (SDHB) [Oryza sativa] >gi_5688949_dbj_BAA82750.1 (AB017429) succinate dehydrogenase iron-protein subunit (SDHB) [Oryza sativa] Seq. No. 411129

Seq. ID uC-osflcyp064g04b1

Method BLASTX
NCBI GI g3122386
BLAST score 442
E value 8.0e-44
Match length 88

```
% identity
NCBI Description WD-40 REPEAT PROTEIN MSI1 >qi 2394227 (AF016845) WD-40
                  repeat protein [Lycopersicon esculentum]
Seq. No.
                  411130
Seq. ID
                  uC-osflcyp064g05b1
Method
                  BLASTX
NCBI GI
                  q4377294
BLAST score
                  151
E value
                   1.0e-09
Match length
                  139
% identity
                   32
NCBI Description
                  (AE001677) Tyrosine Transport [Chlamydia pneumoniae]
                  >gi_4377296_gb_AAD19107_ (AE001677) Tyrosine Transport
                   [Chlamydia pneumoniae]
Seq. No.
                   411131
Seq. ID
                  uC-osflcyp064g07b1
Method
                  BLASTX
NCBI GI
                  q6056196
BLAST score
                  471
E value
                  4.0e-47
Match length
                  138
% identity
                  68
NCBI Description (AC009400) unknown protein [Arabidopsis thaliana]
Seq. No.
                  411132
                  uC-osflcyp064g08b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3294467
BLAST score
                  878
E value
                  8.0e-95
Match length
                  177
% identity
                  95
NCBI Description (U89341) phosphoglucomutase 1 [Zea mays]
Seq. No.
                   411133
Seq. ID
                  uC-osflcyp064g10b1
Method
                  BLASTX
NCBI GI
                  g2407281
BLAST score
                  242
E value
                   6.0e-27
Match length
                  78
                  76
% identity
NCBI Description (AF017363) ribulose 1,5-bisphosphate carboxylase small
                  subunit [Oryza sativa]
Seq. No.
                   411134
Seq. ID
                  uC-osflcyp064g12b1
Method
                  BLASTX
NCBI GI
                  g4874313
BLAST score
                  303
E value
                  2.0e-27
Match length
                  109
% identity
                  (AC006053) putative proton phosphatase [Arabidopsis
NCBI Description
                  thaliana]
```

Seq. No.

411140

Seq. No. 411135 Seq. ID uC-osflcyp064h02b1 Method BLASTX NCBI GI g730456 BLAST score 716 E value 7.0e-76 Match length 140 % identity 98 NCBI Description 40S RIBOSOMAL PROTEIN S19 Seq. No. 411136 uC-osflcyp064h06b1 Seq. ID Method BLASTX NCBI GI a2493650 BLAST score 536 E value 6.0e-55Match length 121 93 % identity NCBI Description RUBISCO SUBUNIT BINDING-PROTEIN BETA SUBUNIT (60 KD CHAPERONIN BETA SUBUNIT) (CPN-60 BETA) >gi_1167858_emb_CAA93139_ (Z68903) chaperonin [Secale cereale] Seq. No. 411137 Seq. ID uC-osflcyp064h07b1 Method BLASTX NCBI GI q5816996 BLAST score 524 E value 2.0e-53 Match length 132 % identity 77 NCBI Description (AL110123) ribosomal protein L32-like protein [Arabidopsis thaliana] Seq. No. 411138 Seq. ID uC-osflcyp064h09b1 Method BLASTX NCBI GI q2980775 BLAST score 160 E value 9.0e-11 77 Match length % identity 51 NCBI Description (AL022198) leucyl aminopeptidase-like protein (partial) [Arabidopsis thaliana] Seq. No. 411139 Seq. ID uC-osflcyp064h11b1 Method BLASTX NCBI GI g1076722 BLAST score 416 E value 1.0e-40 93 Match length % identity NCBI Description hypothetical protein - barley (fragment)

uC-osflcyp064h12b1 Seq. ID Method BLASTX g4586249 NCBI GI BLAST score 281 5.0e-25 E value Match length 116 % identity 48 (AL049640) putative pollen surface protein [Arabidopsis NCBI Description thaliana] Seq. No. 411141 uC-osflcyp065a01b1 Seq. ID Method BLASTX NCBI GI g1009232 BLAST score 202 1.0e-15 E value Match length 49 % identity 80 (L38828) EF-1-alpha-related GTP-binding protein [Nicotiana NCBI Description tabacum] 411142 Seq. No. uC-osflcyp065a03b1 Seq. ID BLASTX Method NCBI GI g2662310 BLAST score 645 E value 1.0e-67 Match length 139 88 % identity NCBI Description (AB009307) bpw1 [Hordeum vulgare] 411143 Seq. No. uC-osflcyp065a05b1 Seq. ID Method BLASTX NCBI GI g3914425 BLAST score 411 E value 2.0e-60 Match length 175 % identity 70 NCBI Description PROTEASOME EPSILON CHAIN PRECURSOR (MACROPAIN EPSILON CHAIN) (MULTICATALYTIC ENDOPEPTIDASE COMPLEX EPSILON CHAIN) >gi_2511596_emb_CAA74029.1_ (Y13695) multicatalytic endopeptidase complex, proteasome precursor, beta subunit [Arabidopsis thaliana] >gi_3421117 (AF043536) 20S proteasome beta subunit PBE1 [Arabidopsis thaliana] >gi 4850389 gb AAD31059.1 AC007357 8 (AC007357) Identical to gb Y13695 multicatalytic endopeptidase complex, proteasome precursor, beta subunit (prce) from Arabidopsis thaliana. ESTs gb_Y09360, gb_F13852, gb_T20555, gb_T44620, gb_AI099779 and gb_AA5861 Seq. No. 411144

Seq. ID uC-osflcyp065a06b1

Method BLASTX
NCBI GI g4689108
BLAST score 156
E value 3.0e-10

Match length 46 % identity 57 (AF077030) hypothetical 43.2 kDa protein [Homo sapiens] NCBI Description >gi 4929577 gb AAD34049.1_AF151812_1 (AF151812) CGI-54 protein [Homo sapiens] Seq. No. 411145 Seq. ID uC-osflcyp065a07b1 Method BLASTX NCBI GI g2130069 BLAST score 780 E value 2.0e-83 Match length 158 % identity 93 NCBI Description catalase (EC 1.11.1.6) catA - rice >gi_1261858_dbj_BAA06232 (D29966) catalase [Oryza sativa] Seq. No. 411146 Seq. ID uC-osflcyp065a08b1 Method BLASTX NCBI GI g1871192 BLAST score 632 E value 5.0e-66 Match length 151 % identity 76 NCBI Description (U90439) Cys3His zinc finger protein isolog [Arabidopsis thaliana] Seq. No. 411147 Seq. ID uC-osflcyp065a09b1 Method BLASTX NCBI GI q4503609 BLAST score 267 E value 1.0e-23 Match length 84 % identity 62 NCBI Description electron-transfer-flavoprotein, beta polypeptide >gi_585110_sp_P38117_ETFB_HUMAN ELECTRON TRANSFER FLAVOPROTEIN BETA-SUBUNIT (BETA-ETF) >gi_479194_pir__\$32482 electron transfer flavoprotein beta chain - human >gi_2781203_pdb_1EFV_B Chain B, Three-Dimensional Structure Of Human Electron Transfer Flavoprotein To 2.1 A Resolution >gi_297902_emb_CAA50441 (X71129) electron transfer flavoprotein beta subunit [Homo sapiens] Seq. No. 411148 Seq. ID uC-osflcyp065a12b1 Method BLASTX NCBI GI q3080398 BLAST score 500

Method BLASTX
NCBI GI g3080398
BLAST score 500
E value 1.0e-50
Match length 137
% identity 32

NCBI Description (AL022603) putative protein [Arabidopsis thaliana]

Seq. No. 411149

Seq. ID uC-osflcyp065b01b1

NCBI GI

BLAST score

g3107903

155

```
Method
                   BLASTX
NCBI GI
                   g3868758
                   594
BLAST score
E value
                   1.0e-61
Match length
                   135
                   81
% identity
NCBI Description
                  (D89802) elongation factor 1B gamma [Oryza sativa]
Seq. No.
                   411150
Seq. ID
                   uC-osflcyp065b03a1
Method
                   BLASTX
NCBI GI
                   g1841464
BLAST score
                   192
                   2.0e-14
E value
Match length
                   45
% identity
                   76
NCBI Description
                  (Y11002) LIM-domain SF3 protein [Nicotiana tabacum]
                   >gi_5932420_gb_AAD56951.1_AF184886_1 (AF184886) LIM domain
                  protein WLIM2 [Nicotiana tabacum]
Seq. No.
                   411151
                  uC-osflcyp065b07b1
Seq. ID
Method
                  BLASTX
NCBI GI
                   q4538959
                   304
BLAST score
E value
                   1.0e-27
Match length
                   84
                   64
% identity
NCBI Description
                  (AL049488) putative protein [Arabidopsis thaliana]
Seq. No.
                   411152
Seq. ID
                  uC-osflcyp065b08b1
Method
                  BLASTX
NCBI GI
                  g3309082
BLAST score
                   470
E value
                   4.0e-47
Match length
                   137
% identity
NCBI Description
                  (AF076251) calcineurin B-like protein 1 [Arabidopsis
                  thaliana]
Seq. No.
                   411153
Seq. ID
                  uC-osflcyp065b09b1
Method
                  BLASTX
NCBI GI
                  q3386614
BLAST score
                  497
E value
                  3.0e-50
Match length
                  137
% identity
                  43
NCBI Description
                  (AC004665) putative transcription factor SF3 [Arabidopsis
                  thaliana]
Seq. No.
                  411154
Seq. ID
                  uC-osflcyp065b11a1
Method
                  BLASTX
```

```
E value
                   4.0e-10
Match length
                   59
% identity
NCBI Description (D83719) polycomb-like protein [Daucus carota]
                   411155
Seq. No.
Seq. ID
                   uC-osflcyp065b11b1
Method
                   BLASTX
NCBI GI
                   q3461848
BLAST score
                   687
E value
                   2.0e-72
Match length
                   159
                   87
% identity
NCBI Description (AC005315) putative ATPase [Arabidopsis thaliana]
Seq. No.
                   411156
Seq. ID
                   uC-osflcyp065c01b1
Method
                   BLASTX
NCBI GI
                   g2129579
BLAST score
                   754
                   2.0e-80
E value
Match length
                   158
% identity
                   84
NCBI Description
                  Dwarf1 protein - Arabidopsis thaliana >gi 516043 (U12400)
                   Dwarf1 [Arabidopsis thaliana]
Seq. No.
                   411157
                   uC-osflcyp065c03b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2352492
BLAST score
                   274
E value
                   5.0e-24
Match length
                   98
% identity
                   56
NCBI Description
                   (AF005047) transport inhibitor response 1 [Arabidopsis
                   thaliana] >gi_2352494 (AF005048) transport inhibitor
                   response 1 [Arabidopsis thaliana]
Seq. No.
                   411158
Seq. ID
                   uC-osflcyp065c07b1
Method
                   BLASTX
NCBI GI
                   g2772934
BLAST score
                   406
E value
                   2.0e-39
Match length
                   126
% identity
                   59
NCBI Description
                   (AF030357) C-8,7 sterol isomerase; aSI1 [Arabidopsis
                   thaliana]
                   411159
Seq. No.
Seq. ID
                   uC-osflcyp065c08b1
Method
                  BLASTX
NCBI GI
                   g4210948
BLAST score
                  768
E value
                   6.0e-82
Match length
                  160
                  86
% identity
```

```
NCBI Description (AF085275) DnaJ protein [Hevea brasiliensis]
Seq. No.
                  411160
Seq. ID
                  uC-osflcyp065c09b1
Method
                  BLASTX
NCBI GI
                  g5915857
BLAST score
                  745
E value
                  4.0e-79
Match length
                  159
% identity
                  91
NCBI Description CYTOCHROME P450 98A1 >gi_2766448 (AF029856) cytochrome P450
                  CYP98A1 [Sorghum bicolor]
                  411161
Seq. No.
                  uC-osflcyp065c11b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4531437
BLAST score
                  425
                  9.0e-42
E value
Match length
                  136
% identity
                  63
NCBI Description (AC006224) putative isopropylmalate dehydratase
                  [Arabidopsis thaliana]
Seq. No.
                  411162
                  uC-osflcyp065d02b1
Seq. ID
Method
                  BLASTX
                  q3668091
NCBI GI
                  197
BLAST score
                  5.0e-15
E value
Match length
                  130
% identity
                  32
NCBI Description (AC004667) hypothetical protein [Arabidopsis thaliana]
                  411163
Seq. No.
Seq. ID
                  uC-osflcyp065d05b1
Method
                  BLASTN
NCBI GI
                  g6041757
BLAST score
                  39
E value
                  2.0e-12
Match length
                  55
% identity
                  93
NCBI Description Genomic Sequence For Oryza sativa Clone 10P20, Lemont
                  Strain, Complete Sequence, complete sequence
Seq. No.
                  411164
                  uC-osflcyp065d07b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1730621
BLAST score
                  198
E value
                   4.0e-15
Match length
                  75
                  52
% identity
                  HYPOTHETICAL 48.1 KD PROTEIN IN TUB1-CPR3 INTERGENIC REGION
NCBI Description
                  >gi 630106 pir S48817 hypothetical protein YML079w - yeast
                   (Saccharomyces cerevisiae) >gi_587531_emb_CAA86498_
                   (Z46373) orf, len: 423, CAI: 0.18, 27.4% identity in 307 aa
```

BLAST score

Match length

% identity

E value

644

160 79

2.0e-67

overlap with S36201 S36201 hypothetical protein 1 - Rhizobium leguminosarum [Saccharomyces cerevisiae]

Seq. No. 411165 Seq. ID uC-osflcyp065d08b1 Method BLASTX NCBI GI q730512 309 BLAST score E value 1.0e-30 Match length 84 84 % identity NCBI Description RAS-RELATED PROTEIN RIC2 >gi 481506 pir S38741 GTP-binding protein ric2 - rice >gi_218228_dbj_BAA02904 (D13758) ras-related GTP binding protein [Oryza sativa] Seq. No. 411166 Seq. ID uC-osflcyp065d09b1 Method BLASTX NCBI GI g1346764 BLAST score 491 E value 2.0e-49 Match length 115 87 % identity NCBI Description SERINE/THREONINE PROTEIN PHOSPHATASE PP1 >gi_951336_gb_AAA74625_ (U31773) protein phosphatase 1 [Oryza sativa] Seq. No. 411167 Seq. ID uC-osflcyp065d11b1 Method BLASTX NCBI GI q4191791 BLAST score 402 E value 4.0e-39 Match length 124 % identity NCBI Description (AC005917) putative sf21 {Helianthus annuus} protein [Arabidopsis thaliana] Seq. No. 411168 Seq. ID uC-osflcyp065e01b1 Method BLASTX NCBI GI g3386614 BLAST score 441 E value 8.0e-44Match length 120 % identity (AC004665) putative transcription factor SF3 [Arabidopsis NCBI Description thaliana] Seq. No. 411169 Seq. ID uC-osflcyp065e02b1 Method BLASTX NCBI GI g3882355

```
NCBI Description
                  (U92460) 12-oxophytodienoate reductase OPR1 [Arabidopsis
                   thaliana]
Seq. No.
                   411170
Seq. ID
                  uC-osflcyp065e03b1
Method
                  BLASTX
NCBI GI
                  g541855
BLAST score
                  496
                  4.0e-50
E value
Match length
                  164
% identity
                  54
NCBI Description cycloartenol synthase (EC 5.4.99.8) - Arabidopsis thaliana
Seq. No.
                  411171
                  uC-osflcyp065e09a1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g5042437
BLAST score
                   403
                  0.0e+00
E value
                  415
Match length
                  100
% identity
NCBI Description Oryza sativa BAC T49B20 genomic sequence, complete sequence
Seq. No.
                  411172
                  uC-osflcyp065e09b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g5042455
                  540
BLAST score
                  2.0e-55
E value
                  115
Match length
                  90
% identity
NCBI Description
                  (AC007789) NADP-dependent isocitrate dehydrogenase [Oryza
                  sativa]
Seq. No.
                   411173
Seq. ID
                  uC-osflcyp065e11b1
Method
                  BLASTX
NCBI GI
                  q1136122
BLAST score
                  701
E value
                   4.0e-74
Match length
                  131
% identity
NCBI Description (X91807) alfa-tubulin [Oryza sativa]
                   411174
Seq. No.
Seq. ID
                  uC-osflcyp065f01b1
Method
                  BLASTX
NCBI GI
                  g2464913
BLAST score
                  167
E value
                   1.0e-11
Match length
                  134
```

Seq. No. 411175

% identity

NCBI Description

Seq. ID uC-osflcyp065f05a1

thaliana]

(Z99708) sugar transporter like protein [Arabidopsis

Method BLASTX g5091509 NCBI GI BLAST score 266 E value 3.0e-23 Match length 48 98 % identity NCBI Description (AB023482) EST AU065533(C2174) corresponds to a region of the predicted gene.; Similar to Homo sapiens splicing factor Prp8 mRNA, complete cds.(AF092565) [Oryza sativa] 411176 Seq. No. Seq. ID uC-osflcyp065f06b1 Method BLASTX NCBI GI g5091509 BLAST score 817 E value 1.0e-87 Match length 164 98 % identity NCBI Description (AB023482) EST AU065533(C2174) corresponds to a region of the predicted gene.; Similar to Homo sapiens splicing factor Prp8 mRNA, complete cds.(AF092565) [Oryza sativa] Seq. No. 411177 Seq. ID uC-osflcyp065f08b1 Method BLASTX NCBI GI q4538923 BLAST score 173 E value 2.0e-12 Match length 95 48 % identity (AL049483) predicted protein destination factor NCBI Description [Arabidopsis thaliana] Seq. No. 411178 Seq. ID uC-osflcyp065f10b1 Method BLASTX NCBI GI g2119278 BLAST score 265 E value 6.0e - 30Match length 96 % identity 81 NCBI Description tubulin beta-1 chain - rice Seq. No. 411179 Seq. ID uC-osflcyp065f12b1 Method BLASTX NCBI GI g4585976 BLAST score 228 E value 1.0e-18 Match length 79 % identity

Seq. No. 411180

Seq. ID uC-osflcyp065g02b1

Method BLASTX NCBI GI g68843

NCBI Description (AC005287) Unknown protein [Arabidopsis thaliana]

359 BLAST score 4.0e-34 E value Match length 91 79 % identity NCBI Description phospholipid transfer protein homolog - rice >gi_4139635_pdb_1RZL_ Rice Nonspecific Lipid Transfer Protein >gi_5107522_pdb_1BV2_ Lipid Transfer Protein From Rice Seeds, Nmr, 14 Structures 411181 Seq. No. uC-osflcyp065g06b1 Seq. ID Method BLASTX g549063 NCBI GI 252 BLAST score E value 3.0e-22Match length 65 91 % identity TRANSLATIONALLY CONTROLLED TUMOR PROTEIN HOMOLOG (TCTP) NCBI Description >gi_1072464_pir__A38958 IgE-dependent histamine-releasing factor homolog - rice >gi_303835_dbj_BAA02151 (D12626) 21kd polypeptide [Oryza sativa] Seq. No. 411182 uC-osflcyp065g07b1 Seq. ID Method BLASTN g1619603 NCBI GI BLAST score 37 2.0e-11 E value Match length 53 % identity 92 NCBI Description O.sativa mRNA for lipid transfer protein >gi 1667589 gb U77295 OSU77295 Oryza sativa lipid transfer protein (LTP) mRNA, complete cds Seq. No. 411183 Seq. ID uC-osflcyp065g09a1 Method BLASTX NCBI GI q5902930 BLAST score 323 E value 1.0e-30 Match length 104 % identity NCBI Description (AB029510) small GTP-binding protein OsRac3 [Oryza sativa] 411184 Seq. No. Seq. ID uC-osflcyp065g09b1 Method BLASTX NCBI GI q4959459

Method BLASTX
NCBI GI g4959459
BLAST score 495
E value 1.0e-57
Match length 119
% identity 95

NCBI Description (AF126052) RACA small GTP binding protein [Zea mays]

Seq. No. 411185

Seq. ID uC-osflcyp065g10b1

Method BLASTN



g3582315 NCBI GI BLAST score 48 1.0e-17 E value 56 Match length 96 % identity Arabidopsis thaliana chromosome II BAC T27A16 genomic NCBI Description sequence, complete sequence [Arabidopsis thaliana] 411186 Seq. No. uC-osflcyp065g11b1 Seq. ID BLASTX Method g4417304 NCBI GI 501 BLAST score 1.0e-50 E value 164 Match length % identity 58 (AC006446) putative beta-1,4-mannosyl-glycoprotein NCBI Description beta-1,4-N-acetylglucosaminyltransferase [Arabidopsis thaliana] 411187 Seq. No. uC-osflcyp065h02b1 Seq. ID Method BLASTX g2130069 NCBI GI 630 BLAST score 8.0e-66 E value 143 Match length % identity 8.5 catalase (EC 1.11.1.6) catA - rice NCBI Description >gi 1261858 dbj BAA06232_ (D29966) catalase [Oryza sativa] 411188 Seq. No. uC-osflcyp065h03b1 Seq. ID BLASTX Method NCBI GI g4887131 504 BLAST score E value 4.0e-51 Match length 117 76 % identity NCBI Description (AF134732) 60S ribosomal protein L1 [Prunus armeniaca] Seq. No. 411189 uC-osflcyp065h04b1 Seq. ID Method BLASTX NCBI GI g3868758 BLAST score 602 E value 1.0e-62 Match length 138 % identity

NCBI Description (D89802) elongation factor 1B gamma [Oryza sativa]

Seq. No. 411190

Seq. ID uC-osflcyp065h05a1

Method BLASTX
NCBI GI g3892048
BLAST score 180
E value 9.0e-16

Seq. No.

411196

```
Match length
                   118
% identity
                   53
NCBI Description
                   (AC002330) putative tryptophan synthase alpha 1-like
                  protein [Arabidopsis thaliana]
Seq. No.
                   411191
Seq. ID
                   uC-osflcyp065h06b1
Method
                   BLASTX
NCBI GI
                   g2662343
BLAST score
                   700
E value
                   5.0e-74
Match length
                   136
% identity
                   99
NCBI Description (D63581) EF-1 alpha [Oryza sativa]
Seq. No.
                   411192
Seq. ID
                   uC-osflcyp065h07b1
Method
                   BLASTX
NCBI GI
                   g2370232
BLAST score
                   428
E value
                   3.0e-42
Match length
                   88
% identity
                   94
NCBI Description (AJ001341) putative acyl-CoA oxidase [Hordeum vulgare]
Seq. No.
                   411193
Seq. ID
                   uC-osflcyp065h08b1
Method
                   BLASTX
NCBI GI
                   g4531444
BLAST score
                   345
E value
                   2.0e-32
Match length
                   95
% identity
                   68
NCBI Description (AC006224) putative protein kinase [Arabidopsis thaliana]
Seq. No.
                   411194
Seq. ID
                   uC-osflcyp065h12b1
Method
                   BLASTX
NCBI GI
                   q1808688
BLAST score
                   153
E value
                   6.0e-10
Match length
                  65
                   49
% identity
NCBI Description (Y10784) hypothetical protein [Sporobolus stapfianus]
Seq. No.
                   411195
Seq. ID
                  uC-osflcyp066a01a1
Method
                  BLASTX
NCBI GI
                   g5816996
BLAST score
                   503
E value
                   6.0e-51
Match length
                   105
% identity
NCBI Description
                  (AL110123) ribosomal protein L32-like protein [Arabidopsis
                  thaliana]
```

NCBI GI

```
Seq. ID
                   uC-osflcyp066a02a1
Method
                   BLASTN
                   q6006355
NCBI GI
BLAST score
                   43
E value
                   2.0e-15
Match length
                   63
                   94
% identity
NCBI Description Oryza sativa genomic DNA, chromosome 6, clone:P0493C11
Seq. No.
                   411197
                   uC-osflcyp066a08a1
Seq. ID
Method
                  BLASTX
NCBI GI
                   g2808638
                   164
BLAST score
E value
                   3.0e-11
Match length
                   52
                   73
% identity
NCBI Description (AJ001367) small GTP-binding protein [Daucus carota]
Seq. No.
                   411198
Seq. ID
                  uC-osflcyp066a09a1
Method
                  BLASTX
NCBI GI
                  g2497820
BLAST score
                  321
E value
                   1.0e-29
Match length
                  74
% identity
                  84
NCBI Description
                 DNA REPLICATION LICENSING FACTOR MCM3 HOMOLOG (REPLICATION
                  ORIGIN ACTIVATOR) (ROA PROTEIN) >gi_1076823_pir__$52247
                  probable replication origin activator protein ROA - maize
                   (fragment) > gi\_609290\_emb\_CAA82556\_ (Z29368) ROA protein
                   [Zea mays]
Seq. No.
                  411199
Seq. ID
                  uC-osflcyp066b02a1
Method
                  BLASTX
NCBI GI
                  q3915826
BLAST score
                  227
E value
                  1.0e-18
Match length
                  54
% identity
                  87
NCBI Description 60S RIBOSOMAL PROTEIN L5
Seq. No.
                  411200
Seq. ID
                  uC-osflcyp066b04a1
Method
                  BLASTX
NCBI GI
                  g3687251
BLAST score
                  207
E value
                  3.0e-16
Match length
                  65
% identity
                  62
NCBI Description (AC005169) unknown protein [Arabidopsis thaliana]
Seq. No.
                  411201
Seq. ID
                  uC-osflcyp066b06a1
Method
                  BLASTX
```

53413

g2130105

192 BLAST score 2.0e-14 E value Match length 42 90 % identity histone H2A type 2 (clone wcH2A-4) - wheat NCBI Description >gi_536892_dbj_BAA07278_ (D38089) protein H2A [Triticum
aestivum] >gi_536896_dbj_BAA07280_ (D38091) protein H2A [Triticum aestivum] Seq. No. 411202 uC-osflcyp066b09a1 Seq. ID BLASTX Method NCBI GI q633110 BLAST score 251 E value 2.0e-21 72 Match length 75 % identity NCBI Description (D31843) plasma membrane H+-ATPase [Oryza sativa] 411203 Seq. No. Seq. ID uC-osflcyp066c02a1 Method BLASTX g4127456 NCBI GI 365 BLAST score E value 9.0e-35 92 Match length % identity 38 NCBI Description (AJ010818) Cpn21 protein [Arabidopsis thaliana] Seq. No. 411204 Seq. ID uC-osflcyp066c04a1 Method BLASTX NCBI GI q1170029 238 BLAST score 7.0e-20 E value Match length 60 % identity GLUTAMATE-1-SEMIALDEHYDE 2,1-AMINOMUTASE PRECURSOR (GSA) NCBI Description (GLUTAMATE-1-SEMIALDEHYDE AMINOTRANSFERASE) (GSA-AT) >gi_100581_pir__A35789 glutamate-1-semialdehyde 2,1-aminomutase (EC 5.4.3.8) - barley >gi_506383 (M31545) glutamate 1-semialdehyde aminotransferase [Hordeum vulgare] 411205 Seq. No. Seq. ID uC-osflcyp066c07a1 Method BLASTX NCBI GI g2267597 BLAST score 365 E value 9.0e-35

Match length 84 % identity 88

NCBI Description (AF009413) 10 kDa chaperonin [Oryza sativa]

Seq. No. 411206

Seq. ID uC-osflcyp066c10a1

Method BLASTX NCBI GI g1169528

```
BLAST score
                  448
                  2.0e-44
E value
Match length
                  90
% identity
                  99
NCBI Description ENOLASE 2 (2-PHOSPHOGLYCERATE DEHYDRATASE 2)
                  (2-PHOSPHO-D-GLYCERATE HYDRO-LYASE 2) >gi 602253 (U17973)
                  enolase [Zea mays]
Seq. No.
                  411207
                  uC-osflcyp066c11a1
Seq. ID
Method
                  BLASTX
                  g6094430
NCBI GI
BLAST score
                  337
E value
                  1.0e-31
Match length
                  67
                  97
% identity
NCBI Description TUBULIN ALPHA-2 CHAIN (ALPHA-TUBULIN 2) >gi 2511533
                  (AF008121) alpha-tubulin 2 [Eleusine indica]
                  411208
Seq. No.
Seq. ID
                  uC-osflcyp066d06a1
Method
                  BLASTN
NCBI GI
                  g2773153
BLAST score
                  486
E value
                  0.0e+00
Match length
                  500
% identity
                  99
NCBI Description Oryza sativa abscisic acid- and stress-inducible protein
                  (Asr1) mRNA, complete cds
Seq. No.
                  411209
Seq. ID
                  uC-osflcyp066d10a1
Method
                  BLASTX
NCBI GI
                  g5902930
BLAST score
                  204
E value
                  7.0e-16
Match length
                  45
% identity
                  91
NCBI Description (AB029510) small GTP-binding protein OsRac3 [Oryza sativa]
Seq. No.
                   411210
Seq. ID
                  uC-osflcyp066d12a1
Method
                  BLASTX
NCBI GI
                  g5701965
BLAST score
                  149
E value
                  2.0e-09
Match length
                  65
% identity
                  40
NCBI Description (AL109736) WD repeat protein [Schizosaccharomyces pombe]
Seq. No.
                   411211
Seq. ID
                  uC-osflcyp066e05a1
Method
                  BLASTN
NCBI GI
                  g2570514
BLAST score
                  264
E value
                  1.0e-146
```

Match length

% identity NCBI Description Oryza sativa glycolate oxidase (GOX) mRNA, complete cds 411212 Seq. No. uC-osflcyp066e09a1 Seq. ID BLASTX Method NCBI GI q3288883 BLAST score 502 E value 8.0e-51 102 Match length % identity 98 NCBI Description (AB015431) SAR DNA binding protein [Oryza sativa] 411213 Seq. No. uC-osflcyp066e10a1 Seq. ID Method BLASTN g3288882 NCBI GI BLAST score 85 6.0e-40 E value Match length 165 % identity 88 NCBI Description Oryza sativa mRNA for SAR DNA binding protein, partial cds 411214 Seq. No. uC-osflcyp066f03a1 Seq. ID Method BLASTN NCBI GI q1632821 BLAST score 144 3.0e-75 E value Match length 268 % identity 88 O.sativa mRNA for transmembrane protein NCBI Description >gi_1667593_gb_U77297_OSU77297 Oryza sativa transmembrane protein mRNA, complete cds Seq. No. 411215 uC-osflcyp066f05a1 Seq. ID Method BLASTX g479406 NCBI GI BLAST score 335 E value 3.0e - 31Match length 68 % identity 94 chlorophyll a/b-binding protein - garden pea NCBI Description >gi_20671_emb_CAA49149_ (X69215) chlorophyll a/b-binding
protein [Pisum sativum] 411216 Seq. No. Seq. ID uC-osflcyp066f07a1 Method BLASTX NCBI GI q5733874 BLAST score 184 E value 1.0e-13 72 Match length 43 % identity

NCBI Description (AC007932) F11A17.8 [Arabidopsis thaliana]

Seq. No. 411217 uC-osflcyp066f10a1 Seq. ID Method BLASTX NCBI GI g1136122 BLAST score 336 2.0e-31 E value Match length 66 100 % identity NCBI Description (X91807) alfa-tubulin [Oryza sativa] 411218 Seq. No. uC-osflcyp066f11a1 Seq. ID Method BLASTX g1351270 NCBI GI BLAST score 168 8.0e-12 E value 37 Match length 89 % identity NCBI Description TRIOSEPHOSPHATE ISOMERASE, CYTOSOLIC (TIM) >gi_478410_pir__JQ2255 triose-phosphate isomerase (EC 5.3.1.1) - rice >gi_169821 (M87064) triosephosphate isomerase [Oryza sativa] 411219 Seq. No. Seq. ID uC-osflcyp066f12a1 Method BLASTN g3075487 NCBI GI BLAST score 34 2.0e-09 E value Match length 46 % identity 93 NCBI Description Oryza sativa chlorophyll a/b-binding protein (RCABP69) mRNA, complete cds Seq. No. 411220 Seq. ID uC-osflcyp066g04a1 Method BLASTX NCBI GI g3169182 BLAST score 283 E value 3.0e-25Match length 62 % identity NCBI Description (AC004401) unknown protein [Arabidopsis thaliana] Seq. No. 411221 Seq. ID uC-osflcyp066g05a1 Method BLASTX NCBI GI g4127456 277 BLAST score E value 2.0e-24 Match length 68 78 % identity

Seq. No. 411222

Seq. ID uC-osflcyp066h02a1

Method BLASTX

NCBI Description (AJ010818) Cpn21 protein [Arabidopsis thaliana]

```
NCBI GI
                   q3885884
BLAST score
                   501
                   1.0e-50
E value
Match length
                   99
% identity
                   98
NCBI Description (AF093630) 60S ribosomal protein L21 [Oryza sativa]
                   411223
Seq. No.
Seq. ID
                  uC-osflcyp066h03a1
Method
                   BLASTN
NCBI GI
                   g1208445
BLAST score
                   246
E value
                   1.0e-136
Match length
                   246
                   100
% identity
NCBI Description Rice (YK426) mRNA, complete cds
                   411224
Seq. No.
Seq. ID
                   uC-osflcyp066h06a1
Method
                   BLASTX
NCBI GI
                   q1762148
BLAST score
                   290
E value
                   6.0e-26
Match length
                   58
% identity
                   88
NCBI Description (U48695) glutamate dehydrogenase [Solanum lycopersicum]
Seq. No.
                   411225
                   uC-osflcyp066h10a1
Seq. ID
Method
                  BLASTX
NCBI GI
                   q547712
BLAST score
                   335
E value
                   3.0e-31
Match length
                   66
                   98
% identity
NCBI Description
                  EUKARYOTIC INITIATION FACTOR 4A (EIF-4A)
                   >gi_542153_pir__S38358 translation initiation factor eIF-4A
                   - rice >gi_303844_dbj_BAA02152_ (D12627) eukaryotic
                   initiation factor 4A [Oryza sativa]
Seq. No.
                   411226
Seq. ID
                   uC-osflcyp066h11a1
Method
                   BLASTX
NCBI GI
                   g2281089
BLAST score
                   320
E value
                   2.0e-29
Match length
                   69
% identity
NCBI Description (AC002333) Sm protein F isolog [Arabidopsis thaliana]
Seq. No.
                   411227
Seq. ID
                   uC-osflcyp066h12a1
Method
                  BLASTX
NCBI GI
                   g733454
BLAST score
                   327
E value
                   2.0e-30
Match length
                   68
```

```
% identity
NCBI Description
                   (U23188) chlorophyll a/b-binding apoprotein CP26 precursor
                   [Zea mays]
                   411228
Seq. No.
                   uC-osflcyp067a02a1
Seq. ID
Method
                  BLASTN
NCBI GI
                   g11954
BLAST score
                   36
E value
                   4.0e-11
Match length
                   68
% identity
                   88
                  Rice chloroplast DNA for ribulose-1,5-biphosphate
NCBI Description
                   carboxylase (clone pCT-1)
                   411229
Seq. No.
                  uC-osflcyp067a05a1
Seq. ID
Method
                  BLASTX
NCBI GI
                   q407940
BLAST score
                   190
E value
                   2.0e-16
Match length
                  71
% identity
                   66
NCBI Description (U02495) epoxide hydrolase [Solanum tuberosum]
Seq. No.
                   411230
Seq. ID
                  uC-osflcyp067b02a1
Method
                  BLASTN
NCBI GI
                   g2331130
BLAST score
                   266
E value
                   1.0e-148
Match length
                   322
% identity
                   96
NCBI Description
                  Oryza sativa glycine-rich protein (OSGRP1) mRNA, complete
Seq. No.
                   411231
Seq. ID
                  uC-osflcyp067b06a1
Method
                  BLASTX
NCBI GI
                   q4512675
BLAST score
                  251
E value
                   2.0e-21
Match length
                  63
                   75
% identity
NCBI Description (AC006931) putative citrate synthase [Arabidopsis thaliana]
Seq. No.
                   411232
Seq. ID
                  uC-osflcyp067b10a1
Method
                  BLASTX
NCBI GI
                  g2335108
BLAST score
                  271
                  1.0e-23
E value
Match length
                  103
                  49
% identity
NCBI Description
                  (AC002339) putative isulinase [Arabidopsis thaliana]
Seq. No.
                  411233
```

```
NCBI GI
                  g3335365
BLAST score
                  274
E value
                  5.0e-24
                  87
Match length
% identity
                  66
NCBI Description (AC003028) high affinity calcium antiporter [Arabidopsis
                  thaliana]
                  416181
Seq. No.
Seq. ID
                  uC-osflm202106h11b1
Method
                  BLASTX
                  g3668091
NCBI GI
BLAST score
                  399
                  4.0e-39
E value
Match length
                  116
% identity
                  38
NCBI Description (AC004667) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  416182
Seq. ID
                  uC-osf1m202106h12b1
Method
                  BLASTN
NCBI GI
                  g297126
BLAST score
                  38
E value
                  1.0e-11
Match length
                  74
                 88
% identity
NCBI Description A.thaliana target DNA
Seq. No.
                  416183
                  uC-osflm202107a01b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4115377
BLAST score
                  344
E value
                  3.0e-32
                 109
Match length
% identity
                  69
NCBI Description (AC005967) unknown protein [Arabidopsis thaliana]
Seq. No.
                  416184
                  uC-osf1m202107a03b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4584343
BLAST score
                  245
E value
                  1.0e-20
Match length
                  69
% identity
                  68
NCBI Description (AC007127) putative ubiquitin protein [Arabidopsis
                  thaliana]
Seq. No.
                  416185
Seq. ID
                  uC-osflm202107a05b1
Method
                  BLASTN
NCBI GI
                  g733457
BLAST score
                  51
E value
                  9.0e-20
Match length
                  123
% identity
                  86
```

Seq. No.

416191

```
NCBI Description Zea mays chlorophyll a/b-binding apoprotein CP24 (Lhcb6-1)
                   mRNA, complete cds
                   416186
Seq. No.
Seq. ID
                   uC-osflm202107a06b1
Method
                   BLASTX
NCBI GI
                   g5881779
BLAST score
                   203
E value
                   4.0e-16
Match length
                   57
% identity
NCBI Description (AL117386) putative protein [Arabidopsis thaliana]
Seq. No.
                   416187
Seq. ID
                   uC-osflm202107a07b1
Method
                   BLASTX
NCBI GI
                   g4490737
BLAST score
                   314
E value
                   9.0e-29
Match length
                   154
% identity
                   51
NCBI Description (AL035708) putative protein [Arabidopsis thaliana]
Seq. No.
                   416188
Seq. ID
                   uC-osflm202107a08b1
Method
                  BLASTX
NCBI GI
                   g3786009
BLAST score
                   319
E value
                   3.0e-29
Match length
                  123
                   57
% identity
NCBI Description (AC005499) unknown protein [Arabidopsis thaliana]
Seq. No.
                   416189
Seq. ID
                  uC-osflm202107b01b1
Method
                  BLASTX
NCBI GI
                  q3688173
BLAST score
                  631
E value
                  7.0e-66
Match length
                  166
% identity
                  69
NCBI Description (AL031804) putative protein [Arabidopsis thaliana]
Seq. No.
                  416190
Seq. ID
                  uC-osflm202107b02b1
                  BLASTX
Method
NCBI GI
                  g135399
BLAST score
                  686
E value
                  2.0e-72
Match length
                  128
% identity
                  100
NCBI Description
                 TUBULIN ALPHA-1 CHAIN >gi_100716_pir S20758 tubulin
                  alpha-1 chain - rice >gi 20379 emb CAA77988 (Z11931) alpha
                  1 tubulin [Oryza sativa] > gi_1136124_emb_CAA62918_ (X91808)
                  alfa-tubulin [Oryza sativa]
```

Seq. No.

416196

Seq. ID uC-osflm202107b03b1 Method BLASTX NCBI GI q1617036 BLAST score 483 E value 1.0e-48 Match length 131 % identity 69 NCBI Description (Y08624) Ted2 [Vigna unguiculata] Seq. No. 416192 Seq. ID uC-osflm202107b05b1 Method BLASTX NCBI GI q5823020 BLAST score 183 E value 2.0e-13 Match length 63 % identity 54 (AF089849) senescence-specific cysteine protease [Brassica NCBI Description napus] 416193 Seq. No. uC-osflm202107b06b1 Seq. ID Method BLASTX NCBI GI g3163946 BLAST score 403 2.0e-39 E value Match length 101 % identity 81 NCBI Description (AJ005599) alpha-tubulin 1 [Eleusine indica] Seq. No. 416194 Seq. ID uC-osflm202107b07b1 Method BLASTX NCBI GI g120668 BLAST score 779 E value 3.0e-83 Match length 171 % identity 89 NCBI Description GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC >gi_82399_pir_ A24159 glyceraldehyde-3-phosphate
dehydrogenase (EC 1.2.1.12), cytosolic - barley (fragment) >gi_167044 (M36650) glyceraldehyde-3-phosphate dehydrogenase [Hordeum vulgare] >gi_225347 prf 1301218A dehydrogenase, glyceraldehydephosphate [Hordeum vulgare var. distichum] Seq. No. 416195 Seq. ID uC-osflm202107b11b1 Method BLASTX NCBI GI g3885888 BLAST score 287 1.0e-25 E value Match length 101 % identity 63 NCBI Description (AF093632) high mobility group protein [Oryza sativa]

```
Seq. ID
                   uC-osflm202107b12b1
Method
                   BLASTX
NCBI GI
                   q4972089
BLAST score
                   229
E value
                   7.0e-23
Match length
                   107
% identity
                   48
NCBI Description
                  (AL078468) acyl-CoA synthetase-like protein [Arabidopsis
                   thaliana]
Seq. No.
                   416197
Seq. ID
                   uC-osflm202107c01b1
Method
                   BLASTX
NCBI GI
                   q3746581
BLAST score
                   762
E value
                   3.0e-81
Match length
                   163
% identity
                   89
NCBI Description (AF062403) glutathione S-transferase II [Oryza sativa]
Seq. No.
                   416198
Seq. ID
                   uC-osflm202107c02b1
Method
                   BLASTX
NCBI GI
                   g4914414
BLAST score
                   340
E value
                   1.0e-31
Match length
                   160
% identity
                   44
NCBI Description
                  (AL050352) Ca2+-transporting ATPase-like protein
                   [Arabidopsis thaliana]
                   416199
Seq. No.
Seq. ID
                   uC-osflm202107c03b1
Method
                  BLASTX
NCBI GI
                  g3128169
BLAST score
                  194
E value
                  1.0e-14
Match length
                  48
% identity
                   73
NCBI Description (AC004521) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  416200
Seq. ID
                  uC-osflm202107c05b1
Method
                  BLASTX
NCBI GI
                  q3319357
BLAST score
                  596
E value
                  8.0e-62
Match length
                  164
% identity
                  70
NCBI Description
                  (AF077407) contains similarity to phosphoenolpyruvate
                  synthase (ppsA) (GB:AE001056) [Arabidopsis thaliana]
Seq. No.
                  416201
Seq. ID
                  uC-osflm202107c06b1
Method
                  BLASTX
NCBI GI
                  g2244908
BLAST score
                  167
```

NCBI GI

E value

BLAST score

```
E value
                    1.0e-11
Match length
                    41
                    76
% identity
NCBI Description
                  (Z97339) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   416202
                   uC-osflm202107c07b1
Seq. ID
                   BLASTX
Method
NCBI GI
                   g114657
BLAST score
                   730
E value
                    2.0e-77
Match length
                   140
                    99
% identity
                   ATP SYNTHASE A CHAIN PRECURSOR (SUBUNIT IV)
NCBI Description
                   >gi_67926_pir__LWRZ6 H+-transporting ATP synthase (EC
                   3.6.1.34) chain a - rice chloroplast
                   >gi_11975_emb_CAA33990_ (X15901) ATPase a subunit [Oryza
sativa] >gi_226693_prf__1603356U ATPase a [Oryza sativa]
Seq. No.
                   416203
                   uC-osflm202107c08b1
Seq. ID
                   BLASTX
Method
NCBI GI
                   g1848212
BLAST score
                   716
                   7.0e-76
E value
Match length
                   148
% identity
                    51
NCBI Description
                   (Y11209) protein disulfide-isomerase precursor [Nicotiana
                   tabacum]
Seq. No.
                    416204
Seq. ID
                   uC-osflm202107c09b1
Method
                   BLASTX
NCBI GI
                   g1362162
BLAST score
                   524
E value
                    2.0e-53
Match length
                   146
% identity
                    66
                   beta-glucosidase BGQ60 precursor - barley >qi 804656
NCBI Description
                    (L41869) beta-glucosidase [Hordeum vulgare]
Seq. No.
                   416205
Seq. ID
                   uC-osflm202107c10b1
Method
                   BLASTX
NCBI GI
                   g1245182
BLAST score
                   301
E value
                   9.0e-56
                   123
Match length
% identity
                   86
NCBI Description (U49398) sterol delta-7 reductase [Arabidopsis thaliana]
Seq. No.
                   416206
Seq. ID
                   uC-osflm202107c11b1
Method
                   BLASTX
```

54385

g2494320

500 8.0e-51

109 Match length % identity EUKARYOTIC TRANSLATION INITIATION FACTOR 5 (EIF-5) NCBI Description >gi 1806575 emb CAA67868 (X99517) Eukaryotic initiation factor-5 [Zea mays] 416207 Seq. No. uC-osflm202107c12b1 Seq. ID Method BLASTX NCBI GI q4646203 BLAST score 167 E value 1.0e-11 Match length 67 43 % identity NCBI Description (AC007230) Belongs to PF 00026 Eukaryotic aspartyl protease family. [Arabidopsis thaliana] 416208 Seq. No. uC-osflm202107d02b1 Seq. ID Method BLASTX NCBI GI q1168654 BLAST score 528 E value 8.0e-54 Match length 170 % identity 56 BETA-GALACTOSIDASE PRECURSOR (LACTASE) NCBI Description >gi_542198_pir__S41889 beta-galactosidase (EC 3.2.1.23) garden asparagus >gi 452712 emb CAA54525 (X77319) beta-galactosidase [Asparagus officinalis] Seq. No. 416209 uC-osflm202107d04b1 Seq. ID Method BLASTX NCBI GI q5280988 BLAST score 268 E value 2.0e-23 Match length 162 % identity NCBI Description (Z97335) hypothetical protein [Arabidopsis thaliana] Seq. No. 416210 uC-osflm202107d05b1 Seq. ID Method BLASTX NCBI GI g115787 BLAST score 559 E value 2.0e-67 Match length 142 % identity 95 CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I NCBI Description CAB-2) (LHCP) >gi_82461_pir__S03706 chlorophyll a/b-binding protein 2R precursor - rice >gi_20182_emb_CAA32109_ (X13909) chlorophyll a/b-binding preprotein (AA -28 to 235) [Oryza sativa] Seq. No. 416211 Seq. ID uC-osflm202107d06b1

54386

BLASTX

Method

Seq. No.

Seq. ID

416216

uC-osflm202107e06b1

```
NCBI GI
                  g1174470
BLAST score
                   319
E value
                  2.0e-29
Match length
                  91
                  60
% identity
NCBI Description OLIGOSACCHARYL TRANSFERASE STT3 SUBUNIT HOMOLOG (B5)
                   (INTEGRAL MEMBRANE PROTEIN 1) >gi 508543 (L34260) integral
                  membrane protein 1 [Mus musculus] >gi_1588285_prf 2208301A
                  integral membrane protein [Mus musculus]
Seq. No.
                  416212
Seq. ID
                  uC-osflm202107e01b1
Method
                  BLASTX
NCBI GI
                  q5902371
BLAST score
                  290
E value
                  6.0e-26
Match length
                  83
% identity
                  63
NCBI Description (AC009322) Hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  416213
Seq. ID
                  uC-osflm202107e02b1
Method
                  BLASTX
NCBI GI
                  q4128197
BLAST score
                  210
E value
                  1.0e-16
Match length
                  119
% identity
                  43
NCBI Description (U75273) acyl-CoA binding protein [Arabidopsis thaliana]
Seq. No.
                  416214
Seq. ID
                  uC-osflm202107e03b1
Method
                  BLASTX
NCBI GI
                  g1352613
BLAST score
                  499
E value
                  1.0e-50
Match length
                  109
% identity
                  93
NCBI Description OCS-ELEMENT BINDING FACTOR 1 (OCSBF-1)
                  >gi_444047_emb_CAA44607_ (X62745) ocs-binding factor 1 [Zea
                  mays]
Seq. No.
                  416215
Seq. ID
                  uC-osflm202107e05b1
Method
                  BLASTX
NCBI GI
                  g2501189
BLAST score
                  536
E value
                  9.0e-55
Match length
                  138
% identity
                  78
NCBI Description
                 THIAMINE BIOSYNTHETIC ENZYME 1-1 PRECURSOR
                  >gi_2130146_pir__S61419 thiamine biosynthetic enzyme thi1-1
                  - maize >gi_596078 (U17350) thiamine biosynthetic enzyme
                  [Zea mays]
```

```
Method
                   BLASTX
NCBI GI
                   g1167836
BLAST score
                   378
E value
                   3.0e-36
Match length
                   102
% identity
                   63
                   (Z68893) protein with incomplete signal sequence [Holcus
NCBI Description
Seq. No.
                   416217
Seq. ID
                   uC-osflm202107e07b1
Method
                   BLASTX
NCBI GI
                   g2244750
BLAST score
                   730
E value
                   1.0e-77
Match length
                   146
% identity
                   96
                   (Z97335) adenosylhomocysteinase [Arabidopsis thaliana]
NCBI Description
                   >gi_3088579_gb_AAC14714.1_ (AF059581)
                   S-adenosyl-L-homocysteine hydrolase [Arabidopsis thaliana]
Seq. No.
                   416218
Seq. ID
                   uC-osflm202107e09b1
Method
                   BLASTX
NCBI GI
                   q4539459
BLAST score
                   300
E value
                   4.0e-27
Match length
                   88
% identity
                   68
NCBI Description (AL049500) putative protein [Arabidopsis thaliana]
Seq. No.
                   416219
Seq. ID
                   uC-osflm202107e10b1
Method
                   BLASTX
NCBI GI
                   g3249070
BLAST score
                   229
E value
                   9.0e-19
Match length
                  76
% identity
                   67
NCBI Description
                  (AC004473) Contains similarity to siah binding protein 1
                   (SiahBP1) gb U51586 from Homo sapiens. ESTs gb T43314,
                   gb_T43315 and gb_R90521, gb_T75905 [Arabidopsis thaliana]
Seq. No.
                   416220
Seq. ID
                  uC-osflm202107f01b1
Method
                  BLASTX
                  g2673917
                  381
                  2.0e-44
                  152
```

NCBI GI BLAST score E value Match length % identity

NCBI Description (AC002561) putative ATP-dependent RNA helicase [Arabidopsis

thaliana]

Seq. No. 416221

Seq. ID uC-osflm202107f02b1

Method BLASTX

```
NCBI GI
                   g4204257
BLAST score
                   460
E value
                   6.0e-46
Match length
                   143
% identity
NCBI Description (AC005223) 5493 [Arabidopsis thaliana]
                   416222
Seq. No.
Seq. ID
                   uC-osflm202107f03b1
Method
                   BLASTX
NCBI GI
                   g5921647
BLAST score
                   322
E value
                   6.0e-30
Match length
                   102
% identity
                   63
NCBI Description (AF155332) flavonoid 3'-hydroxylase [Petunia x hybrida]
                   416223
Seq. No.
Seq. ID
                   uC-osflm202107f04b1
Method
                   BLASTX
NCBI GI
                   g2335108
BLAST score
                   490
E value
                   2.0e-51
Match length
                   162
% identity
                   60
NCBI Description (AC002339) putative isulinase [Arabidopsis thaliana]
Seq. No.
                   416224
Seq. ID
                   uC-osflm202107f06b1
Method
                   BLASTX
NCBI GI
                   g1730560
BLAST score
                   434
E value
                   8.0e-43
Match length
                   106
% identity
                   75
                  ALPHA-GLUCAN PHOSPHORYLASE, H ISOZYME (STARCH PHOSPHORYLASE
NCBI Description
                   H) >gi_510932_emb_CAA84494_ (Z35117) alpha 1,4-glucan phosphorylase type H [Vicia faba]
Seq. No.
                   416225
                   uC-osflm202107f07b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   q4972686
BLAST score
                   217
E value
                   2.0e-17
Match length
                   128
% identity
                   42
NCBI Description (AF132150) unknown [Drosophila melanogaster]
Seq. No.
                   416226
Seq. ID
                   uC-osflm202107f08b1
Method
                   BLASTX
```

Method BLASTX
NCBI GI g4885026
BLAST score 450
E value 9.0e-45
Match length 139
% identity 63

```
NCBI Description (AF147738) myosin VIII ZMM3 [Zea mays]
Seq. No.
                   416227
Seq. ID
                   uC-osflm202107f09b1
Method
                   BLASTX
NCBI GI
                   g871931
BLAST score
                   526
E value
                   1.0e-53
Match length
                   131
% identity
                   82
NCBI Description (D30763) ferredoxin [Oryza sativa]
Seq. No.
                   416228
Seq. ID
                   uC-osflm202107f10b1
Method
                   BLASTX
                   q4835797
NCBI GI
BLAST score
                   391
E value
                   9.0e-38
Match length
                   141
% identity
NCBI Description
                   (AC007296) Strong similarity to gb_U61231 cytochrome P450
                   from Arabidopsis thaliana and is a member of the PF 00067
                   Cytochrome P450 family. ESTs gb_Z30775 and gb_Z3077\overline{6} come
                   from this gene
Seq. No.
                   416229
Seq. ID
                   uC-osflm202107q02b1
Method
                   BLASTX
NCBI GI
                   q3096927
BLAST score
                   480
E value
                   2.0e-48
Match length
                   127
% identity
                   69
NCBI Description (AL023094) putative protein [Arabidopsis thaliana]
Seq. No.
                   416230
Seq. ID
                   uC-osflm202107q03b1
Method
                   BLASTN
NCBI GI
                   g4097337
BLAST score
                   441
E value
                   0.0e + 00
Match length
                   548
% identity
                   95
NCBI Description
                  Oryza sativa metallothionein-like protein mRNA, complete
                   cds
Seq. No.
                   416231
Seq. ID
                   uC-osflm202107g04b1
Method
                   BLASTX
NCBI GI
                   q82734
BLAST score
                   741
E value
                   8.0e-79
Match length
                  149
                   30
% identity
NCBI Description
                  ubiquitin precursor - maize (fragment)
```

>gi_226763 prf 1604470A poly-ubiquitin [Zea mays]

416232 Seq. No. Seq. ID uC-osflm202107q06b1 Method BLASTN g2446999 NCBI GI BLAST score 45 3.0e-16E value 53 Match length 96 % identity NCBI Description Zea mays FAD8 gene for fatty acid desaturase, partial cds 416233 Seq. No. uC-osflm202107g07b1 Seq. ID Method BLASTX NCBI GI g132105 BLAST score 538 4.0e-55 E value Match length 118 % identity NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR (RUBISCO SMALL SUBUNIT C) >gi_68094_pir__RKRZS9 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_ (D00643) small subunit of ribulose-1,5-bisphosphate carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa] >gi 226375 prf 1508256A ribulose bisphosphate carboxylase S [Oryza sativa] 416234 Seq. No. Seq. ID uC-osflm202107g08b1 Method BLASTX NCBI GI g4101707 BLAST score 358 E value 7.0e-34 Match length 122 % identity 53 NCBI Description (AF006080) glucose acyltransferase [Solanum berthaultii] 416235 Seq. No. Seq. ID uC-osflm202107g09b1 Method BLASTX NCBI GI g4503521 BLAST score 323 E value 9.0e-30 Match length 124 % identity 53 NCBI Description murine mammary tumor integration site 6 (oncogene homolog) >gi 2498490 sp Q64252 INT6 MOUSE VIRAL INTEGRATION SITE PROTEIN INT-6 >gi 2114363 (U62962) similar to mouse Int-6 [Homo sapiens] $>q\bar{i}$ 2351382 (U54562) eIF3-p48 [Homo sapiens] >gi 2688818 (U85947) Int-6 [Homo sapiens] >gi 2695701

Seq. No. 416236

Seq. ID uC-osflm202107g10b1

sapiens]

Method BLASTX

(U94175) mammary tumor-associated protein INT6 [Homo

```
NCBI GI
                   q4538923
BLAST score
                   169
E value
                   1.0e-11
Match length
                   64
% identity
                   [Arabidopsis thaliana]
```

NCBI Description (AL049483) predicted protein destination factor

Seq. No. 416237

uC-osflm202107g11b1 Seq. ID

BLASTX Method NCBI GI q6006864 BLAST score 188 E value 6.0e-1471 Match length % identity 54

NCBI Description (AC009540) hypothetical protein [Arabidopsis thaliana]

Seq. No. 416238

uC-osflm202107h01b1 Seq. ID

Method BLASTX NCBI GI g3023816 BLAST score 186 2.0e-14 E value Match length 44% identity 82

NCBI Description GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC

>gi 968996 (U31676) glyceraldehyde-3-phosphate

dehydrogenase [Oryza sativa]

416239 Seq. No.

Seq. ID uC-osflm202107h04b1

Method BLASTX NCBI GI g1710807 BLAST score 474 2.0e-47 E value Match length 110 87 % identity

NCBI Description RUBISCO SUBUNIT BINDING-PROTEIN ALPHA SUBUNIT PRECURSOR (60

KD CHAPERONIN ALPHA SUBUNIT) (CPN-60 ALPHA) >gi 1185390

(U21105) alphacpn60 [Pisum sativum]

Seq. No. 416240

uC-osflm202107h05b1 Seq. ID

Method BLASTX NCBI GI q2832717 BLAST score 888 5.0e-96 E value Match length 175 % identity

NCBI Description (AJ003114) alkaline/neutral invertase [Lolium temulentum]

Seq. No. 416241

Seq. ID uC-osflm202107h06b1

Method BLASTX NCBI GI g2865394 BLAST score 205

```
E value
                   6.0e-16
Match length
                   92
% identity
                   61
NCBI Description (AF036949) basic leucine zipper protein [Zea mays]
Seq. No.
                   416242
Seq. ID
                  uC-osflm202107h09b1
Method
                  BLASTX
NCBI GI
                  g6006270
BLAST score
                  193
E value
                  1.0e-14
Match length
                  98
% identity
                  39
NCBI Description (AB022692) TAF-Ibeta2 [Xenopus laevis]
Seq. No.
                  416243
Seq. ID
                  uC-osflm202107h10b1
Method
                  BLASTX
NCBI GI
                  g2739044
BLAST score
                  524
E value
                  2.0e-53
Match length
                  129
                  74
% identity
NCBI Description (AF024651) polyphosphoinositide binding protein Sshlp
                  [Glycine max]
Seq. No.
                  416244
Seq. ID
                  uC-osflm202107h11b1
Method
                  BLASTX
                  g2130069
NCBI GI
BLAST score
                  646
E value
                  1.0e-67
Match length
                  133
% identity
                  92
NCBI Description catalase (EC 1.11.1.6) catA - rice
                  >gi_1261858_dbj_BAA06232_ (D29966) catalase [Oryza sativa]
Seq. No.
                  416245
Seq. ID
                  uC-osflm202107h12b1
Method
                  BLASTX
NCBI GI
                  g2624326
BLAST score
                  469
E value
                  3.0e-47
Match length
                  92
% identity
                  99
NCBI Description (AJ002893) OsGRP1 [Oryza sativa]
Seq. No.
                  416246
Seq. ID
                  uC-osflm202108a02b1
Method
                  BLASTX
NCBI GI
                  g1706331
BLAST score
                  717
E value
                  4.0e-81
Match length
                  179
% identity
                  87
                 PYRUVATE DECARBOXYLASE ISOZYME 3 (PDC) >gi_476284 (U07338)
NCBI Description
                  pyruvate decarboxylase [Oryza sativa]
```

Seq. ID

Method

416247 Seq. No. uC-osflm202108a04b1 Seq. ID Method BLASTX g3935181 NCBI GI 207 BLAST score 2.0e-16 E value Match length 46 % identity 76 NCBI Description (AC004557) F17L21.24 [Arabidopsis thaliana] Seq. No. 416248 uC-osflm202108a05b1 Seq. ID BLASTX Method NCBI GI g3395443 BLAST score 364 1.0e-34 E value 95 Match length % identity 67 NCBI Description (AC004683) putative ammonium transporter, 3' partial [Arabidopsis thaliana] Seq. No. 416249 Seq. ID uC-osflm202108a10b1 Method BLASTX NCBI GI g2262170 259 BLAST score 3.0e-22E value Match length 101 57 % identity NCBI Description (AC002329) predicted glycosyl hydrolase [Arabidopsis thaliana] Seq. No. 416250 Seq. ID uC-osflm202108a12b1 Method BLASTN NCBI GI g2305114 BLAST score 91 E value 4.0e-4499 Match length % identity 98 NCBI Description Oryza sativa ferredoxin mRNA, complete cds Seq. No. 416251 Seq. ID uC-osflm202108b02b1 Method BLASTX NCBI GI q5824531 BLAST score 179 E value 7.0e-13 Match length 141 % identity 30 (AL024499) cDNA EST EMBL:C10123 comes from this gene NCBI Description [Caenorhabditis elegans] Seq. No. 416252

uC-osflm202108b03b1

BLASTX

```
NCBI GI
                   q4678323
BLAST score
                   170
E value
                   7.0e-12
Match length
                   164
% identity
                   34
NCBI Description (AL049658) putative protein [Arabidopsis thaliana]
Seq. No.
                   416253
Seq. ID
                   uC-osflm202108b07b1
Method
                   BLASTX
NCBI GI
                   q5912299
BLAST score
                   791
E value
                   1.0e-84
Match length
                   162
% identity
                   98
NCBI Description (AJ133787) gigantea homologue [Oryza sativa]
Seq. No.
                   416254
Seq. ID
                   uC-osflm202108b09b1
Method
                   BLASTX
NCBI GI
                   q3415115
BLAST score
                   203
E value
                   5.0e-16
                  72
Match length
% identity
                   51
NCBI Description (AF081202) villin 2 [Arabidopsis thaliana]
Seq. No.
                   416255
Seq. ID
                  uC-osflm202108b10b1
Method
                  BLASTX
NCBI GI
                   g2982451
BLAST score
                   392
E value
                   7.0e-38
Match length
                  143
% identity
                   62
NCBI Description (AL022223) putative protein [Arabidopsis thaliana]
Seq. No.
                   416256
Seq. ID
                  uC-osflm202108c01b1
Method
                  BLASTX
NCBI GI
                  g82496
BLAST score
                  568
E value
                  2.0e-58
Match length
                  153
% identity
                  75
NCBI Description phenylalanine ammonia-lyase (EC 4.3.1.5) - rice
                  416257
Seq. No.
Seq. ID
                  uC-osflm202108c02b1
Method
                  BLASTX
NCBI GI
                  g3540190
BLAST score
                  226
E value
                  2.0e-18
Match length
                  86
% identity
                  48
```

NCBI Description (AC004122) Hypothetical protein [Arabidopsis thaliana]

```
Seq. No.
                   416258
                  uC-osflm202108c03b1
Seq. ID
Method
                  BLASTX
                  q131770
NCBI GI
BLAST score
                  532
                  3.0e-54
E value
Match length
                  146
% identity
                   68
                  40S RIBOSOMAL PROTEIN S9 (40S RIBOSOMAL PROTEIN 1024)
NCBI Description
                   (VEGETATIVE SPECIFIC PROTEIN V12) >gi 70880 pir R3DO24
                  ribosomal protein S9.e - slime mold (Dictyostelium
                  discoideum) >gi 7353 emb CAA29844 (X06636) rp1024 protein
                   [Dictyostelium discoideum]
Seq. No.
                   416259
Seq. ID
                  uC-osflm202108c06b1
Method
                  BLASTX
NCBI GI
                  q2129825
BLAST score
                  347
                  1.0e-32
E value
Match length
                  120
                  59
% identity
NCBI Description
                  dynamin-like protein phragmoplastin 12 - soybean
                  >gi_1217994 (U25547) SDL [Glycine max]
                   416260
Seq. No.
                  uC-osflm202108c07b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4895226
BLAST score
                   697
                  1.0e-73
E value
Match length
                  159
                  82
% identity
NCBI Description (AC007660) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   416261
                  uC-osflm202108c08b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4760553
                   763
BLAST score
                   2.0e-81
E value
                  156
Match length
                   96
% identity
NCBI Description (AB019533) Nad-dependent formate dehydrogenase [Oryza
                   sativa]
                   416262
Seq. No.
Seq. ID
                  uC-osflm202108c09b1
Method
                  BLASTX
                  g4262174
NCBI GI
BLAST score
                   287
E value
                   2.0e-25
Match length
                  104
% identity
                   57
                  (AC005508) 9058 [Arabidopsis thaliana]
NCBI Description
                   416263
Seq. No.
```

Seq. ID uC-osflm202108c10b1
Method BLASTX
NCBI GI g132105
BLAST score 712
E value 2.0e-75
Match length 143

93

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR

(RUBISCO SMALL SUBUNIT C) >gi 68094 pir RKRZS9

ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor (clone pOSSS1139) - rice >gi 218208 dbj BAA00538

(D00643) small subunit of ribulose-1,5-bisphosphate

carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa] >gi 226375 prf 1508256A ribulose bisphosphate

carboxylase S [Oryza sativa]

Seq. No. 416264

% identity

Seq. ID uC-osflm202108c12b1

Method BLASTX
NCBI GI g6016720
BLAST score 345
E value 2.0e-32
Match length 100
% identity 59

NCBI Description (AC009325) hypothetical protein [Arabidopsis thaliana]

Seq. No. 416265

Seq. ID uC-osflm202108d01b1

Method BLASTX
NCBI GI g4539414
BLAST score 239
E value 5.0e-20
Match length 137
% identity 36

NCBI Description (AL049524) putative subtilisin-like protease [Arabidopsis

thaliana]

Seq. No. 416266

Seq. ID uC-osflm202108d02b1

Method BLASTX
NCBI GI g1777312
BLAST score 367
E value 5.0e-35
Match length 94
% identity 74

NCBI Description (D30622) novel serine/threonine protein kinase [Arabidopsis

thaliana]

Seq. No. 416267

Seq. ID uC-osflm202108d03b1

Method BLASTX
NCBI GI g4309732
BLAST score 235
E value 2.0e-19
Match length 57
% identity 70

```
NCBI Description (AC006439) hypothetical protein [Arabidopsis thaliana]
                  416268
Seq. No.
Seq. ID
                  uC-osflm202108d06b1
Method
                  BLASTX
NCBI GI
                  g4835767
BLAST score
                  415
E value
                  1.0e-40
Match length
                  145
% identity
                  54
NCBI Description (AC007202) T8K14.16 [Arabidopsis thaliana]
Seq. No.
                  416269
Seq. ID
                  uC-osflm202108d07b1
Method
                  BLASTX
NCBI GI
                  g3970652
BLAST score
                  402
E value
                  5.0e-39
Match length
                  105
% identity
                  70
NCBI Description (X77499) amino acid permease [Arabidopsis thaliana]
Seq. No.
                  416270
Seq. ID
                  uC-osflm202108d08b1
Method
                  BLASTX
NCBI GI
                  q1708191
BLAST score
                  207
E value
                  3.0e-31
Match length
                  101
% identity
                  67
NCBI Description HEXOSE CARRIER PROTEIN HEX6 >gi 467319 (L08188) hexose
                  carrier protein [Ricinus communis]
Seq. No.
                  416271
Seq. ID
                  uC-osflm202108d12b1
Method
                  BLASTX
NCBI GI
                  g4582468
BLAST score
                  476
E value
                  8.0e-48
Match length
                  109
% identity
                  87
NCBI Description (AC007071) putative 40S ribosomal protein; contains
                  C-terminal domain [Arabidopsis thaliana]
Seq. No.
                  416272
Seq. ID
                  uC-osflm202108e01b1
Method
                  BLASTX
NCBI GI
                  q5263320
BLAST score
                  354
E value
                  2.0e-33
Match length
                  79
% identity
                  85
NCBI Description
                 (AC007727) Similar to gb M87339 replication factor C,
                  37-kDa subunit from Homo sapiens and is a member of
```

activities. [Arabidopsis thaliana]

PF_00004 ATPases associated with various cellular

BLAST score

396

```
Seq. No.
                   416273
Seq. ID
                   uC-osflm202108e02b1
Method
                   BLASTX
NCBI GI
                   g3482918
BLAST score
                   881
E value
                   4.0e-95
Match length
                   189
% identity
                   87
                  (AC003970) Similar to ATP-citrate-lyase [Arabidopsis
NCBI Description
                   thaliana]
                   416274
Seq. No.
                   uC-osflm202108e03b1
Seq. ID
Method
                  BLASTX
NCBI GI
                   q5802606
BLAST score
                   432
E value
                   1.0e-42
Match length
                   93
% identity
                   83
NCBI Description (AF174486) methylenetetrahydrofolate reductase [Zea mays]
Seq. No.
                   416275
Seq. ID
                   uC-osflm202108e07b1
Method
                   BLASTX
NCBI GI
                   q3850108
BLAST score
                   289
E value
                   9.0e-26
Match length
                   160
% identity
                   42
NCBI Description (AL033388) putative calcium-transporting atpase
                   [Schizosaccharomyces pombe]
                   416276
Seq. No.
Seq. ID
                   uC-osflm202108e09b1
Method
                  BLASTX
NCBI GI
                   q2244855
BLAST score
                   308
E value
                   3.0e-28
Match length
                  107
% identity
                   64
NCBI Description (Z97337) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   416277
Seq. ID
                   uC-osflm202108e10b1
Method
                  BLASTX
                  g4455335
NCBI GI
BLAST score
                   492
E value
                  1.0e-49
Match length
                  175
% identity
                   58
NCBI Description (AL035525) putative protein [Arabidopsis thaliana]
Seq. No.
                   416278
Seq. ID
                  uC-osflm202108e11b1
Method
                  BLASTX
NCBI GI
                   g1167836
```

E value 2.0e-38 Match length 104 % identity 63

NCBI Description (Z68893) protein with incomplete signal sequence [Holcus

lanatus]

Seq. No. 416279

Seq. ID uC-osflm202108f02b1

Method BLASTX
NCBI GI g1170851
BLAST score 145
E value 6.0e-09
Match length 92
% identity 42

NCBI Description MANNOSYL-OLIGOSACCHARIDE ALPHA-1,2-MANNOSIDASE

(MAN(9)-ALPHA-MANNOSIDASE) (ALPHA-MANNOSIDASE 1A) >gi_1083410_pir__A54408 mannosyl-oligosaccharide

1,2-alpha-mannosidase (EC 3.2.1.113) - mouse >gi_474280 (U04299) mannosyl-oligosaccharide alpha-1,2-mannosidase

[Mus musculus]

Seq. No. 416280

Seq. ID uC-osflm202108f03b1

Method BLASTX
NCBI GI g4972062
BLAST score 275
E value 3.0e-24
Match length 93
% identity 63

NCBI Description (AL078470) putative protein [Arabidopsis thaliana]

Seq. No. 416281

Seq. ID uC-osflm202108f05b1

Method BLASTX
NCBI GI g3318615
BLAST score 558
E value 3.0e-57
Match length 132
% identity 83

NCBI Description (AB016065) mitochondrial phosphate transporter [Oryza

sativa]

Seq. No. 416282

Seq. ID uC-osflm202108f06b1

Method BLASTX
NCBI GI g2829275
BLAST score 339
E value 1.0e-31
Match length 114
% identity 62

NCBI Description (AF044265) nucleoside diphosphate kinase 3 [Arabidopsis

thaliana] >gi_3513740 (AF080118) contains similarity to nucleoside diphosphate kinases (Pfam: NDK.hmm, score: 301.12) [Arabidopsis thaliana] >gi_4539375_emb_CAB40069.1_

(AL049525) nucleoside diphosphate kinase 3 (ndpk3)

[Arabidopsis thaliana]

Match length

79

```
416283
Seq. No.
Seq. ID
                  uC-osflm202108f07b1
Method
                  BLASTX
NCBI GI
                  q3213227
BLAST score
                  156
E value
                  3.0e-10
Match length
                  148
% identity
                  25
NCBI Description
                  (AF035209) putative v-SNARE Vtila [Mus musculus]
                  >qi 3421062 (AF035823) 29-kDa Golgi SNARE [Mus musculus]
Seq. No.
                  416284
                  uC-osflm202108f08b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q121631
BLAST score
                  200
                  1.0e-15
E value
                  83
Match length
% identity
                  52
NCBI Description GLYCINE-RICH CELL WALL STRUCTURAL PROTEIN 2 PRECURSOR
                  >gi_72323_pir__KNNT2S glycine-rich protein 2 - wood tobacco
                  >gi_19743_emb_CAA42622_ (X60007) nsGRP-2 [Nicotiana
                   sylvestris]
Seq. No.
                  416285
Seq. ID
                  uC-osflm202108f10b1
Method
                  BLASTX
NCBI GI
                  q1168609
BLAST score
                  428
                   5.0e-42
E value
Match length
                  133
% identity
NCBI Description AUXIN-RESISTANCE PROTEIN AXR1 >gi 479664 pir S35071
                   auxin-resistance protein AXR1 - Arabidopsis thaliana
                   >gi 304104 (L13922) ubiquitin-activating enzyme E1
                   [Arabidopsis thaliana] >gi_2388579 (AC000098) Match to
                   Arabidopsis AXR1 (gb_ATHAXR1122). [Arabidopsis thaliana]
                   >gi 448755 prf 1917337A ubiquitin-activating enzyme E1
                   [Arabidopsis thaliana]
Seq. No.
                   416286
Seq. ID
                  uC-osflm202108f11b1
Method
                  BLASTX
NCBI GI
                  g3688808
BLAST score
                  257
E value
                   5.0e-22
Match length
                  172
                   37
% identity
NCBI Description (AF084104) AcsA [Bacillus firmus]
Seq. No.
                   416287
Seq. ID
                  uC-osflm202108f12b1
                  BLASTX
Method
NCBI GI
                  g2829275
BLAST score
                  373
E value
                  1.0e-35
```

% identity (AF044265) nucleoside diphosphate kinase 3 [Arabidopsis NCBI Description thaliana] >gi_3513740 (AF080118) contains similarity to nucleoside diphosphate kinases (Pfam: NDK.hmm, score: 301.12) [Arabidopsis thaliana] >gi 4539375 emb CAB40069.1 (AL049525) nucleoside diphosphate kinase 3 (ndpk3) [Arabidopsis thaliana] Seq. No. 416288 uC-osflm202108g01b1 Seq. ID Method BLASTX g2258315 NCBI GI BLAST score 162 6.0e-11 E value Match length 124 % identity NCBI Description (AF004878) resistance complex protein I2C-1 [Lycopersicon esculentum] Seq. No. 416289 uC-osflm202108g02b1 Seq. ID Method BLASTX NCBI GI g5903104 BLAST score 161 E value 7.0e-11 Match length 115 % identity 37 (AC008017) Highly similar to non intermediate filament IFA NCBI Description binding protein [Arabidopsis thaliana] Seq. No. 416290 uC-osflm202108g03b1 Seq. ID Method BLASTX NCBI GI g129591 BLAST score 412 E value 2.0e-40 Match length 100 81 % identity NCBI Description PHENYLALANINE AMMONIA-LYASE >gi 295824 emb CAA34226 (X16099) phenylalanine ammonia-lyase [Oryza sativa]

Seq. No. 416291 Seq. ID uC-osflm202108g07b1

Method BLASTX NCBI GI g2662341 BLAST score 826 E value 9.0e-89 170 Match length 93 % identity

NCBI Description (D63580) EF-1 alpha [Oryza sativa]

>gi_2662345_dbj_BAA23659_ (D63582) EF-1 alpha [Oryza satīva] >gi_2662347_dbj_BAA23660_ (D63583) EF-1 alpha

[Oryza sativa]

Seq. No. 416292

Seq. ID uC-osflm202108g08b1

Method BLASTX

E value

Match length

3.0e-27

71

```
g4079798
NCBI GI
                  534
BLAST score
                  1.0e-54
E value
                  140
Match length
                  76
% identity
                  (AF052203) 23 kDa polypeptide of photosystem II [Oryza
NCBI Description
                  sativa]
                  416293
Seq. No.
                  uC-osflm202108g12b1
Seq. ID
Method
                  BLASTX
                  g1070494
NCBI GI
BLAST score
                  225
                  2.0e-18
E value
                  94
Match length
                  52
% identity
NCBI Description serine-type carboxypeptidase (EC 3.4.16.1) precursor -
                  barley
                  416294
Seq. No.
                  uC-osflm202108h01b1
Seq. ID
                  BLASTX
Method
NCBI GI
                  g4406756
                  581
BLAST score
E value
                  4.0e-60
                  143
Match length
% identity
                  77
NCBI Description (AC006836) putative integral membrane protein A3
                   [Arabidopsis thaliana]
Seq. No.
                   416295
                  uC-osflm202108h02b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4455304
BLAST score
                  167
E value
                   1.0e-11
Match length
                  108
% identity
                   32
NCBI Description (AL035528) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   416296
                  uC-osflm202108h03b1
Seq. ID
Method
                  BLASTX
NCBI GI
                   g2342724
BLAST score
                  206
E value
                  2.0e-16
Match length
                  80
% identity
NCBI Description (AC002341) unknown protein [Arabidopsis thaliana]
Seq. No.
                   416297
Seq. ID
                  uC-osflm202108h04b1
Method
                  BLASTX
NCBI GI
                  g4581156
BLAST score
                  302
```

Seq. No.

```
% identity
NCBI Description (AC006919) putative pyruvate kinase [Arabidopsis thaliana]
Seq. No.
                   416298
                  uC-osflm202108h06b1
Seq. ID
                  BLASTX
Method
NCBI GI
                  g2130073
BLAST score
                  683
E value
                   5.0e-72
Match length
                  133
% identity
                   99
NCBI Description
                  fructose-bisphosphate aldolase (EC 4.1.2.13) isoenzyme C-1,
                  cytosolic - rice >gi_786178_dbj_BAA08845_ (D50307) aldolase
                  C-1 [Oryza sativa] >gi_790970_dbj_BAA08830_ (D50301)
                  aldolase C-1 [Oryza sativa]
Seq. No.
                   416299
Seq. ID
                  uC-osflm202108h09b1
Method
                  BLASTX
NCBI GI
                  g2827619
BLAST score
                  433
E value
                  8.0e-43
Match length
                  105
% identity
NCBI Description (AL021636) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   416300
                  uC-osflm202108h10b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3668069
BLAST score
                  155
E value
                  4.0e-10
                  86
Match length
% identity
                  44
NCBI Description (U28007) Pto kinase interactor 1 [Lycopersicon esculentum]
Seq. No.
                  416301
Seq. ID
                  uC-osflm202108h11b1
Method
                  BLASTX
NCBI GI
                  g2330885
BLAST score
                  166
E value
                  1.0e-11
Match length
                  116
% identity
NCBI Description (AJ000486) methionine gamma-lyase [Trichomonas vaginalis]
Seq. No.
                  416302
                  uC-osflm202108h12b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q5123951
BLAST score
                  211
E value
                  8.0e-17
Match length
                  51
% identity
NCBI Description
                 (AL079349) putative protein [Arabidopsis thaliana]
```

```
uC-osflm202109a01b1
Seq. ID
Method
                   BLASTX
                   g4895197
NCBI GI
BLAST score
                   167
E value
                   2.0e-11
Match length
                   94
% identity
                   38
NCBI Description (AC007661) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   416304
                   uC-osflm202109a02b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   q5902390
BLAST score
                   453
E value
                   4.0e-45
Match length
                   146
% identity
                   61
NCBI Description (AC008148) Unknown protein [Arabidopsis thaliana]
Seq. No.
                   416305
                   uC-osflm202109a03b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3264767
BLAST score
                   157
E value
                   3.0e-10
Match length
                   110
% identity
                   37
NCBI Description (AF071893) AP2 domain containing protein [Prunus armeniaca]
Seq. No.
                   416306
                   uC-osflm202109a06b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   q1184774
BLAST score
                   252
E value
                   7.0e-22
                  58
Match length
                   81
% identity
NCBI Description (U45856) cytosolic glyceroldehyde-3-phosphate dehydrogenase
                  GAPC3 [Zea mays]
Seq. No.
                   416307
Seq. ID
                   uC-osflm202109a08b1
Method
                   BLASTX
NCBI GI
                   g82496
BLAST score
                   652
E value
                   2.0e-68
Match length
                  151
% identity
                   87
NCBI Description phenylalanine ammonia-lyase (EC 4.3.1.5) - rice
Seq. No.
                   416308
                   uC-osflm202109a09b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3023816
BLAST score
                   479
E value
                   3.0e-48
Match length
                  108
```

```
% identity
NCBI Description
                  GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC
                   >qi 968996 (U31676) glyceraldehyde-3-phosphate
                  dehydrogenase [Oryza sativa]
                   416309
Seq. No.
Seq. ID
                  uC-osflm202109a10b1
Method
                  BLASTX
NCBI GI
                  q1352830
BLAST score
                  682
E value
                   6.0e-72
Match length
                  150
                  89
% identity
                  VACUOLAR ATP SYNTHASE CATALYTIC SUBUNIT A (V-ATPASE 69 KD
NCBI Description
                   SUBUNIT) >gi_1049253 (U36436) vacuolar ATPase 69 kDa
                  subunit [Zea mays]
                   416310
Seq. No.
Seq. ID
                  uC-osflm202109a12b1
Method
                  BLASTN
NCBI GI
                  q2570516
BLAST score
                  103
E value
                   7.0e-51
Match length
                  215
% identity
                  86
NCBI Description Oryza sativa thioredoxin F isoform mRNA, complete cds
                  416311
Seq. No.
                  uC-osflm202109b02b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q6014701
BLAST score
                  536
E value
                   9.0e-55
Match length
                  168
% identity
                   59
NCBI Description (AF190450) enoyl-CoA-hydratase [Avicennia marina]
Seq. No.
                   416312
Seq. ID
                  uC-osflm202109b04b1
Method
                  BLASTX
NCBI GI
                  g2117355
BLAST score
                  374
E value
                  9.0e-36
                  129
Match length
% identity
                  61
NCBI Description
                  mitochondrial processing peptidase (EC 3.4.99.41) alpha-II
                   chain precursor - potato >gi_587562_emb_CAA56520_ (X80236)
                  mitochondrial processing peptidase [Solanum tuberosum]
Seq. No.
                   416313
Seq. ID
                  uC-osflm202109b05b1
Method
                  BLASTN
NCBI GI
                  g5852170
BLAST score
                  71
E value
                  7.0e-32
Match length
                  83
```

% identity

NCBI Description Oryza sativa indica(GLA4) genomic DNA, chromosome 4, BAC clone:t17804 416314 Seq. No. uC-osflm202109b06b1 Seq. ID BLASTX Method NCBI GI g5091498 BLAST score 418 2.0e-64 E value 145 Match length % identity 86 (AB023482) ESTs AU058067(E20733), AAU058070(E20873) NCBI Description correspond to a region of the predicted gene.; Similar to Populus tremuloides caffeoyl-CoA 3-0-methyltransferase mRNA, complete cds.(U27116) [Oryza sativa] Seq. No. 416315 uC-osflm202109b07b1 Seq. ID BLASTX Method g4539453 NCBI GI 388 BLAST score E value 2.0e-37 115 Match length 65 % identity (AL049500) putative protein [Arabidopsis thaliana] NCBI Description 416316 Seq. No. uC-osflm202109b08b1 Seq. ID BLASTX Method NCBI GI q4455180 163 BLAST score E value 6.0e-20 86 Match length 60 % identity NCBI Description (AL035521) putative protein [Arabidopsis thaliana] Seq. No. 416317 uC-osflm202109b10b1 Seq. ID Method BLASTX NCBI GI a5689136 BLAST score 420 E value 4.0e-41Match length 86 % identity NCBI Description (AB023479) transcription factor Ntlim1 [Nicotiana tabacum] Seq. No. 416318 uC-osflm202109c03b1 Seq. ID Method BLASTX

Method BLASTX
NCBI GI g5007084
BLAST score 950
E value 1.0e-103
Match length 180
% identity 99

NCBI Description (AF155333) NADP-specific isocitrate dehydrogenase [Oryza

sativa]

```
416319
Seq. No.
                  uC-osflm202109c04b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2194119
BLAST score
                  322
                  1.0e-29
E value
Match length
                  104
                  55
% identity
NCBI Description
                  (AC002062) No definition line found [Arabidopsis thaliana]
                  416320
Seq. No.
                  uC-osflm202109c05b1
Seq. ID
Method
                  BLASTN
                  g2443456
NCBI GI
BLAST score
                  111
E value
                  2.0e-55
Match length
                  134
                  96
% identity
                  Oryza sativa ethylene responsive element binding protein
NCBI Description
                   (Os-EREBP1) mRNA, complete cds
                  416321
Seq. No.
                  uC-osflm202109c06b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3122858
BLAST score
                  533
E value
                  2.0e-54
Match length
                  156
% identity
                  65
                  D-3-PHOSPHOGLYCERATE DEHYDROGENASE PRECURSOR (PGDH)
NCBI Description
                  >gi_2189964_dbj_BAA20405_ (AB003280) Phosphoglycerate
                  dehydrogenase [Arabidopsis thaliana]
                  >gi_2804258_dbj_BAA24440_ (AB010407) phosphoglycerate
                  dehydrogenase [Arabidopsis thaliana]
Seq. No.
                   416322
                  uC-osflm202109c08b1
Seq. ID
Method
                  BLASTN
NCBI GI
                  q14264
BLAST score
                  58
E value
                  8.0e-24
                  78
Match length
                  94
% identity
NCBI Description T.aestivum gene for sedoheptulose-1,7-bisphoshatase
Seq. No.
                   416323
Seq. ID
                  uC-osflm202109c09b1
                  BLASTX
Method
NCBI GI
                  q2501189
BLAST score
                  438
E value
                   4.0e-51
Match length
                  141
                  77
% identity
                  THIAMINE BIOSYNTHETIC ENZYME 1-1 PRECURSOR
NCBI Description
                  >gi 2130146 pir S61419 thiamine biosynthetic enzyme thi1-1
                   - maize >gi_596078 (U17350) thiamine biosynthetic enzyme
```

[Zea mays]

Seq. No. 416324 uC-osflm202109c11b1 Seq. ID Method BLASTX g3914005 NCBI GI BLAST score 504 E value 4.0e-51 Match length 119 87 % identity NCBI Description MITOCHONDRIAL LON PROTEASE HOMOLOG 1 PRECURSOR >gi_1816586 (U85494) LON1 protease [Zea mays] Seq. No. 416325 Seq. ID uC-osflm202109d01b1 Method BLASTX NCBI GI g4587611 BLAST score 229 E value 7.0e-19 Match length 104 46 % identity NCBI Description (AC006951) putative 40S ribosomal protein S17 [Arabidopsis thaliana] 416326 Seq. No. uC-osflm202109d02b1 Seq. ID Method BLASTX NCBI GI g134595 BLAST score 675 E value 4.0e-71 Match length 129 % identity 98 SUPEROXIDE DISMUTASE-1 [CU-ZN] >gi_280412_pir_ S22508 superoxide dismutase (EC 1.15.1.1) (Cu-Zn) sodA - rice NCBI Description >gi_218224_dbj_BAA00799_ (D00999) copper/zinc-superoxide dismutase [Oryza sativa] >gi_685242 (L19435) cytosolic copper/zinc-superoxide dismutase [Oryza sativa] >gi_1096504_prf__2111424A Cu/Zn superoxide dismutase [Oryza sativa] Seq. No. 416327 Seq. ID uC-osflm202109d04b1 Method BLASTX NCBI GI g294845 BLAST score 731 E value 1.0e-77 Match length 179 % identity 79 (L13655) membrane protein [Saccharum hybrid cultivar NCBI Description H65-7052] Seq. No. 416328

Seq. ID uC-osflm202109d05b1

Method BLASTX NCBI GI g1890575 BLAST score 403 E value 4.0e-39 Match length 127

```
% identity
NCBI Description
                  (X93174) xyloglucan endotransglycosylase (XET) [Hordeum
                  vulgare]
                  416329
Seq. No.
                  uC-osflm202109d07b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4587611
BLAST score
                  456
E value
                  2.0e-45
Match length
                  135
% identity
                  67
NCBI Description
                  (AC006951) putative 40S ribosomal protein S17 [Arabidopsis
                  thaliana]
                  416330
Seq. No.
                  uC-osflm202109d10b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2952328
BLAST score
                  656
E value
                  2.0e-72
Match length
                  144
                  98
% identity
NCBI Description
                  (AF049889) 1-aminocyclopropane-1-carboxylate oxidase [Oryza
                  sativa]
                  416331
Seq. No.
                  uC-osflm202109d11b1
Seq. ID
Method
                  BLASTN
NCBI GI
                  q218154
BLAST score
                  80
E value
                  7.0e-37
Match length
                  135
                  100
% identity
NCBI Description Oryza sativa gene for cytoplasmic aldolase, complete cds,
                  clone:Aldp
Seq. No.
                  416332
                  uC-osflm202109e01b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2827537
BLAST score
                  488
E value
                  3.0e-49
Match length
                  130
% identity
                  66
NCBI Description
                  (AL021633) putative zinc finger protein [Arabidopsis
                  thaliana]
                  416333
Seq. No.
                  uC-osflm202109e02b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3721942
BLAST score
                  603
E value
                  9.0e-63
Match length
                  127
% identity
                  87
NCBI Description (AB018248) chitinase [Oryza sativa]
```

Seq. No. 416334
Seq. ID uC-osflm202109e03b1
Method BLASTX

NCBI GI g1076531 BLAST score 182 E value 2.0e-13 Match length 60 % identity 53

NCBI Description hypothetical protein, pollen allergen homolog - garden pea

>gi_2129891_pir__S65056 pollen allergen homolog precursor
(clone PPA1) - garden pea >gi_732905_emb_CAA59470_ (X85187)

homology with pollen allergens [Pisum sativum]

Seq. No. 416335

Seq. ID uC-osflm202109e04b1

Method BLASTX
NCBI GI g3879914
BLAST score 192
E value 2.0e-14
Match length 129
% identity 40

NCBI Description (Z74043) predicted using Genefinder; cDNA EST EMBL:C13850

comes from this gene; cDNA EST EMBL:C11575 comes from this

gene; cDNA EST yk343f4.5 comes from this gene

[Caenorhabditis elegans]

Seq. No. 416336

Seq. ID uC-osflm202109e05b1

Method BLASTX
NCBI GI g121349
BLAST score 471
E value 5.0e-68
Match length 141
% identity 86

NCBI Description GLUTAMINE SYNTHETASE SHOOT ISOZYME (GLUTAMATE--AMMONIA

LIGASE) (CLONE LAMBDA-GS28) >gi_20368_emb_CAA32461_

(X14245) cytosolic glutamine synthetase (AA 1-356) [Oryza

sativa]

Seq. No. 416337

Seq. ID uC-osflm202109e06b1

Method BLASTX
NCBI GI g1136120
BLAST score 556
E value 1.0e-72
Match length 145
% identity 94

NCBI Description (X91806) alpha-tubulin [Oryza sativa]

Seq. No. 416338

Seq. ID uC-osflm202109e07b1

Method BLASTX
NCBI GI g1922251
BLAST score 385
E value 5.0e-37
Match length 109

```
% identity
NCBI Description
                   (Y12072) farnesyl pyrophosphate synthase [Gossypium
                  arboreum]
                  416339
Seq. No.
                  uC-osflm202109e08b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g283008
BLAST score
                  641
E value
                  4.0e-67
Match length
                  146
% identity
                  86
                  sucrose synthase (EC 2.4.1.13) - rice
NCBI Description
                  >gi_20366_emb_CAA46017_ (X64770) sucrose synthase [Oryza
                  sativa]
Seq. No.
                  416340
                  uC-osflm202109e10b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1621463
BLAST score
                  463
E value
                  3.0e-46
Match length
                  117
                  69
% identity
NCBI Description (U73104) laccase [Liriodendron tulipifera]
Seq. No.
                  416341
                  uC-osflm202109e12b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q421855
BLAST score
                  151
E value
                   9.0e-10
Match length
                  94
                  35
% identity
NCBI Description alanine--tRNA ligase (EC 6.1.1.7) - Arabidopsis thaliana
                   (fragment)
Seq. No.
                   416342
                  uC-osflm202109f01b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g129591
BLAST score
                  147
E value
                   1.0e-09
Match length
                  38
% identity
                   74
NCBI Description PHENYLALANINE AMMONIA-LYASE >gi 295824 emb CAA34226
                   (X16099) phenylalanine ammonia-lyase [Oryza sativa]
Seq. No.
                   416343
                  uC-osflm202109f02b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2739044
BLAST score
                  441
E value
                  1.0e-43
Match length
                  117
% identity
NCBI Description (AF024651) polyphosphoinositide binding protein Sshlp
```

```
[Glycine max]
Seq. No.
                   416344
Seq. ID
                   uC-osflm202109f03b1
Method
                   BLASTX
                   g4678280
NCBI GI
BLAST score
                   231
E value
                   6.0e-19
Match length
                   137
% identity
                   35
NCBI Description (AL049660) zinc finger-like protein [Arabidopsis thaliana]
Seq. No.
                   416345
                   uC-osflm202109f05b1
Seq. ID
Method
                   BLASTX
                   g5734634
NCBI GI
BLAST score
                   296
E value
                   6.0e-27
Match length
                   113
                   59
% identity
                  (AP000391) Similar to putative lipase (AC006232) [Oryza
NCBI Description
                   sativa]
                   416346
Seq. No.
                   uC-osflm202109f06b1
Seq. ID
Method
                   BLASTX
                   g4406767
NCBI GI
BLAST score
                   184
                   7.0e-19
E value
Match length
                   112
% identity
                   45
                  (AC006836) putative flavonol sulfotransferase [Arabidopsis
NCBI Description
                   thaliana]
                   416347
Seq. No.
Seq. ID
                   uC-osflm202109f08b1
Method
                   BLASTX
NCBI GI
                   q1946300
BLAST score
                   549
E value
                   3.0e-56
Match length
                   168
% identity
                   37
NCBI Description (Y12529) hypothetical protein [Silene latifolia]
                   416348
Seq. No.
Seq. ID
                   uC-osflm202109f09b1
Method
                   BLASTX
NCBI GI
                   g4590326
                   881
BLAST score
E value
                   4.0e-95
Match length
                   187
```

Seq. No. 416349

% identity

Seq. ID uC-osflm202109f10b1

95

Method BLASTX

NCBI Description (AF083327) 101 kDa heat shock protein [Zea mays]

E value

2.0e-61

```
g3335378
NCBI GI
                   288
BLAST score
                   7.0e-26
E value
                  109
Match length
% identity
                   52
                  (AC003028) Myb-related transcription activator [Arabidopsis
NCBI Description
                  thaliana]
                   416350
Seq. No.
Seq. ID
                  uC-osflm202109f12b1
Method
                  BLASTX
NCBI GI
                  g5734779
BLAST score
                  498
E value
                   3.0e-50
Match length
                  154
% identity
                  58
NCBI Description (AC007980) 78688 [Arabidopsis thaliana]
                   416351
Seq. No.
                  uC-osflm202109g01b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3023947
BLAST score
                  189
                   5.0e-17
E value
Match length
                  89
% identity
                   60
NCBI Description PROBABLE HISTONE DEACETYLASE (RPD3 HOMOLOG) >gi 2665840
                   (AF035815) putative histone deacetylase RPD3 [Zea mays]
                   416352
Seq. No.
Seq. ID
                  uC-osflm202109q03b1
Method
                  BLASTX
NCBI GI
                  g4585882
BLAST score
                  548
E value
                   4.0e-56
Match length
                  146
% identity
                   72
NCBI Description (AC005850) PSI type III chlorophyll a/b-binding protein
                   [Arabidopsis thaliana]
Seq. No.
                   416353
Seq. ID
                  uC-osflm202109q04b1
Method
                  BLASTX
NCBI GI
                  q3763927
BLAST score
                  306
E value
                   9.0e-28
Match length
                  94
% identity
NCBI Description
                   (AC004450) putative carboxyphosphoenolpyruvate mutase
                   [Arabidopsis thaliana]
Seq. No.
                   416354
Seq. ID
                  uC-osflm202109q05b1
Method
                  BLASTX
NCBI GI
                  g3927825
BLAST score
                  593
```

Match length 138 % identity 83

NCBI Description (AC005727) putative dTDP-glucose 4-6-dehydratase

[Arabidopsis thaliana]

Seq. No. 416355

Seq. ID uC-osflm202109g06b1

Method BLASTX
NCBI GI g421989
BLAST score 279
E value 1.0e-24
Match length 133
% identity 50

NCBI Description serpin - barley >gi 19071 emb CAA78822 (Z15116) protein zx

[Hordeum vulgare] >gi_444778_prf__1908213A protein Zx

[Hordeum vulgare]

Seq. No. 416356

Seq. ID uC-osflm202109g07b1

Method BLASTN
NCBI GI g1304265
BLAST score 99
E value 3.0e-48
Match length 209
% identity 87

NCBI Description Triticum aestivum mRNA for HALF-1, complete cds

Seq. No. 416357

Seq. ID uC-osflm202109g08b1

Method BLASTX
NCBI GI g4539009
BLAST score 203
E value 1.0e-15
Match length 68
% identity 56

NCBI Description (AL049481) putative protein [Arabidopsis thaliana]

Seq. No. 416358

Seq. ID uC-osflm202109g09b1

Method BLASTX
NCBI GI g3885888
BLAST score 196
E value 5.0e-15
Match length 86
% identity 53

NCBI Description (AF093632) high mobility group protein [Oryza sativa]

Seq. No. 416359

Seq. ID uC-osflm202109g11b1

Method BLASTX
NCBI GI g3927825
BLAST score 351
E value 3.0e-33
Match length 108
% identity 66

NCBI Description (AC005727) putative dTDP-glucose 4-6-dehydratase

[Arabidopsis thaliana]

```
Seq. No.
                  416360
Seq. ID
                  uC-osflm202109q12b1
Method
                  BLASTX
NCBI GI
                  q2497543
BLAST score
                  292
E value
                  1.0e-48
Match length
                  131
% identity
                  84
NCBI Description PYRUVATE KINASE, CYTOSOLIC ISOZYME >gi_542061_pir S41379
                  pyruvate kinase - common tobacco >gi_444023_emb_CAA82628_
                  (Z29492) pyruvate kinase [Nicotiana tabacum]
                  416361
Seq. No.
Seq. ID
                  uC-osflm202109h01b1
Method
                  BLASTX
NCBI GI
                  q1168408
BLAST score
                  397
E value
                  9.0e-39
Match length
                  93
% identity
                  84
NCBI Description
                  FRUCTOSE-BISPHOSPHATE ALDOLASE, CYTOPLASMIC ISOZYME 1
                  >gi_2118268_pir__S58168 fructose-bisphosphate aldolase (EC
                  4.1.2.13) - garden pea >gi_927507_emb CAA61946 (X89828)
                  fructose-1,6-bisphosphate aldolase [Pisum sativum]
                  416362
Seq. No.
Seq. ID
                  uC-osflm202109h04b1
Method
                  BLASTX
NCBI GI
                  g4107009
BLAST score
                  451
E value
                  8.0e-45
Match length
                  87
% identity
                  98
NCBI Description (D82039) OSK1 [Oryza sativa]
Seq. No.
                  416363
Seq. ID
                  uC-osflm202109h05b1
Method
                  BLASTX
NCBI GI
                  g4033424
BLAST score
                  653
E value
                  3.0e-74
Match length
                  165
% identity
                  84
NCBI Description SOLUBLE INORGANIC PYROPHOSPHATASE (PYROPHOSPHATE
                  PHOSPHO-HYDROLASE) (PPASE) >gi_2668746 (AF034947) inorganic
                  pyrophosphatase [Zea mays]
Seq. No.
                  416364
Seq. ID
                  uC-osflm202109h06b1
Method
                  BLASTX
NCBI GI
                  g4887543
BLAST score
                  503
E value
                  7.0e-51
Match length
                  116
% identity
                  83
NCBI Description (AJ012278) ATP-dependent Clp protease subunit ClpP
```

Seq. No.

416370

```
(AB022326) nClpP1 [Arabidopsis thaliana]
                  416365
Seq. No.
                  uC-osflm202109h08b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4220533
BLAST score
                  147
                   3.0e-09
E value
                  94
Match length
                   39
% identity
                  (AL035356) putative mitochondrial uncoupling protein
NCBI Description
                   [Arabidopsis thaliana]
                   416366
Seq. No.
                  uC-osflm202109h09b1
Seq. ID
                  BLASTN
Method
NCBI GI
                  q21834
                   45
BLAST score
                   4.0e-16
E value
                  77
Match length
% identity
                   90
                  Wheat mRNA for cytosolic phosphoglycerate kinase (EC
NCBI Description
                   2.7.2.3)
                   416367
Seq. No.
Seq. ID
                   uC-osflm202109h10b1
Method
                  BLASTX
                  g2911072
NCBI GI
                  160
BLAST score
                   9.0e-11
E value
Match length
                   48
                   67
% identity
NCBI Description (AL021960) putative protein [Arabidopsis thaliana]
                   416368
Seq. No.
Seq. ID
                   uC-osflm202109h11b1
                   BLASTX
Method
NCBI GI
                   q862310
BLAST score
                   208
E value
                   1.0e-16
Match length
                   78
% identity
NCBI Description (L28001) G protein alpha-subunit [Oryza sativa]
                   416369
Seq. No.
Seq. ID
                   uC-osflm202110a03b1
Method
                   BLASTX
NCBI GI
                   q4220533
BLAST score
                   337
E value
                   2.0e-31
Match length
                   137
% identity
                   54
                  (AL035356) putative mitochondrial uncoupling protein
NCBI Description
                   [Arabidopsis thaliana]
```

[Arabidopsis thaliana] >gi_5360579_dbj_BAA82065.1_

```
uC-osflm202110a04b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1946371
BLAST score
                  174
E value
                  2.0e-12
                  92
Match length
                  45
% identity
                  (U93215) regulatory protein Viviparous-1 isolog
NCBI Description
                  [Arabidopsis thaliana]
                  416371
Seq. No.
                  uC-osflm202110a07b1
Seq. ID
Method
                  BLASTX
                  q1168537
NCBI GI
BLAST score
                  508
                  2.0e-51
E value
Match length
                  147
% identity
                  66
NCBI Description ASPARTIC PROTEINASE PRECURSOR >gi 82458 pir JS0732
                  aspartic proteinase (EC 3.4.23.-) - rice
                  >gi_218143_dbj_BAA02242_ (D12777) aspartic proteinase
                  [Oryza sativa]
Seq. No.
                  416372
                  uC-osflm202110a08b1
Seq. ID
Method
                  BLASTX
                  q4033424
NCBI GI
BLAST score
                  617
E value
                  3.0e-64
Match length
                  130
% identity
                  93
NCBI Description SOLUBLE INORGANIC PYROPHOSPHATASE (PYROPHOSPHATE
                  PHOSPHO-HYDROLASE) (PPASE) >gi 2668746 (AF034947) inorganic
                  pyrophosphatase [Zea mays]
                  416373
Seq. No.
                  uC-osflm202110a09b1
Seq. ID
                  BLASTX
Method
NCBI GI
                  g82496
BLAST score
                  450
                  1.0e-58
E value
Match length
                  140
                  79
% identity
NCBI Description phenylalanine ammonia-lyase (EC 4.3.1.5) - rice
                  416374
Seq. No.
                  uC-osflm202110a10b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g136057
                  512
BLAST score
E value
                  5.0e-52
Match length
                  130
% identity
                  76
                  TRIOSEPHOSPHATE ISOMERASE, CYTOSOLIC (TIM)
NCBI Description
                  >gi_99499_pir__A32187 (S)-tetrahydroberberine oxidase -
                  Coptis japonica >gi_556171 (J04121) triosephosphate
```

54418

isomerase [Coptis japonica]

416375 Seq. No. Seq. ID uC-osflm202110a12b1 Method BLASTX NCBI GI g3914425 BLAST score 440 E value 2.0e-43 Match length 154 % identity 60 NCBI Description PROTEASOME EPSILON CHAIN PRECURSOR (MACROPAIN EPSILON CHAIN) (MULTICATALYTIC ENDOPEPTIDASE COMPLEX EPSILON CHAIN) >gi_2511596_emb_CAA74029.1_ (Y13695) multicatalytic endopeptidase complex, proteasome precursor, beta subunit [Arabidopsis thaliana] >gi_3421117 (AF043536) 20S proteasome beta subunit PBE1 [Arabidopsis thaliana] >gi 4850389 gb AAD31059.1 AC007357 8 (AC007357) Identical to gb Y13695 multicatalytic endopeptidase complex, proteasome precursor, beta subunit (prce) from Arabidopsis thaliana. ESTs gb_Y09360, gb_F13852, gb_T20555, gb_T44620, gb AI099779 and gb AA5861 Seq. No. 416376 Seq. ID uC-osflm202110b01b1 BLASTX Method NCBI GI q485742 BLAST score 524 E value 1.0e-57 Match length 147 82 % identity NCBI Description (L32791) pyrophosphatase [Beta vulgaris] 416377 Seq. No. Seq. ID uC-osflm202110b02b1 BLASTX Method NCBI GI g5002521 BLAST score 193 E value 1.0e-14 Match length 78 % identity NCBI Description (AL078606) putative protein [Arabidopsis thaliana] Seq. No. 416378 Seq. ID uC-osflm202110b09b1 Method BLASTX NCBI GI q2146739 BLAST score 587

9.0e-61 E value Match length 162

% identity 70

NCBI Description hexokinase (EC 2.7.1.1) 1 - Arabidopsis thaliana >gi 881521

(U28214) hexokinase 1 [Arabidopsis thaliana]

>gi_4972059_emb_CAB43927.1_ (AL078470) hexokinase

[Arabidopsis thaliana]

Seq. No. 416379

Seq. ID uC-osflm202110b10b1

Method BLASTX

```
Seq. ID
                   uC-osflcyp067b11a1
Method
                   BLASTX
NCBI GI
                   q115813
BLAST score
                   332
E value
                   8.0e-31
Match length
                   96
                   74
% identity
NCBI Description
                   CHLOROPHYLL A-B BINDING PROTEIN 8 PRECURSOR (LHCI TYPE III
                   CAB-8) >gi 19182 emb CAA33330 (X15258) Type III
                   chlorophyll a/b-binding protein [Lycopersicon esculentum]
Seq. No.
                   411234
Seq. ID
                   uC-osflcyp067b12a1
Method
                   BLASTX
NCBI GI
                   g2341025
BLAST score
                   248
E value
                   5.0e-21
Match length
                   65
% identity
                   72
NCBI Description (AC000104) F19P19.2 [Arabidopsis thaliana]
Seq. No.
                   411235
Seq. ID
                   uC-osflcyp067c02a1
Method
                   BLASTN
                   g1917018
NCBI GI
BLAST score
                   46
E value
                   2.0e-16
Match length
                   90
% identity
                   88
NCBI Description Zea mays ribosomal protein S6 RPS6-1 (rps6-1) mRNA,
                   complete cds
Seq. No.
                   411236
Seq. ID
                   uC-osflcyp067c12a1
Method
                   BLASTX
NCBI GI
                   q4567229
BLAST score
                   163
E value
                   6.0e-11
Match length
                   75
% identity
                   41
NCBI Description
                   (AC007119) putative pectin methylesterase [Arabidopsis
                   thaliana]
Seq. No.
                   411237
Seq. ID
                   uC-osflcyp067d02a1
Method
                   BLASTX
NCBI GI
                   g115787
BLAST score
                   541
E value
                   2.0e-55
Match length
                   103
% identity
                   100
                   CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I
NCBI Description
                   CAB-2) (LHCP) >gi_82461_pir__S03706 chlorophyll a/b-binding protein 2R precursor - rice >gi_20182_emb_CAA32109_
                   (X13909) chlorophyll a/b-binding preprotein (AA -28 to 235)
```

[Oryza sativa]

Method

NCBI GI

BLASTX

g480109

```
Seq. No.
                   411238
Seq. ID
                   uC-osflcyp067d06a1
Method
                   BLASTN
                   g4105602
NCBI GI
BLAST score
                   57
E value
                   7.0e-24
Match length
                   85
                   94
% identity
NCBI Description Oryza sativa metallothionein (MTe) gene, complete cds
Seq. No.
                   411239
Seq. ID
                   uC-osflcyp067d08a1
Method
                   BLASTX
NCBI GI
                   q5929928
BLAST score
                   174
E value
                   2.0e-12
Match length
                   40
% identity
                   88
                  (AF178950) voltage-dependent anion channel protein 1a [Zea
NCBI Description
                  mays]
Seq. No.
                   411240
Seq. ID
                   uC-osflcyp067d09a1
Method
                  BLASTX
NCBI GI
                  g3033398
BLAST score
                   348
E value
                   1.0e-32
Match length
                   89
% identity
                   75
NCBI Description
                  (AC004238) putative phosphoribosylaminoimidazolecarboxamide
                  formyltransferase [Arabidopsis thaliana]
Seq. No.
                   411241
Seq. ID
                   uC-osflcyp067d10a1
Method
                  BLASTX
NCBI GI
                  g2988398
BLAST score
                  173
E value
                   4.0e-12
Match length
                  113
% identity
NCBI Description (AC004381) Unknown gene product [Homo sapiens]
Seq. No.
                   411242
Seq. ID
                  uC-osflcyp067d11a1
Method
                  BLASTN
NCBI GI
                  g4097337
BLAST score
                  469
E value
                  0.0e + 00
Match length
                  469
% identity
                  100
NCBI Description Oryza sativa metallothionein-like protein mRNA, complete
                  cds
Seq. No.
                  411243
Seq. ID
                  uC-osflcyp067e04a1
```

BLAST score

Match length

E value

187

39

3.0e-14

```
BLAST score
                   160
                   1.0e-10
E value
                   79
Match length
% identity
                   1
                  EPPT protein - hydromedusa (Podocoryne carnea) (fragment)
NCBI Description
                   >gi 396743 emb CAA52402 (X74358) Pod-EPPT [Podocoryne
                   carnea]
                   411244
Seq. No.
                   uC-osflcyp067e11a1
Seq. ID
Method
                   BLASTN
NCBI GI
                   g3986152
BLAST score
                   61
E value
                   1.0e-25
                   226
Match length
% identity
                   82
NCBI Description Oryza sativa gene for plastidic ATP sulfurylase, complete
                   cds
                   411245
Seq. No.
                   uC-osflcyp067e12a1
Seq. ID
Method
                  BLASTX
NCBI GI
                   g1653665
BLAST score
                   263
E value
                   9.0e-23
Match length
                   81
% identity
                   62
NCBI Description (D90915) peptide chain release factor [Synechocystis sp.]
Seq. No.
                   411246
                   uC-osflcyp067f03a1
Seq. ID
Method
                  BLASTN
NCBI GI
                   g3721941
BLAST score
                   144
E value
                   2.0e-75
Match length
                  184
% identity
                   95
NCBI Description Oryza sativa mRNA for chitinase, complete cds
Seq. No.
                   411247
Seq. ID
                  uC-osflcyp067f04a1
Method
                  BLASTN
NCBI GI
                   q968995
BLAST score
                   145
E value
                   1.0e-75
Match length
                   216
% identity
                   93
NCBI Description Oryza sativa clone glyceraldehyde-3-phosphate dehydrogenase
                   (Gpc) mRNA, complete cds
                   411248
Seq. No.
Seq. ID
                  uC-osflcyp067f07a1
Method
                  BLASTX
NCBI GI
                   g671737
```

```
% identity
                   87
NCBI Description
                   (X74731) Chloropyll a/b binding protein [Amaranthus
                   hypochondriacus]
Seq. No.
                   411249
Seq. ID
                   uC-osflcyp067f11a1
Method
                  BLASTX
                   g4191785
NCBI GI
BLAST score
                  174
E value
                   2.0e-12
Match length
                   50
% identity
                   62
NCBI Description
                 (AC005917) putative hydrolase [Arabidopsis thaliana]
                   411250
Seq. No.
Seq. ID
                   uC-osflcyp067g06a1
Method
                  BLASTX
NCBI GI
                   q4581156
BLAST score
                   143
                   6.0e-09
E value
Match length
                   32
% identity
                   88
NCBI Description (AC006919) putative pyruvate kinase [Arabidopsis thaliana]
Seq. No.
                   411251
                   uC-osflcyp067g08a1
Seq. ID
Method
                  BLASTN
NCBI GI
                   q2072726
BLAST score
                   366
E value
                   0.0e + 00
Match length
                   411
% identity
                   98
NCBI Description O.sativa mRNA for Fd-GOGAT, partial, clone OsGog2
                   411252
Seq. No.
Seq. ID
                  uC-osflcyp067h03a1
Method
                  BLASTX
NCBI GI
                   q2494320
BLAST score
                   159
E value
                   1.0e-10
Match length
                   39
% identity
                   74
NCBI Description
                  EUKARYOTIC TRANSLATION INITIATION FACTOR 5 (EIF-5)
                   >gi_1806575_emb_CAA67868_ (X99517) Eukaryotic initiation
                   factor-5 [Zea mays]
Seq. No.
                   411253
Seq. ID
                   uC-osflcyp067h04a1
Method
                  BLASTX
NCBI GI
                  g3695392
BLAST score
                  172
E value
                   4.0e-12
                  98
Match length
% identity
                   43
NCBI Description (AF096371) No definition line found [Arabidopsis thaliana]
Seq. No.
                   411254
```

% identity

```
Seq. ID
                  uC-osflcyp067h05a1
Method
                  BLASTX
NCBI GI
                  q4539389
BLAST score
                  376
E value
                   6.0e-36
Match length
                  176
                   47
% identity
NCBI Description
                  (AL035526) putative protein kinase [Arabidopsis thaliana]
Seq. No.
                  411255
Seq. ID
                  uC-osflcyp067h12a1
Method
                  BLASTN
                  q3859567
NCBI GI
BLAST score
                  199
E value
                  1.0e-108
Match length
                  274
                  92
% identity
NCBI Description Oryza sativa clone FIL1 unknown mRNA
Seq. No.
                  411256
                  uC-osflcyp068a09b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q483412
BLAST score
                  207
                   3.0e-16
E value
Match length
                  125
% identity
                   44
NCBI Description (L01497) calmodulin-binding protein [Zea mays]
                   411257
Seq. No.
Seq. ID
                   uC-osflcyp068c09b1
Method
                  BLASTX
NCBI GI
                   g1408222
BLAST score
                  520
E value
                   7.0e-53
Match length
                  151
                   70
% identity
NCBI Description (U60764) pathogenesis-related protein [Sorghum bicolor]
Seq. No.
                   411258
Seq. ID
                   uC-osflcyp068d05b1
Method
                  BLASTX
NCBI GI
                  g1261917
BLAST score
                   315
E value
                   9.0e-29
                  90
Match length
% identity
                   60
NCBI Description (X96979) lipid transfer protein 7a2b [Hordeum vulgare]
Seq. No.
                   411259
Seq. ID
                  uC-osflcyp068e01b1
Method
                  BLASTX
NCBI GI
                  g3482933
BLAST score
                  384
E value
                   6.0e-37
Match length
                  157
```

```
NCBI Description
                   (AC003970) Similar to cdc2 protein kinases [Arabidopsis
                   thaliana]
                   411260
Seq. No.
Seq. ID
                  uC-osflcyp068h05b1
Method
                  BLASTX
NCBI GI
                  g3668097
BLAST score
                  548
                   4.0e-56
E value
Match length
                  143
% identity
                  70
NCBI Description (AC004667) putative glycine cleavage system protein H
                  precursor [Arabidopsis thaliana]
                  411261
Seq. No.
Seq. ID
                  uC-osflcyp070a08a1
Method
                  BLASTX
NCBI GI
                  q4678260
BLAST score
                  198
                  3.0e-15
E value
Match length
                  68
                  54
% identity
NCBI Description (AL049657) putative protein [Arabidopsis thaliana]
                  411262
Seq. No.
                  uC-osflcyp070b07a1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g6063536
BLAST score
                  219
E value
                  1.0e-17
Match length
                  48
% identity
                  88
                  (AP000615) ESTs C22369(C12239), C22370(C12239),
NCBI Description
                  AU057852(S21844), AU057853(S21844) correspond to a region of
                  the predicted gene.; similar to calcium dependent protein
                  kinase. (AF048691) [Oryza sativa]
                  411263
Seq. No.
Seq. ID
                  uC-osflcyp070b10a1
Method
                  BLASTX
NCBI GI
                  g4574139
BLAST score
                  283
E value
                  7.0e-30
Match length
                  95
% identity
NCBI Description (AF073697) cysteine synthase [Oryza sativa]
Seq. No.
                  411264
Seq. ID
                  uC-osflcyp070c08a1
Method
                  BLASTX
NCBI GI
                  g2773154
BLAST score
                  228
E value
                  1.0e-18
Match length
                  58
                  76
% identity
NCBI Description
                  (AF039573) abscisic acid- and stress-inducible protein
                  [Oryza sativa]
```

53425

a waterday)

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Seq. No.
                   411265
Seq. ID
                   uC-osflcyp070d01a1
Method
                   BLASTX
NCBI GI
                   g6017110
BLAST score
                   209
E value
                   2.0e-16
Match length
                   52
% identity
                   71
NCBI Description (AC009895) unknown protein [Arabidopsis thaliana]
Seq. No.
                   411266
Seq. ID
                  uC-osflcyp070h07a1
Method
                  BLASTN
NCBI GI
                  g20191
BLAST score
                   372
E value
                   0.0e+00
Match length
                   455
% identity
                   96
NCBI Description O.sativa mRNA for catalase
                   411267
Seq. No.
Seq. ID
                  uC-osflcyp070h12a1
Method
                  BLASTX
NCBI GI
                  g5541723
BLAST score
                  189
E value
                   3.0e-14
Match length
                  53
% identity
                   62
NCBI Description (AL096856) betaine aldehyde dehydrogenase-like protein
                   [Arabidopsis thaliana]
Seq. No.
                   411268
Seq. ID
                  uC-osflcyp071a01b1
Method
                  BLASTX
NCBI GI
                  g3402711
BLAST score
                  164
E value
                   4.0e-11
Match length
                  81
% identity
                   41
NCBI Description
                   (AC004261) putative RNA-binding protein [Arabidopsis
                  thaliana]
                   411269
Seq. No.
Seq. ID
                  uC-osflcyp071a03b1
Method
                  BLASTX
NCBI GI
                  g4063751
BLAST score
                  256
E value
                  6.0e-22
Match length
                  134
% identity
                  44
NCBI Description
                  (AC005851) putative white protein [Arabidopsis thaliana]
                  >gi_4510409_gb_AAD21495.1_ (AC006929) putative white
                  protein [Arabidopsis thaliana]
Seq. No.
                  411270
Seq. ID
                  uC-osflcyp071a07b1
```

```
Method
                   BLASTX
NCBI GI
                   g2244847
BLAST score
                   168
                   1.0e-11
E value
Match length
                   130
% identity
                   32
                  (Z97337) hydroxyproline-rich glycoprotein homolog
NCBI Description
                   [Arabidopsis thaliana]
                   411271
Seq. No.
                   uC-osflcyp071a08b1
Seq. ID
Method
                   BLASTX
                   g5802225
NCBI GI
BLAST score
                   335
                   4.0e-36
E value
Match length
                   99
                   76
% identity
NCBI Description (AF166262) HAL3A protein [Arabidopsis thaliana]
Seq. No.
                   411272
                   uC-osflcyp071a09a1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g5802225
BLAST score
                   254
E value
                   1.0e-21
                   65
Match length
% identity
                   74
NCBI Description (AF166262) HAL3A protein [Arabidopsis thaliana]
Seq. No.
                   411273
Seq. ID
                   uC-osflcyp071a09b1
Method
                   BLASTX
NCBI GI
                   g3402675
BLAST score
                   160
                   1.0e-10
E value
Match length
                   73
% identity
                   48
NCBI Description
                  (AC004697) hypothetical protein [Arabidopsis thaliana]
                   411274
Seq. No.
Seq. ID
                   uC-osflcyp071a10b1
Method
                   BLASTX
NCBI GI
                   g3413511
BLAST score
                   306
E value
                   2.0e-42
                   124
% identity
                   70
NCBI Description
                   (AJ000265) glucose-6-phosphate isomerase [Spinacia
```

Match length

oleracea]

411275 Seq. No.

Seq. ID uC-osflcyp071a12b1

Method BLASTX NCBI GI g128388 BLAST score 198 E value 2.0e-15 Match length 61

% identity NCBI Description NONSPECIFIC LIPID-TRANSFER PROTEIN PRECURSOR (LTP) (PHOSPHOLIPID TRANSFER PROTEIN) (PLTP) >gi_82711_pir__A31779 phospholipid transfer protein 9C2 precursor - maize >gi_168576 (J04176) phospholipid transfer protein precursor [Zea mays] Seq. No. 411276 Seq. ID uC-osflcyp071b02b1 Method BLASTX NCBI GI g1136122 BLAST score 750 E value 8.0e-80 Match length 140 % identity 100 NCBI Description (X91807) alfa-tubulin [Oryza sativa] 411277 Seq. No. Seq. ID uC-osflcyp071b03b1 Method BLASTX NCBI GI q1708107 BLAST score 162 E value 6.0e-21Match length 71 % identity 89 NCBI Description HISTONE H2B >gi 473605 (U08226) histone H2B [Zea mays] Seq. No. 411278 Seq. ID uC-osflcyp071b04b1 Method BLASTX NCBI GI g2914710 BLAST score 304 E value 7.0e-40Match length 156 % identity 57 NCBI Description (AC003974) putative beta-D-galactosidase [Arabidopsis thaliana Seq. No. 411279 Seq. ID uC-osflcyp071b05b1 Method BLASTX NCBI GI g3983665 BLAST score 731 E value 1.0e-77 Match length 156 % identity 92 NCBI Description (AB011271) importin-beta2 [Oryza sativa] Seq. No. 411280 Seq. ID uC-osflcyp071b06b1 Method BLASTX NCBI GI g5263310 BLAST score 214 E value 6.0e-17 Match length 76 % identity

NCBI Description (AC007727) EST gb_N95925 comes from this gene. [Arabidopsis

```
thaliana]
Seq. No.
                   411281
Seq. ID
                  uC-osflcyp071b11b1
Method
                  BLASTX
NCBI GI
                  g2055262
BLAST score
                  472
E value
                  2.0e-47
Match length
                  125
                  73
% identity
NCBI Description (AB003194) chitinase IIb [Oryza sativa]
Seq. No.
                  411282
Seq. ID
                  uC-osflcyp071b12b1
Method
                  BLASTX
NCBI GI
                  g2827516
BLAST score
                  319
E value
                  2.0e-29
Match length
                  134
% identity
                  46
NCBI Description (AL021633) DNA topoisomerase like-protein [Arabidopsis
                  thaliana]
                  411283
Seq. No.
Seq. ID
                  uC-osflcyp071c01a1
Method
                  BLASTX
NCBI GI
                  g2492519
BLAST score
                  586
E value
                  1.0e-60
Match length
                  112
% identity
                  100
NCBI Description
                  26S PROTEASE REGULATORY SUBUNIT 7 (26S PROTEASOME SUBUNIT
                   7) >gi_1395191_dbj_BAA13021_ (D86121) 26S proteasome ATPase
                  subunit [Spinacia oleracea]
Seq. No.
                  411284
Seq. ID
                  uC-osflcyp071c01b1
                  BLASTX
Method
NCBI GI
                  g6056388
BLAST score
                  696
E value
                  2.0e-73
Match length
                  150
% identity
                  89
                  (AC009324) 26S proteasome ATPase subunit [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  411285
Seq. ID
                  uC-osflcyp071c02b1
```

Method BLASTX

NCBI GI g1076800 BLAST score 481 E value 2.0e-48 Match length 131 % identity 69

NCBI Description L-ascorbate peroxidase (EC 1.11.1.11), cytosolic isozyme maize >gi 600116 emb CAA84406 (Z34934) cytosolic ascorbate peroxidase [Zea mays] >gi_1096503_prf__2111423A ascorbate

Seq. No.

Seq. ID

Method

NCBI GI

411291

BLASTX

g5360230

uC-osflcyp071d02b1

peroxidase [Zea mays] Seq. No. 411286 Seq. ID uC-osflcyp071c03b1 Method BLASTX NCBI GI g671740 BLAST score 397 E value 2.0e-38 Match length 72 % identity 100 (X84730) ribulose-bisphosphate carboxylase [synthetic NCBI Description construct] Seq. No. 411287 Seq. ID uC-osflcyp071c05b1 Method BLASTX NCBI GI g2245125 BLAST score 163 E value 6.0e-11 Match length 87 % identity 44 NCBI Description (Z97343) hypothetical protein [Arabidopsis thaliana] Seq. No. 411288 uC-osflcyp071c07b1 Seq. ID Method BLASTX NCBI GI q4158219 BLAST score 365 E value 1.0e-34 Match length 80 90 % identity NCBI Description (Y18623) amylogenin [Oryza sativa] 411289 Seq. No. Seq. ID uC-osflcyp071c10b1 BLASTN Method NCBI GI g312180 BLAST score 45 E value 6.0e-16 Match length 101 % identity 86 NCBI Description Z.mays GapC4 gene Seq. No. 411290 Seq. ID uC-osflcyp071c11b1 Method BLASTX NCBI GI g2293480 BLAST score 402 E value 3.0e-39 Match length 85 % identity NCBI Description (AF011331) glycine-rich protein [Oryza sativa]

Seq. No.

411297

```
BLAST score
                   836
E value
                   7.0e-90
Match length
                   164
% identity
                   94
NCBI Description (AB015287) Ran [Oryza sativa]
Seq. No.
                   411292
Seq. ID
                  uC-osflcyp071d04b1
Method
                  BLASTX
NCBI GI
                   g4835767
BLAST score
                   544
E value
                   1.0e-55
Match length
                   166
% identity
                   61
NCBI Description (AC007202) T8K14.16 [Arabidopsis thaliana]
Seq. No.
                   411293
Seq. ID
                  uC-osflcyp071d06b1
Method
                  BLASTX
NCBI GI
                  g5031281
BLAST score
                  277
E value
                   2.0e-24
Match length
                   113
% identity
                   58
NCBI Description (AF139499) unknown [Prunus armeniaca]
Seq. No.
                   411294
Seq. ID
                  uC-osflcyp071d07b1
Method
                  BLASTN
NCBI GI
                  g2822482
BLAST score
                  40
E value
                  3.0e-13
Match length
                  64
% identity
                  91
NCBI Description Maackia amurensis 14-3-3 protein homolog mRNA, complete cds
Seq. No.
                   411295
Seq. ID
                  uC-osflcyp071d09b1
Method
                  BLASTX
NCBI GI
                  g3128173
BLAST score
                  364
E value
                  1.0e-34
                  97
Match length
                  75
% identity
NCBI Description (AC004521) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  411296
Seq. ID
                  uC-osflcyp071d10b1
Method
                  BLASTX
                  g1498388
NCBI GI
BLAST score
                  769
E value
                  4.0e-82
Match length
                  169
% identity
                  90
NCBI Description (U60510) actin [Zea mays]
```

BLAST score

```
Seq. ID
                   uC-osflcyp071d11b1
Method
                   BLASTX
NCBI GI
                   q5802606
BLAST score
                   757
E value
                   1.0e-80
Match length
                   152
% identity
NCBI Description (AF174486) methylenetetrahydrofolate reductase [Zea mays]
Seq. No.
                   411298
Seq. ID
                   uC-osflcyp071d12b1
Method
                   BLASTX
NCBI GI
                   q2286153
BLAST score
                   828
E value
                   5.0e-89
Match length
                   169
% identity
NCBI Description (AF007581) cytoplasmic malate dehydrogenase [Zea mays]
Seq. No.
                   411299
Seq. ID
                   uC-osflcyp071e02b1
Method
                   BLASTX
NCBI GI
                   q4678376
BLAST score
                   293
E value
                   3.0e-26
Match length
                   71
% identity
NCBI Description (AL049656) putative protein [Arabidopsis thaliana]
Seq. No.
                   411300
Seq. ID
                   uC-osflcyp071e03b1
Method
                   BLASTX
NCBI GI
                   q5263314
BLAST score
                   370
E value
                   2.0e-35
Match length
                   122
% identity
                   57
NCBI Description
                   (AC007727) Similar to gb_X84260 POS5 gene product from
                   Saccharomyces cerevisiae. EST gb W43879 comes from this
                   gene. [Arabidopsis thaliana]
Seq. No.
                   411301
Seq. ID
                   uC-osflcyp071e06b1
Method
                   BLASTX
NCBI GI
                   g5731737
BLAST score
                   322
E value
                   7.0e-30
Match length
                   66
% identity
                   91
NCBI Description
                   (AB021878) similar to yeast sodium/proton exchanger [Oryza
                   sativa]
Seq. No.
                   411302
Seq. ID
                  uC-osflcyp071e07b1
Method
                  BLASTX
NCBI GI
                  g1872521
```

E value 2.0e-29 Match length 122 % identity 55 NCBI Description (U87833) zinc-finger protein Lsd1 [Arabidopsis thaliana] >gi_1872523 (U87834) zinc-finger protein Lsd1 [Arabidopsis thaliana] >gi_5262161_emb_CAB45804.1 (AL080253) zinc-finger protein Lsdl [Arabidopsis thaliana] Seq. No. 411303 uC-osflcyp071e09b1 Seq. ID Method BLASTX NCBI GI q4105561 BLAST score 339 E value 5.0e-32 Match length 97 % identity 75 NCBI Description (AF047444) ribulose-5-phosphate-3-epimerase [Oryza sativa] Seq. No. 411304 Seq. ID uC-osflcyp071f01b1 Method BLASTX NCBI GI g3914685 BLAST score 687 E value 1.0e-72Match length 140 % identity 93 NCBI Description 60S RIBOSOMAL PROTEIN L17 >gi 2668748 (AF034948) ribosomal protein L17 [Zea mays] Seq. No. 411305 Seq. ID uC-osflcyp071f02b1 Method BLASTX NCBI GI q1706260 BLAST score 566 E value 2.0e-58 Match length 120 % identity 90 CYSTEINE PROTEINASE 1 PRECURSOR >gi 2118131 pir S59597 NCBI Description cysteine proteinase 1 precursor - maize >gi_643597_dbj_BAA08244_ (D45402) cysteine proteinase [Zea mays] Seq. No. 411306 Seq. ID uC-osflcyp071f03b1 Method BLASTX NCBI GI g477819 BLAST score 529 E value 7.0e-54 179 Match length 56 % identity NCBI Description mitochondrial processing peptidase (EC 3.4.99.41) beta chain precursor - potato >gi_410634_bbs_136741 cytochrome c reductase-processing peptidase subunit II, MPP subunit II, P53 [potatoes, var. Marfona, tuber, Peptide Mitochondrial,

Seq. No. 411307

530 aa]

```
Seq. ID
                  uC-osflcyp071f07b1
Method
                  BLASTX
NCBI GI
                  a3075488
BLAST score
                  513
E value
                  4.0e-52
Match length
                  116
                  84
% identity
NCBI Description
                 (AF058796) chlorophyll a/b-binding protein [Oryza sativa]
Seq. No.
                  411308
                  uC-osflcyp071f08b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3183991
BLAST score
                  383
E value
                  7.0e-37
Match length
                  143
                  57
% identity
NCBI Description
                 (AJ005173) P69F protein [Lycopersicon esculentum]
                  411309
Seq. No.
Seq. ID
                  uC-osflcyp071f10b1
Method
                  BLASTX
NCBI GI
                  q3914140
BLAST score
                  414
E value
                  2.0e-40
Match length
                  91
                  87
% identity
                  NONSPECIFIC LIPID-TRANSFER PROTEIN 5 PRECURSOR (LTP 5)
NCBI Description
                  >gi 3172343 (AF051369) lipid transfer protein [Oryza
                  sativa]
Seq. No.
                  411310
Seq. ID
                  uC-osflcyp071f11b1
Method
                  BLASTX
NCBI GI
                  q4455208
BLAST score
                  672
E value
                  1.0e-70
Match length
                  181
                  71
% identity
NCBI Description (AL035440) putative protein [Arabidopsis thaliana]
Seq. No.
                  411311
Seq. ID
                  uC-osflcyp071f12b1
Method
                  BLASTX
NCBI GI
                  q3023751
BLAST score
                  302
E value
                  3.0e-27
Match length
                  153
% identity
                  44
NCBI Description
                  70 KD PEPTIDYLPROLYL ISOMERASE (PEPTIDYLPROLYL CIS-TRANS
                  ISOMERASE) (CYCLOPHILIN) (PPIASE) >gi 1076772 pir S55383
                  peptidylprolyl isomerase (EC 5.2.1.8) - wheat
                  >gi 854626 emb CAA60505 (X86903) peptidylprolyl isomerase
                  [Triticum aestivum]
Seq. No.
                  411312
Seq. ID
                  uC-osflcyp071g03b1
```

```
Method
                  BLASTX
NCBI GI
                  g5730132
BLAST score
                   284
E value
                   2.0e-25
Match length
                  73
                   73
% identity
NCBI Description (AL109796) snRNP Sm protein F-like [Arabidopsis thaliana]
                   411313
Seq. No.
Seq. ID
                  uC-osflcyp071g05b1
Method
                  BLASTX
NCBI GI
                  g2842493
BLAST score
                   306
E value
                   7.0e-28
Match length
                  87
% identity
                   66
NCBI Description (AL021749) predicted protein [Arabidopsis thaliana]
                   411314
Seq. No.
                  uC-osflcyp071g06b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4104220
BLAST score
                   502
E value
                   9.0e-51
Match length
                  158
                   68
% identity
NCBI Description
                  (AF033538) caffeic acid O-methyltransferase; LPOMT1 [Lolium
                  perenne]
                   411315
Seq. No.
Seq. ID
                  uC-osflcyp071g07b1
Method
                  BLASTX
NCBI GI
                   q3043612
BLAST score
                  171
E value
                   5.0e-12
Match length
                  141
% identity
                   35
NCBI Description (AB011116) KIAA0544 protein [Homo sapiens]
Seq. No.
                   411316
Seq. ID
                  uC-osflcyp071g08b1
Method
                  BLASTX
NCBI GI
                  g5903091
BLAST score
                  166
E value
                  2.0e-11
Match length
                  90
% identity
                   43
NCBI Description (AC008017) Hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   411317
Seq. ID
                  uC-osflcyp071g10b1
Method
                  BLASTX
NCBI GI
                  g2120736
BLAST score
                  178
E_value
                  9.0e-13
Match length
                  152
% identity
                  30
```

X-Pro dipeptidyl-peptidase (EC 3.4.14.11) - Xanthomonas NCBI Description maltophilia >gi_1753197_dbj_BAA11872_ (D83263) dipeptidyl peptidase IV [Stenotrophomonas maltophilia] 411318 Seq. No. uC-osflcyp071g11b1 Seq. ID Method BLASTX g2739383 NCBI GI 455 BLAST score 3.0e-45E value Match length 155 % identity 61 (AC002505) unknown protein [Arabidopsis thaliana] NCBI Description 411319 Seq. No. uC-osflcyp071g12b1 Seq. ID Method BLASTX NCBI GI g1362051 BLAST score 351 5.0e-33 E value 131 Match length 60 % identity protein kinase 3 - soybean >gi_310582 (L19361) protein NCBI Description kinase 3 [Glycine max] Seq. No. 411320 Seq. ID uC-osflcyp071h02b1 Method BLASTN NCBI GI q2773153 250 BLAST score 1.0e-138 E value Match length 250 100 % identity NCBI Description Oryza sativa abscisic acid- and stress-inducible protein (Asr1) mRNA, complete cds Seq. No. 411321 uC-osflcyp071h03b1 Seq. ID Method BLASTN NCBI GI q3335356 35 BLAST score E value 4.0e-10 51 Match length % identity NCBI Description Arabidopsis thaliana chromosome II BAC F16M14 genomic sequence, complete sequence [Arabidopsis thaliana] Seq. No. 411322 Seq. ID uC-osflcyp071h04b1 BLASTX Method NCBI GI q2829275 BLAST score 144 E value 5.0e-09 Match length 85 % identity (AF044265) nucleoside diphosphate kinase 3 [Arabidopsis NCBI Description

thaliana] >gi_3513740 (AF080118) contains similarity to

```
nucleoside diphosphate kinases (Pfam: NDK.hmm, score: 301.12) [Arabidopsis thaliana] >gi_4539375_emb_CAB40069.1_(AL049525) nucleoside diphosphate kinase 3 (ndpk3) [Arabidopsis thaliana]
```

Seq. No. 411323

Seq. ID uC-osflcyp071h05b1

Method BLASTX
NCBI GI g1213601
BLAST score 484
E value 1.0e-48
Match length 93
% identity 100

NCBI Description (X15901) ribosomal protein S19 [Oryza sativa]

>gi_226648_prf__1603356BY ribosomal protein S19 [Oryza

sativa]

Seq. No. 411324

Seq. ID uC-osflcyp071h06b1

Method BLASTN
NCBI GI g2182028
BLAST score 64
E value 1.0e-27
Match length 64
% identity 100

NCBI Description Oryza sativa mRNA for shaggy-like kinase etha

Seq. No. 411325

Seq. ID uC-osflcyp071h09b1

Method BLASTX
NCBI GI g1777312
BLAST score 218
E value 2.0e-17
Match length 99
% identity 48

NCBI Description (D30622) novel serine/threonine protein kinase [Arabidopsis

thaliana]

Seq. No. 411326

Seq. ID uC-osflcyp071h10b1

Method BLASTX
NCBI GI g3785989
BLAST score 588
E value 8.0e-61
Match length 176
% identity 68

NCBI Description (AC005560) unknown protein [Arabidopsis thaliana]

Seq. No. 411327

Seq. ID uC-osflcyp071h11b1

Method BLASTX
NCBI GI g3068705
BLAST score 161
E value 9.0e-11
Match length 97
% identity 35

NCBI Description (AF049236) unknown [Arabidopsis thaliana]

Method

BLASTX

```
411328
Seq. No.
                   uC-osflcyp071h12b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g6102610
                   171
BLAST score
E value
                   5.0e-12
                   107
Match length
% identity
                   35
NCBI Description (AF187317) CAF protein [Arabidopsis thaliana]
Seq. No.
                   411329
                   uC-osflcyp073a01a1
Seq. ID
Method
                   BLASTN
NCBI GI
                   a3885887
BLAST score
                   364
E value
                   0.0e + 00
                   412
Match length
                   97
% identity
NCBI Description Oryza sativa high mobility group protein (HMG) mRNA,
                   complete cds
Seq. No.
                   411330
Seq. ID
                   uC-osflcyp073a01b1
Method
                   BLASTN
NCBI GI
                   g3885887
BLAST score
                   360
                   0.0e + 00
E value
Match length
                   389
% identity
NCBI Description Oryza sativa high mobility group protein (HMG) mRNA,
                   complete cds
Seq. No.
                   411331
Seq. ID
                   uC-osflcyp073a02b1
Method
                   BLASTX
NCBI GI
                   g5734712
BLAST score
                   152
E value
                   5.0e-10
Match length
                   51
% identity
                   57
NCBI Description
                  (AC008075) ESTs gb_T41781 and gb_AA586096 come from this
                   gene. [Arabidopsis thaliana]
Seq. No.
                   411332
Seq. ID
                   uC-osflcyp073a03b1
Method
                   BLASTX
NCBI GI
                   g1350548
                   230
BLAST score
                   6.0e-19
E value
Match length
                   69
% identity
                   59
NCBI Description (L47609) heat shock-like protein [Picea glauca]
Seq. No.
                   411333
Seq. ID
                   uC-osflcyp073b02b1
```

```
NCBI GI
                   q5881784
BLAST score
                   191
E value
                   1.0e-21
Match length
                   81
% identity
                   74
NCBI Description
                   (AJ249442) putative AUX1-like permease [Arabidopsis
                   thaliana]
Seq. No.
                   411334
Seq. ID
                   uC-osflcyp073b04b1
Method
                   BLASTX
NCBI GI
                   q2982289
BLAST score
                   391
E value
                   2.0e-40
Match length
                   90
                   98
% identity
NCBI Description (AF051229) 60S ribosomal protein L17 [Picea mariana]
                   411335
Seq. No.
Seq. ID
                   uC-osflcyp073b11b1
Method
                   BLASTX
NCBI GI
                   g4099408
BLAST score
                   172
E value
                   8.0e-22
Match length
                   72
% identity
                   79
                  (U86763) delta-type tonoplast intrinsic protein [Triticum
NCBI Description
                   aestivuml
Seq. No.
                   411336
Seq. ID
                   uC-osflcyp073b12b1
Method
                   BLASTX
NCBI GI
                   g4191778
BLAST score
                   344
E value
                   2.0e-32
Match length
                   81
% identity
                   83
                   (AC005917) putative nucleosome assembly protein I
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                   411337
Seq. ID
                   uC-osflcyp073c05b1
Method
                   BLASTX
NCBI GI
                   g2129774
BLAST score
                   386
E value
                   3.0e-37
Match length
                   120
% identity
NCBI Description
                  xyloglucan endotransglycosylase-related protein XTR4 -
                   Arabidopsis thaliana (fragment) >qi 1244754 (U43486)
                   {\tt xyloglucan\ endotransglycosylase-related\ protein}
                   [Arabidopsis thaliana]
```

Seq. No. 411338

Seq. ID uC-osflcyp073c06b1

Method BLASTX NCBI GI g2832630

```
BLAST score
                  243
                  2.0e-20
E value
                  78
Match length
                  58
% identity
NCBI Description
                 (AL021711) putative protein [Arabidopsis thaliana]
                  411339
Seq. No.
                  uC-osflcyp073c07b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2497746
BLAST score
                  194
E value
                  8.0e-15
Match length
                  113
                  42
% identity
                 NONSPECIFIC LIPID-TRANSFER PROTEIN 2 PRECURSOR (LTP 2)
NCBI Description
                  >gi 951334 (U31766) lipid transfer protein precursor [Oryza
                  satīva]
                  411340
Seq. No.
Seq. ID
                  uC-osflcyp073c08b1
Method
                  BLASTN
NCBI GI
                  g1532047
BLAST score
                  83
E value
                  1.0e-38
Match length
                  177
                  89
% identity
NCBI Description O.sativa mRNA for S-adenosylmethionine decarboxylase
                  411341
Seq. No.
                  uC-osflcyp073d01b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q5734748
BLAST score
                  239
E value
                  4.0e-20
Match length
                  79
% identity
                  57
NCBI Description (AC007651) Unknown protein [Arabidopsis thaliana]
Seq. No.
                  411342
Seq. ID
                  uC-osflcyp073d03b1
Method
                  BLASTX
NCBI GI
                  g2880048
BLAST score
                  400
                  2.0e-53
E value
                  127
Match length
% identity
                  75
NCBI Description (AC002340) unknown protein [Arabidopsis thaliana]
                  411343
Seq. No.
Seq. ID
                  uC-osflcyp073d04b1
Method
                  BLASTX
NCBI GI
                  g100638
BLAST score
                  402
E value
                  3.0e-39
                  105
Match length
% identity
                  65
NCBI Description pollen allergen Lol p I precursor (clone 5A) - perennial
```

Method

NCBI GI

E value

BLAST score

Match length

% identity

BLASTX

196

93

41

g729478

3.0e-15



perenne]

```
Seq. No.
                  411344
Seq. ID
                  uC-osflcyp073d06b1
                  BLASTX
Method
                  g5668812
NCBI GI
BLAST score
                  203
E value
                  1.0e-23
Match length
                  113
                  49
% identity
NCBI Description
                  (AC007519) Contains 3 PF 00076 RNA recognition motif
                  domains. ESTs gb_R30092, gb_R30093, gb_AA394338, gb_N65719
                  and gb AA597577 come from this gene. [Arabidopsis thaliana]
Seq. No.
                  411345
Seq. ID
                  uC-osflcyp073d07b1
Method
                  BLASTX
                  g543711
NCBI GI
BLAST score
                  156
E value
                  2.0e-10
Match length
                  35
                  94
% identity
NCBI Description
                  14-3-3-LIKE PROTEIN S94 >gi_419796_pir__S30927 14-3-3
                  protein homolog - rice >gi_303859_dbj_BAA03711_ (D16140)
                  brain specific protein [Oryza sativa]
Seq. No.
                  411346
Seq. ID
                  uC-osflcyp073d08b1
Method
                  BLASTX
NCBI GI
                  g3157927
BLAST score
                  210
E value
                   1.0e-16
Match length
                  78
% identity
                  59
NCBI Description
                   (AC002131) Contains similarity to GDP-dissociation
                  inhibitor gb L07918 from Mus musculus. [Arabidopsis
                  thaliana]
Seq. No.
                   411347
Seq. ID
                  uC-osflcyp073d09b1
Method
                  BLASTX
NCBI GI
                  g553107
BLAST score
                  325
E value
                  2.0e-38
Match length
                  97
% identity
                  80
NCBI Description (L04967) triosephosphate isomerase [Oryza sativa]
Seq. No.
                  411348
Seq. ID
                  uC-osflcyp073d10b1
```

ryegrass >gi 168316 (M57474) pollen allergen [Lolium

Match length

124

```
NCBI Description FERREDOXIN--NADP REDUCTASE, LEAF ISOZYME PRECURSOR (FNR)
                   >gi_442481_dbj_BAA04616_ (D17790) ferredoxin-NADP+
reductase [Oryza sativa] >gi_6069649_dbj_BAA85425.1
                   (AP000616) ESTs AU078647(E1557), C72400(E1557) correspond to
                   a region of the predicted gene.; similar to
                   ferredoxin-NADP+ reductase (D17790) [Oryza sativa]
                   411349
Seq. No.
                   uC-osflcyp073d11b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3789954
BLAST score
                   345
E value
                   6.0e - 33
Match length
                   77
% identity
                   87
NCBI Description (AF094776) chlorophyll a/b-binding protein precursor [Oryza
                   sativa]
                   411350
Seq. No.
                   uC-osflcyp073d12b1
Seq. ID
Method
                   BLASTN
NCBI GI
                   g3885887
BLAST score
                   183
E value
                   2.0e-98
Match length
                   285
% identity
                   98
NCBI Description Oryza sativa high mobility group protein (HMG) mRNA,
                   complete cds
Seq. No.
                   411351
Seq. ID
                   uC-osflcyp073e01b1
Method
                   BLASTX
NCBI GI
                   q3169719
BLAST score
                   226
E value
                   2.0e-27
Match length
                   100
% identity
NCBI Description (AF007109) similar to yeast dcp1 [Arabidopsis thaliana]
Seq. No.
                   411352
Seq. ID
                   uC-osflcyp073e03b1
Method
                   BLASTN
NCBI GI
                   g1778820
BLAST score
                   206
E value
                   1.0e-112
Match length
                   293
% identity
                   93
NCBI Description Oryza sativa S-adenosyl-L-methionine synthetase (pOS-SAMS2)
                   mRNA, complete cds
Seq. No.
                   411353
Seq. ID
                   uC-osflcyp073e04b1
Method
                   BLASTX
NCBI GI
                   g2117937
BLAST score
                   585
E value
                   1.0e-60
```



% identity 94

NCBI Description UTP--glucose-1-phosphate uridylyltransferase (EC 2.7.7.9) -

barley >gi_1212996_emb_CAA62689_ (X91347) UDP-glucose

pyrophosphorylase [Hordeum vulgare]

Seq. No. 411354

Seq. ID uC-osflcyp073e07b1

Method BLASTX
NCBI GI g4455296
BLAST score 163
E value 3.0e-11
Match length 55
% identity 53

NCBI Description (AL035528) hypothetical protein [Arabidopsis thaliana]

Seq. No. 411355

Seq. ID uC-osflcyp073e08b1

Method BLASTX
NCBI GI 94895197
BLAST score 197
E value 3.0e-15
Match length 92
% identity 38

NCBI Description (AC007661) hypothetical protein [Arabidopsis thaliana]

Seq. No. 411356

Seq. ID uC-osflcyp073e10b1

Method BLASTX
NCBI GI g2293566
BLAST score 438
E value 6.0e-46
Match length 100
% identity 92

NCBI Description (AF012896) ADP-ribosylation factor 1 [Oryza sativa]

Seq. No. 411357

Seq. ID uC-osflcyp073e11b1

Method BLASTX
NCBI GI 94508073
BLAST score 196
E value 3.0e-19
Match length 113
% identity 46

NCBI Description (AC005882) 43220 [Arabidopsis thaliana]

Seq. No. 411358

Seq. ID uC-osflcyp073f02b1

Method BLASTN
NCBI GI 94097337
BLAST score 284
E value 1.0e-158
Match length 300
% identity 99

NCBI Description Oryza sativa metallothionein-like protein mRNA, complete

cds

Seq. No. 411359

NCBI GI

```
uC-osflcyp073f03b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   q4885026
BLAST score
                   536
E value
                   7.0e-55
Match length
                   139
                   79
% identity
NCBI Description
                 (AF147738) myosin VIII ZMM3 [Zea mays]
                   411360
Seq. No.
Seq. ID
                   uC-osflcyp073f05b1
Method
                  BLASTX
                  g464621
NCBI GI
BLAST score
                   349
E value
                   4.0e-33
Match length
                   105
                   70
% identity
NCBI Description 60S RIBOSOMAL PROTEIN L6 (YL16-LIKE) >gi 280374 pir S28586
                   ribosomal protein ML16 - common ice plant
                   >gi 19539 emb CAA49175 (X69378) ribosomal protein YL16
                   [Mesembryanthemum crystallinum]
Seq. No.
                   411361
Seq. ID
                   uC-osflcyp073f06b1
Method
                  BLASTX
NCBI GI
                   g2827709
BLAST score
                   287
E value
                   1.0e-25
Match length
                   113
% identity
NCBI Description
                 (AL021684) predicted protein [Arabidopsis thaliana]
                   411362
Seq. No.
Seq. ID
                  uC-osflcyp073f07b1
Method
                  BLASTX
NCBI GI
                   q1184774
BLAST score
                   389
E value
                   7.0e - 38
Match length
                   106
% identity
                   73
NCBI Description
                   (U45856) cytosolic glyceroldehyde-3-phosphate dehydrogenase
                  GAPC3 [Zea mays]
Seq. No.
                   411363
Seq. ID
                  uC-osflcyp073f08b1
Method
                  BLASTX
NCBI GI
                  g5802627
BLAST score
                   411
E value
                  3.0e-40
                  99
Match length
                  83
% identity
NCBI Description (AF176089) COP8 [Arabidopsis thaliana]
Seq. No.
                  411364
Seq. ID
                  uC-osflcyp073f10b1
Method
                  BLASTX
```

53444

g1184774

BLAST score 510 E value 5.0e-52 Match length 102 % identity 94

NCBI Description (U45856) cytosolic glyceroldehyde-3-phosphate dehydrogenase

GAPC3 [Zea mays]

Seq. No. 411365

Seq. ID uC-osflcyp073f11b1

Method BLASTN
NCBI GI g4680488
BLAST score 43
E value 2.0e-15
Match length 85
% identity 100

NCBI Description Oryza sativa BAC clone 1.H19, complete sequence

Seq. No. 411366

Seq. ID uC-osflcyp073g01b1

Method BLASTX
NCBI GI g4455250
BLAST score 184
E value 2.0e-28
Match length 135
% identity 53

NCBI Description (AL035523) putative protein [Arabidopsis thaliana]

Seq. No. 411367

Seq. ID uC-osflcyp073g05b1

Method BLASTX
NCBI GI g115787
BLAST score 381
E value 6.0e-37
Match length 97
% identity 81

NCBI Description CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I

CAB-2) (LHCP) >gi_82461_pir__S03706 chlorophyll a/b-binding

protein 2R precursor - rice >gi 20182 emb CAA32109

(X13909) chlorophyll a/b-binding preprotein (AA -28 to 235)

[Oryza sativa]

Seq. No. 411368

Seq. ID uC-osflcyp073g07b1

Method BLASTX
NCBI GI g3355477
BLAST score 371
E value 5.0e-36
Match length 77
% identity 46

NCBI Description (AC004218) putative P-glycoprotein, pgpl [Arabidopsis

thaliana]

Seq. No. 411369

Seq. ID uC-osflcyp073g09b1

Method BLASTX NCBI GI g3914422 BLAST score 623

Match length

NCBI Description

% identity

133

69

```
E value
                    4.0e-65
  Match length
                    120
                    93
  % identity
  NCBI Description PROFILIN >gi 2154728 emb CAA69669 (Y08389) profilin 2
                    [Cynodon dactylon] >gi 2154730 emb CAA69670 (Y08390)
                    profilin 1 [Cynodon dactylon]
  Seq. No.
                    411370
  Seq. ID
                    uC-osflcyp073g10b1
 Method
                    BLASTX
 NCBI GI
                    g5902380
  BLAST score
                    207
 E value
                    3.0e-16
 Match length
                    56
                    64
  % identity
 NCBI Description (AC009322) Hypothetical protein [Arabidopsis thaliana]
Seq. No.
                    411371
 Seq. ID
                    uC-osflcyp073h01b1
 Method
                    BLASTN
 NCBI GI
                    g3885887
 BLAST score
                    95
 E value
                    4.0e-46
 Match length
                    162
  % identity
                    90
 NCBI Description Oryza sativa high mobility group protein (HMG) mRNA,
                    complete cds
 Seq. No.
                    411372
 Seq. ID
                    uC-osflcyp073h07a1
 Method
                    BLASTN
 NCBI GI
                    g20163
 BLAST score
                    82
 E value
                    2.0e-38
 Match length
                    152
  % identity
                    90
 NCBI Description O.sativa Rrl5 mRNA for 5S ribosomal RNA
  Seq. No.
                    411373
  Seq. ID
                    uC-osflcyp073h07b1
 Method
                    BLASTX
 NCBI GI
                    g3915826
 BLAST score
                    309
 E value
                    1.0e-28
 Match length
                    79
  % identity
                    80
 NCBI Description 60S RIBOSOMAL PROTEIN L5
 Seq. No.
                    411374
 Seq. ID
                    uC-osflcyp073h10b1
 Method
                    BLASTX
 NCBI GI
                    g719291
 BLAST score
                    429
 E value
                    5.0e-43
```

(U19134) unknown [Arabidopsis thaliana]

```
>gi 1095007 prf 2107236A SABRE gene [Arabidopsis thaliana]
                  411375
Seq. No.
Seq. ID
                  uC-osflcyp073h11b1
Method
                  BLASTX
                  g730580
NCBI GI
BLAST score
                  436
                  7.0e-53
E value
Match length
                  114
% identity
                  99
NCBI Description 60S ACIDIC RIBOSOMAL PROTEIN PO >gi 455401 dbj BAA04668
                   (D21130) acidic ribosomal protein PO [Oryza sativa]
Seq. No.
                  411376
                  uC-osflcyp073h12b1
Seq. ID
Method
                  BLASTX
                  g3319776
NCBI GI
BLAST score
                  715
E value
                  7.0e-76
Match length
                  141
% identity
                  92
NCBI Description (AJ007665) seryl-tRNA synthetase [Zea mays]
                  411377
Seq. No.
                  uC-osflcyp074a03b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3023816
BLAST score
                  230
E value
                  3.0e-19
Match length
                  84
% identity
                  60
                  GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC
NCBI Description
                  >gi_968996 (U31676) glyceraldehyde-3-phosphate
                  dehydrogenase [Oryza sativa]
Seq. No.
                  411378
Seq. ID
                  uC-osflcyp074a04b1
Method
                  BLASTN
NCBI GI
                  q5042437
BLAST score
                  46
E value
                  1.0e-16
                  74
Match length
                  91
% identity
NCBI Description Oryza sativa BAC T49B20 genomic sequence, complete sequence
Seq. No.
                  411379
Seq. ID
                  uC-osflcyp074a06b1
Method
                  BLASTX
NCBI GI
                  g5929932
BLAST score
                  283
E value
                  3.0e-25
Match length
                  94
% identity
                  61
NCBI Description
                  (AF178952) voltage-dependent anion channel protein 2 [Zea
                  mays]
Seq. No.
                  411380
```

E value

2.0e-19

```
Seq. ID
                   uC-osflcyp074a07b1
Method
                   BLASTX
NCBI GI
                   q6016708
BLAST score
                   154
E value
                   2.0e-10
Match length
                   49
                   59
% identity
NCBI Description
                  (AC009325) putative protein kinase [Arabidopsis thaliana]
Seq. No.
                   411381
Seq. ID
                  uC-osflcyp074a10b1
Method
                  BLASTX
NCBI GI
                   q5381253
BLAST score
                   382
E value
                   6.0e-37
Match length
                   121
% identity
                   63
                  (AB027752) peroxidase [Nicotiana tabacum]
NCBI Description
Seq. No.
                   411382
                  uC-osflcyp074a11a1
Seq. ID
Method
                  BLASTX
NCBI GI
                   g5929932
BLAST score
                   198
E value
                   3.0e-15
Match length
                   47
                   87
% identity
NCBI Description
                   (AF178952) voltage-dependent anion channel protein 2 [Zea
                  mays]
Seq. No.
                   411383
Seq. ID
                   uC-osflcyp074a11b1
Method
                   BLASTX
NCBI GI
                   q3599491
BLAST score
                   389
E value
                   2.0e-37
                   92
Match length
                   79
% identity
NCBI Description (AF085149) putative aminotransferase [Capsicum chinense]
Seq. No.
                   411384
Seq. ID
                   uC-osflcyp074b02b1
Method
                   BLASTX
NCBI GI
                   g1747296
BLAST score
                   338
E value
                   1.0e-31
                  84
Match length
% identity
                   85
                  (D45384) vacuolar H+-pyrophosphatase [Oryza sativa]
NCBI Description
                  >gi 3298476 dbj BAA31524 (AB012766) ovp2 [Oryza sativa]
                   411385
Seq. No.
Seq. ID
                  uC-osflcyp074b04b1
                  BLASTN
Method
NCBI GI
                   g4160401
                  51
BLAST score
```

```
79
Match length
                  92
% identity
NCBI Description Zea mays eIF-5 gene, exons 1-2
Seq. No.
                  411386
                  uC-osflcyp074b06b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1705678
BLAST score
                  588
E value
                  7.0e-61
                  134
Match length
% identity
                  86
NCBI Description CELL DIVISION CYCLE PROTEIN 48 HOMOLOG (VALOSIN CONTAINING
                  PROTEIN HOMOLOG) (VCP) >gi 862480 (U20213)
                  valosin-containing protein [Glycine max]
                  411387
Seq. No.
Seq. ID
                  uC-osflcyp074b08b1
Method
                  BLASTX
NCBI GI
                  g1747296
BLAST score
                  670
E value
                  1.0e-70
Match length
                  140
                  94
% identity
NCBI Description
                  (D45384) vacuolar H+-pyrophosphatase [Oryza sativa]
                  >gi 3298476 dbj BAA31524 (AB012766) ovp2 [Oryza sativa]
                  411388
Seq. No.
                  uC-osflcyp074b11b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1815681
BLAST score
                  194
E value
                   3.0e-16
Match length
                  78
% identity
NCBI Description (U85246) expansin [Oryza sativa]
Seq. No.
                  411389
                  uC-osflcyp074c03b1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g6041757
BLAST score
                  42
E value
                  3.0e-14
Match length
                  62
% identity
                  92
NCBI Description
                  Genomic Sequence For Oryza sativa Clone 10P20, Lemont
                  Strain, Complete Sequence, complete sequence
                  411390
Seq. No.
Seq. ID
                  uC-osflcyp074c04b1
Method
                  BLASTX
NCBI GI
                  g3850582
BLAST score
                  360
E value
                  3.0e-34
Match length
                  82
% identity
NCBI Description (AC005278) F15K9.14 [Arabidopsis thaliana]
```

NCBI GI

BLAST score

g82496

675

411391 Seq. No. Seq. ID uC-osflcyp074c05b1 Method BLASTX NCBI GI g2407275 295 BLAST score 1.0e-26 E value 98 Match length % identity 63 (AF017360) lipid transfer protein LPT III [Oryza sativa] NCBI Description Seq. No. 411392 Seq. ID uC-osflcyp074c06b1 Method BLASTX NCBI GI q6049841 BLAST score 552 E value 1.0e-56 Match length 151 70 % identity NCBI Description (AF190728) asparagine synthetase [Helianthus annuus] 411393 Seq. No. uC-osflcyp074c08b1 Seq. ID Method BLASTX NCBI GI g2055230 BLAST score 177 E value 1.0e-12 Match length 133 % identity 37 NCBI Description (AB000130) SRC2 [Glycine max] 411394 Seq. No. Seq. ID uC-osflcyp074c11b1 Method BLASTX NCBI GI q3193313 BLAST score 277 E value 1.0e-24Match length 82 % identity 61 NCBI Description (AF069299) contains similarity to pectinesterase [Arabidopsis thaliana] Seq. No. 411395 Seq. ID uC-osflcyp074c12b1 Method BLASTX NCBI GI q4490706 BLAST score 142 E value 8.0e-09 Match length 43 % identity NCBI Description (AL035680) putative protein [Arabidopsis thaliana] Seq. No. 411396 Seq. ID uC-osflcyp074d04b1 Method BLASTX

BLAST score

Match length

% identity

E value

811

157

97

5.0e-87

```
5.0e-71
E value
Match length
                  152
                   87
% identity
NCBI Description
                  phenylalanine ammonia-lyase (EC 4.3.1.5) - rice
                   411397
Seq. No.
                  uC-osflcyp074d09b1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g175854
BLAST score
                   42
E value
                  2.0e-14
Match length
                  42
% identity
                  100
NCBI Description O.sativa 28S large subunit rRNA, 5' end
                  411398
Seq. No.
                  uC-osflcyp074d11b1
Seq. ID
Method
                  BLASTN
                  g6041757
NCBI GI
BLAST score
                   42
E value
                   4.0e-14
Match length
                  75
                   47
% identity
NCBI Description
                  Genomic Sequence For Oryza sativa Clone 10P20, Lemont
                   Strain, Complete Sequence, complete sequence
Seq. No.
                   411399
                  uC-osflcyp074d12b1
Seq. ID
Method
                  BLASTX
NCBI GI
                   g585095
BLAST score
                   183
                   1.0e-13
E value
Match length
                   84
% identity
                   44
                  ENOLASE (2-PHOSPHOGLYCERATE DEHYDRATASE)
NCBI Description
                   (2-PHOSPHO-D-GLYCERATE HYDRO-LYASE) >gi_2118305_pir__A41835
                  phosphopyruvate hydratase (EC 4.2.1.11) - Bacillus subtilis
                   >gi_460259 (L29475) enolase [Bacillus subtilis]
                   411400
Seq. No.
Seq. ID
                   uC-osflcyp074e01b1
Method
                   BLASTX
NCBI GI
                   g1747294
BLAST score
                   352
E value
                   2.0e-37
Match length
                   138
% identity
                   68
NCBI Description
                  (D45383) vacuolar H+-pyrophosphatase [Oryza sativa]
Seq. No.
                   411401
Seq. ID
                   uC-osflcyp074e04b1
Method
                  BLASTX
NCBI GI
                   g3913018
```

Match length

64

NCBI Description FRUCTOSE-BISPHOSPHATE ALDOLASE, CHLOROPLAST PRECURSOR (ALDP) >gi_218155 dbj_BAA02730_ (D13513) chloroplastic aldolase [Oryza sativa] 411402 Seq. No. uC-osflcyp074e10b1 Seq. ID Method BLASTX NCBI GI g3913018 BLAST score 654 1.0e-68 E value Match length 133 99 % identity NCBI Description FRUCTOSE-BISPHOSPHATE ALDOLASE, CHLOROPLAST PRECURSOR (ALDP) >gi 218155 dbj BAA02730 (D13513) chloroplastic aldolase [Oryza sativa] Seq. No. 411403 uC-osflcyp074f03b1 Seq. ID Method BLASTX NCBI GI q3914422 BLAST score 344 3.0e-32 E value 106 Match length 65 % identity NCBI Description PROFILIN >gi 2154728 emb CAA69669 (Y08389) profilin 2 [Cynodon dactylon] >gi 2154730 emb CAA69670 (Y08390) profilin 1 [Cynodon dactylon] Seq. No. 411404 uC-osflcyp074f05b1 Seq. ID Method BLASTX NCBI GI g2130069 BLAST score 604 E value 7.0e-63 Match length 119 % identity NCBI Description catalase (EC 1.11.1.6) catA - rice >gi_1261858_dbj_BAA06232 (D29966) catalase [Oryza sativa] Seq. No. 411405 Seq. ID uC-osflcyp074f06b1 Method BLASTX NCBI GI g4581162 BLAST score 526 E value 1.0e-53 Match length 117 % identity 85 (AC006220) putative symbiosis-related protein [Arabidopsis NCBI Description thaliana] Seq. No. 411406 Seq. ID uC-osflcyp074f09b1 Method BLASTX NCBI GI g3914422 BLAST score 259 E value 3.0e-23



% identity 83 PROFILIN >gi_2154728_emb_CAA69669_ (Y08389) profilin 2 NCBI Description [Cynodon dactylon] >gi 2154730 emb CAA69670 (Y08390) profilin 1 [Cynodon dactylon] 411407 Seq. No. Seq. ID uC-osflcyp074f11b1 Method BLASTX NCBI GI g5262784 BLAST score 262 E value 4.0e-23 Match length 134 % identity NCBI Description (AL080282) putative protein [Arabidopsis thaliana] Seq. No. 411408 Seq. ID uC-osflcyp074g02b1 Method BLASTX NCBI GI g218179 BLAST score 211 E value 5.0e-17 Match length 75 % identity 57 NCBI Description (D10207) H-ATPase [Oryza sativa] >gi_444339_prf__1906387A H ATPase [Oryza sativa] Seq. No. 411409 Seq. ID uC-osflcyp074g11b1 Method BLASTX NCBI GI q4538911 BLAST score 154 E value 4.0e-10 Match length 96 % identity 34 NCBI Description (AL049482) hypothetical protein [Arabidopsis thaliana] Seq. No. 411410 Seq. ID uC-osflcyp074h04b1 Method BLASTX NCBI GI q1911774 BLAST score 190 E value 3.0e-14Match length 81 % identity NCBI Description (S83364) putative Rab5-interacting protein {clone L1-57} [human, HeLa cells, Peptide Partial, 122 aa] [Homo sapiens] Seq. No. 411411

Seq. ID uC-osflcyp074h12b1

Method BLASTX
NCBI GI 94886280
BLAST score 256
E value 6.0e-22
Match length 103
% identity 44

NCBI Description (AL050300) putative protein [Arabidopsis thaliana]

Seq. No. 411412 Seq. ID uC-osflcyp075a09b1 Method BLASTX NCBI GI q3004565 BLAST score 427 E value 6.0e-42Match length 182 49 % identity NCBI Description (AC003673) putative protein kinase [Arabidopsis thaliana] Seq. No. 411413 Seq. ID uC-osflcyp075b07b1 Method BLASTX NCBI GI g3643596 BLAST score 403 E value 4.0e-39 Match length 117 67 % identity (AC005395) hypothetical protein [Arabidopsis thaliana] NCBI Description Seq. No. 411414 uC-osflcyp075c03b1 Seq. ID Method BLASTX NCBI GI g2342676 BLAST score 369 E value 4.0e-35 Match length 109 % identity 66 (AC000106) Strong similarity to Oryza NADPH oxidase NCBI Description (gb X93301). [Arabidopsis thaliana] 411415 Seq. No. Seq. ID uC-osflcyp075c11b1 Method BLASTX NCBI GI q4126809 BLAST score 336 E value 2.0e-31 Match length 69 97 % identity NCBI Description (AB017042) glyoxalase I [Oryza sativa] Seq. No. 411416 Seq. ID uC-osflcyp075d07b1 Method BLASTX NCBI GI g2801538 BLAST score 569 E value 1.0e-58 Match length 126 % identity 90 NCBI Description (AF039532) harpin induced gene 1 homolog [Oryza sativa] Seq. No. 411417 Seq. ID uC-osflcyp075e03b1 Method BLASTX NCBI GI g544242 551 BLAST score E value 2.0e-56

BLAST score

513

```
Match length
                  147
                   78
% identity
                  ENDOPLASMIN HOMOLOG PRECURSOR (GRP94 HOMOLOG)
NCBI Description
                  >gi 485498 pir S33533 heat shock protein 90 homolog
                  precursor - barley >gi_22652_emb_CAA48143 (X67960) GRP94
                  homologue [Hordeum vulgare]
Seq. No.
                  411418
                  uC-osflcyp075e11b1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g5441876
BLAST score
                  183
E value
                  3.0e-98
                  259
Match length
% identity
                  93
NCBI Description Oryza sativa genomic DNA, chromosome 2, clone:P0437H03
                  (contig b)
                  411419
Seq. No.
Seq. ID
                  uC-osflcyp075f07b1
Method
                  BLASTN
NCBI GI
                  g11957
BLAST score
                  171
                  2.0e-91
E value
Match length
                  223
% identity
                  95
NCBI Description Rice complete chloroplast genome
                  411420
Seq. No.
                  uC-osflcyp075g03b1
Seq. ID
Method
                  BLASTX
                  g5231113
NCBI GI
BLAST score
                  255
E value
                  6.0e-22
Match length
                  135
% identity
                  38
NCBI Description
                  (AF141202) EIN2 [Arabidopsis thaliana]
                  >gi_5231115_gb_AAD41077.1_AF141203_1 (AF141203) EIN2
                  [Arabidopsis thaliana]
Seq. No.
                  411421
Seq. ID
                  uC-osflcyp075q11b1
Method
                  BLASTX
NCBI GI
                  q3913018
BLAST score
                  830
E value
                  4.0e-89
Match length
                  171
% identity
                  97
NCBI Description
                 FRUCTOSE-BISPHOSPHATE ALDOLASE, CHLOROPLAST PRECURSOR
                   (ALDP) >gi_218155_dbj_BAA02730 (D13513) chloroplastic
                  aldolase [Oryza sativa]
Seq. No.
                  411422
Seq. ID
                  uC-osflcyp075h08b1
Method
                  BLASTX
NCBI GI
                  g113172
```



```
4.0e-52
E value
Match length
                  122
                  83
% identity
                  ACYL CARRIER PROTEIN III PRECURSOR (ACP III)
NCBI Description
                  >gi_100561_pir__S17928 acyl carrier protein 3 - barley
                  >gi 166971 (M58754) acyl carrier protein III [Hordeum
                  vulgare]
                  411423
Seq. No.
                  uC-osflcyp075h09b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4938477
BLAST score
                  198
E value
                  3.0e-15
                  72
Match length
                  54
% identity
                  (AL078464) putative protein [Arabidopsis thaliana]
NCBI Description
                   411424
Seq. No.
                  uC-osflcyp077d03b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4835791
                  431
BLAST score
                  2.0e-42
E value
Match length
                  134
% identity
                   60
NCBI Description
                  (AC007296) Strong similarity to gb Z70314 heat-shock
                  protein from Arabidopsis thaliana and is a member of the
                  PF_00012 Hsp70 protein family
Seq. No.
                   411425
                  uC-osflcyp077d08b1
Seq. ID
Method
                  BLASTX
NCBI GI
                   q1619300
BLAST score
                   532
E value
                   3.0e-54
Match length
                  133
% identity
NCBI Description (X95269) LRR protein [Lycopersicon esculentum]
Seq. No.
                   411426
Seq. ID
                  uC-osflcyp077e04b1
Method
                  BLASTX
NCBI GI
                  g2570511
BLAST score
                  219
E value
                   7.0e-18
Match length
                  102
% identity
                   49
                  (AF022738) chlorophyll a-b binding protein [Oryza sativa]
NCBI Description
                   411427
Seq. No.
```

Seq. ID uC-osflcyp077g12b1

Method BLASTX
NCBI GI g4102839
BLAST score 455
E value 3.0e-45
Match length 141

```
% identity
NCBI Description
                  (AF016713) LeOPT1 [Lycopersicon esculentum]
                   411428
Seq. No.
Seq. ID
                  uC-osflcyp077h11b1
Method
                  BLASTX
                  g4582468
NCBI GI
BLAST score
                   379
E value
                   2.0e-36
Match length
                  91
% identity
                  85
NCBI Description
                  (AC007071) putative 40S ribosomal protein; contains
                  C-terminal domain [Arabidopsis thaliana]
                   411429
Seq. No.
Seq. ID
                  uC-osflcyp077h12b1
Method
                  BLASTX
NCBI GI
                   q1658313
BLAST score
                   446
E value
                   4.0e-44
Match length
                  151
% identity
                   29
NCBI Description
                 (Y08987) osr40g2 [Oryza sativa]
Seq. No.
                  411430
Seq. ID
                  uC-osflcyp078a01a1
Method
                  BLASTX
NCBI GI
                  a4006818
BLAST score
                  291
E value
                   5.0e-26
Match length
                  75
% identity
                   72
NCBI Description
                  (AC005970) putative translation initiation factor eIF-2B,
                  alpha subunit [Arabidopsis thaliana]
Seq. No.
                   411431
Seq. ID
                  uC-osflcyp078a01b1
Method
                  BLASTX
NCBI GI
                  q4006818
BLAST score
                   329
E value
                  2.0e-30
Match length
                  89
                  70
% identity
NCBI Description
                  (AC005970) putative translation initiation factor eIF-2B,
                  alpha subunit [Arabidopsis thaliana]
Seq. No.
                   411432
Seq. ID
                  uC-osflcyp078a05b1
Method
                  BLASTX
NCBI GI
                  g5922612
BLAST score
                  385
```

E value 3.0e-37 Match length 115

% identity 64 NCBI Description

(AP000492) EST AU078118(E3904) corresponds to a region of the predicted gene.; similar to Arabidopsis thaliana BAC IG002P16; No definition line found. (AF007270) [Oryza

```
sativa]
Seq. No.
                   411433
                   uC-osflcyp078a07a1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g6017109
BLAST score
                   192
                   2.0e-14
E value
                   45
Match length
                   73
% identity
NCBI Description
                   (AC009895) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   411434
                   uC-osflcyp078a08a1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3860329
BLAST score
                   219
                   1.0e-17
E value
                   44
Match length
                   95
% identity
NCBI Description
                   (AJ012691) superoxide dismutase [Cicer arietinum]
                   >gi_3892130_emb_CAA10160_ (AJ012739) superoxide dismutase
                   [Cicer arietinum]
Seq. No.
                   411435
                   uC-osflcyp078a08b1
Seq. ID
Method
                   BLASTX
                   g134595
NCBI GI
BLAST score
                   732
E value
                   9.0e-78
Match length
                   140
% identity
                   99
                   SUPEROXIDE DISMUTASE-1 [CU-ZN] >gi_280412_pir__S22508
NCBI Description
                   superoxide dismutase (EC 1.15.1.1) (Cu-Zn) sodA - rice
                   >gi_218224_dbj_BAA00799 (D00999) copper/zinc-superoxide
dismutase [Oryza sativa] >gi_685242 (L19435) cytosolic
                   copper/zinc-superoxide dismutase [Oryza sativa]
                   >gi_1096504_prf__2111424A Cu/Zn superoxide dismutase [Oryza
                   sativa]
Seq. No.
                   411436
Seq. ID
                   uC-osflcyp078a09a1
Method
                   BLASTX
NCBI GI
                   g1498315
BLAST score
                   159
E value
                   3.0e-14
Match length
                   78
% identity
NCBI Description
                  (U56419) IAP100 [Pisum sativum]
Seq. No.
                   411437
Seq. ID
                   uC-osflcyp078a10a1
```

Method BLASTX
NCBI GI g2499005
BLAST score 163
E value 4.0e-11
Match length 81

```
% identity
                   44
                   4-METHYL-5 (B-HYDROXYETHYL) -THIAZOLE MONOPHOSPHATE
NCBI Description
                   BIOSYNTHESIS ENZYME >gi_1100872 (U34923) ThiJ [Escherichia
                   coli] >gi 1773108 (U82664)
                   4-methyl-\overline{5} (b-hydroxyethyl)-thiazole monophosphate
                   biosynthesis protein [Escherichia coli] >gi 1786626
                   (AE000148) 4-methyl-5(beta-hydroxyethyl)-thiazole
                  monophosphate synthesis [Escherichia coli]
Seq. No.
                   411438
                  uC-osflcyp078a10b1
Seq. ID
Method
                  BLASTX
NCBI GI
                   q2911060
BLAST score
                   201
E value
                   2.0e-15
Match length
                  157
                   27
% identity
NCBI Description
                  (AL021961) putative protein [Arabidopsis thaliana]
                   >gi_3297826_emb_CAA19884.1_ (AL031032) putative protein
                   [Arabidopsis thaliana]
                   411439
Seq. No.
Seq. ID
                   uC-osflcyp078a11b1
Method
                   BLASTX
NCBI GI
                   q4895248
BLAST score
                   675
                   4.0e-71
E value
Match length
                  148
                   87
% identity
NCBI Description
                  (AC007659) putative mitochondrial elongation factor G
                   [Arabidopsis thaliana]
                   411440
Seq. No.
Seq. ID
                   uC-osflcyp078a12a1
Method
                   BLASTX
NCBI GI
                   q5080798
BLAST score
                   160
E value
                   1.0e-10
Match length
                   53
% identity
                   49
NCBI Description
                  (AC007576) Very similar to ribonucleases [Arabidopsis
                   thaliana]
Seq. No.
                   411441
Seq. ID
                   uC-osflcyp078a12b1
Method
                  BLASTX
NCBI GI
                   q1698670
                   217
BLAST score
E value
                   2.0e-17
Match length
                  122
                   34
% identity
NCBI Description (U66241) S-like RNase [Zea mays]
                   411442
Seq. No.
Seq. ID
                  uC-osflcyp078b01b1
Method
                  BLASTX
NCBI GI
                   g629592
```

```
246
BLAST score
                  8.0e-21
E value
                  91
Match length
                  52
% identity
NCBI Description
                  hypothetical protein - rape >gi 6065752 emb CAB58175.1
                   (X74225) putative pod-specific dehydrogenase SAC25
                   [Brassica napus]
                  411443
Seq. No.
Seq. ID
                  uC-osflcyp078b03b1
Method
                  BLASTX
                  g548485
NCBI GI
BLAST score
                  141
E value
                  9.0e-09
                  71
Match length
                  51
% identity
                  POLYGALACTURONASE INHIBITOR PRECURSOR
NCBI Description
                   (POLYGALACTURONASE-INHIBITING PROTEIN)
                  >gi_478677_pir__S23764 polygalacturanase-inhibiting protein
                  precursor - kidney bean >gi_21029_emb_CAA46016_ (X64769)
                  polygalacturanase-inhibiting protein [Phaseolus vulgaris]
                   411444
Seq. No.
                  uC-osflcyp078b04b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3421096
BLAST score
                  366
E value
                  8.0e-35
                  80
Match length
% identity
                   88
                   (AF043528) 20S proteasome subunit PAG1 [Arabidopsis
NCBI Description
                   thaliana] >gi 3885332 (AC005623) proteasome component
                   [Arabidopsis Thaliana]
Seq. No.
                   411445
Seq. ID
                  uC-osflcyp078b06b1
Method
                  BLASTX
NCBI GI
                   g485518
BLAST score
                   148
E value
                   2.0e-10
Match length
                   95
% identity
                   49
NCBI Description
                  ubiquitin / ribosomal protein CEP52 - rice
                   >gi 303857 dbj BAA02154 (D12629) ubiquitin/ribosomal
                  polyprotein [Oryza sativa]
Seq. No.
                   411446
Seq. ID
                   uC-osflcyp078b07b1
Method
                   BLASTX
NCBI GI
                   q4104220
BLAST score
                   444
E value
                   5.0e-44
Match length
                  153
% identity
                   63
                   (AF033538) caffeic acid O-methyltransferase; LPOMT1 [Lolium
NCBI Description
```

perenne]

Seq. No. 411447 uC-osflcyp078b08b1 Seq. ID Method BLASTX NCBI GI q4741844 529 BLAST score 6.0e-54E value Match length 115 95 % identity NCBI Description (AF112964) small GTP-binding protein [Triticum aestivum] 411448 Seq. No. uC-osflcyp078b11a1 Seq. ID Method BLASTX NCBI GI q417744 BLAST score 243 E value 2.0e-20 Match length 48 96 % identity NCBI Description ADENOSYLHOMOCYSTEINASE (S-ADENOSYL-L-HOMOCYSTEINE HYDROLASE) (ADOHCYASE) >gi 169663 (M81885) S-adenosylhomocysteine hydrolase [Petroselinum crispum] 411449 Seq. No. uC-osflcyp078b11b1 Seq. ID Method BLASTN NCBI GI g170772 BLAST score 329 E value 0.0e + 00Match length 433 94 % identity NCBI Description Triticum aestivum S-adenosyl-L-homocysteine hydrolase (SH6.2) mRNA, complete cds 411450 Seq. No. Seq. ID uC-osflcyp078b12b1 Method BLASTX NCBI GI q485518 BLAST score 549 E value 2.0e-56 Match length 111 % identity 96 NCBI Description ubiquitin / ribosomal protein CEP52 - rice >gi 303857 dbj BAA02154 (D12629) ubiquitin/ribosomal polyprotein [Oryza sativa] Seq. No. 411451 Seq. ID uC-osflcyp078c02b1 Method BLASTX NCBI GI g5668813 BLAST score 177 E value 1.0e-12

Match length 108 32 % identity

NCBI Description (AC007519) Similar to gb_X77136 HSR203J protein from Nicotiana tabacum and is a member of the PF_00135

Carboxylesterase family. ESTs gb_Z25688 and gb_F14025 come

from this gene. [Arabidopsis thaliana]

Seq. No.

411457

```
411452
Seq. No.
                   uC-osflcyp078c03a1
Seq. ID
Method
                   BLASTX
NCBI GI
                   q5002520
BLAST score
                   404
E value
                   3.0e-39
                   139
Match length
                   55
% identity
                  (AL078606) putative phospholipase D-gamma [Arabidopsis
NCBI Description
                   thaliana]
                   411453
Seq. No.
                   uC-osflcyp078c03b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3850819
BLAST score
                   527
                   1.0e-53
E value
                   103
Match length
                   95
% identity
                  (Y18349) U2 snRNP auxiliary factor, small subunit [Oryza
NCBI Description
                   sativa]
                   411454
Seq. No.
                   uC-osflcyp078c08a1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g4928472
BLAST score
                   407
                   1.0e-39
E value
                   101
Match length
                   75
% identity
NCBI Description
                  (AF133302) type 2 peroxiredoxin [Brassica rapa subsp.
                   pekinensis]
Seq. No.
                   411455
Seq. ID
                   uC-osflcyp078c08b1
Method
                   BLASTX
NCBI GI
                   q4928472
BLAST score
                   525
E value
                   1.0e-53
Match length
                   128
% identity
                   75
NCBI Description
                   (AF133302) type 2 peroxiredoxin [Brassica rapa subsp.
                   pekinensis]
Seq. No.
                   411456
Seq. ID
                   uC-osflcyp078c09a1
Method
                   BLASTX
NCBI GI
                   q550452
BLAST score
                   258
E value
                   3.0e-22
Match length
                   72
% identity
                   68
                   (U08469) 3-methylcrotonyl-CoA carboxylase, biotin-carrier
NCBI Description
                   domain [Glycine max]
```



Seq. ID uC-osflcyp078c09b1

Method BLASTX
NCBI GI g550452
BLAST score 604
E value 3.0e-64
Match length 156
% identity 78

NCBI Description (U08469) 3-methylcrotonyl-CoA carboxylase, biotin-carrier

domain [Glycine max]

Seq. No. 411458

Seq. ID uC-osflcyp078c12b1

Method BLASTX
NCBI GI g3219164
BLAST score 663
E value 1.0e-69
Match length 162
% identity 80

NCBI Description (AB006210) glutamine amidotransferase/cyclase [Arabidopsis

thaliana]

Seq. No. 411459

Seq. ID uC-osflcyp078d01a1

Method BLASTN
NCBI GI g20367
BLAST score 71
E value 1.0e-31
Match length 254
% identity 85

NCBI Description Oryza sativa shoot GS1 mRNA for cytosolic glutamine

synthetase (EC 6.3.1.2) (clone lambda-GS28)

Seq. No. 411460

Seq. ID uC-osflcyp078d01b1

Method BLASTN
NCBI GI g20367
BLAST score 199
E value 1.0e-108
Match length 268
% identity 100

NCBI Description Oryza sativa shoot GS1 mRNA for cytosolic glutamine

synthetase (EC 6.3.1.2) (clone lambda-GS28)

Seq. No. 411461

Seq. ID uC-osflcyp078d03b1

Method BLASTX
NCBI GI g2501190
BLAST score 440
E value 2.0e-43
Match length 112
% identity 82

NCBI Description THIAMINE BIOSYNTHETIC ENZYME 1-2 PRECURSOR

>gi_2130147_pir__S61420 thiamine biosynthetic enzyme thi1-2
- maize >gi 596080 (U17351) thiamine biosynthetic enzyme

[Zea mays]

Seq. No. 411462

```
Seq. ID
                  uC-osflcyp078d04b1
                  BLASTX
Method
NCBI GI
                  g1350777
BLAST score
                  193
E value
                  1.0e-14
Match length
                  44
                  86
% identity
NCBI Description 60S RIBOSOMAL PROTEIN L9 >gi 971282 dbj BAA07209 (D38012)
                  ribosomal protein L9 [Oryza sativa]
Seq. No.
                   411463
Seq. ID
                  uC-osflcyp078d06a1
Method
                  BLASTX
NCBI GI
                  g2809262
BLAST score
                  267
E value
                  3.0e-23
Match length
                  107
                  50
% identity
NCBI Description (AC002560) F21B7.31 [Arabidopsis thaliana]
Seq. No.
                  411464
                  uC-osflcyp078d06b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2809262
BLAST score
                  220
                  1.0e-17
E value
Match length
                  141
% identity
                  35
NCBI Description (AC002560) F21B7.31 [Arabidopsis thaliana]
Seq. No.
                  411465
                  uC-osflcyp078d08b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4895220
BLAST score
                  568
E value
                  2.0e-58
Match length
                  163
% identity
                  69
NCBI Description (AC007660) unknown protein [Arabidopsis thaliana]
Seq. No.
                  411466
Seq. ID
                  uC-osflcyp078d11b1
Method
                  BLASTX
                  g3395938
NCBI GI
BLAST score
                  429
E value
                  3.0e-42
Match length
                  109
% identity
                  73
NCBI Description
                  (AF076924) polypyrimidine tract-binding protein homolog
                  [Arabidopsis thaliana]
Seq. No.
                  411467
Seq. ID
                  uC-osflcyp078d12a1
```

Method BLASTX NCBI GI g2827702 BLAST score 346 E value 3.0e-58

Match length 147 % identity 75 NCBI Description (AL021684) predicted protein [Arabidopsis thaliana] Seq. No. 411468 uC-osflcyp078d12b1 Seq. ID Method BLASTX NCBI GI g2827702 BLAST score 243 E value 2.0e-20 Match length 52 % identity 79 NCBI Description (ALO21684) predicted protein [Arabidopsis thaliana] 411469 Seq. No. Seq. ID uC-osflcyp078e01b1 Method BLASTX NCBI GI g3928150 BLAST score 660 E value 3.0e-69 Match length 165 % identity 78 NCBI Description (AJ131049) hypothetical protein [Cicer arietinum] Seq. No. 411470 Seq. ID uC-osflcyp078e02a1 Method BLASTX NCBI GI g1136122 BLAST score 157 E value 2.0e-10 Match length 46 % identity 65 NCBI Description (X91807) alfa-tubulin [Oryza sativa] Seq. No. 411471 Seq. ID uC-osflcyp078e02b1 Method BLASTX NCBI GI q1136122 BLAST score 743 E value 4.0e-79 Match length 144 % identity 95 NCBI Description (X91807) alfa-tubulin [Oryza sativa] Seq. No. 411472 Seq. ID uC-osflcyp078e04a1 Method BLASTN NCBI GI q11957 BLAST score 152 E value 6.0e-80 Match length 248 % identity 46

NCBI Description Rice complete chloroplast genome

Seq. No. 411473

Seq. ID uC-osflcyp078e06b1

Method BLASTX

Seq. No.

Seq. ID

411478

uC-osflcyp078e10b1



```
g1888357
NCBI GI
BLAST score
                  456
                  2.0e-45
E value
                  156
Match length
                  55
% identity
                  (X98130) alpha-mannosidase [Arabidopsis thaliana]
NCBI Description
                  >gi_1890154_emb_CAA72432_ (Y11767) alpha-mannosidase
                  precursor [Arabidopsis thaliana]
Seq. No.
                  411474
                  uC-osflcyp078e08b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4467116
BLAST score
                  218
                  1.0e-17
E value
Match length
                  113
                   40
% identity
                 (AL035538) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                  411475
Seq. No.
                  uC-osflcyp078e09a1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q283008
BLAST score
                  447
E value
                   2.0e-44
                  84
Match length
% identity
                  100
                  sucrose synthase (EC 2.4.1.13) - rice
NCBI Description
                   >gi 20366 emb CAA46017 (X64770) sucrose synthase [Oryza
                   sativa]
                   411476
Seq. No.
                  uC-osflcyp078e09b1
Seq. ID
Method
                  BLASTX
NCBI GI
                   q283008
BLAST score
                   756
E value
                   6.0e-92
Match length
                   184
                   99
% identity
                  sucrose synthase (EC 2.4.1.13) - rice
NCBI Description
                   >gi 20366 emb CAA46017 (X64770) sucrose synthase [Oryza
                   sativa]
                   411477
Seq. No.
Seq. ID
                   uC-osflcyp078e10a1
Method
                   BLASTX
NCBI GI
                   g283008
BLAST score
                   231
E value
                   4.0e-19
Match length
                   62
                   77
% identity
NCBI Description
                  sucrose synthase (EC 2.4.1.13) - rice
                   >gi 20366 emb CAA46017 (X64770) sucrose synthase [Oryza
                   sativa]
```

Method BLASTX g6041804 NCBI GI BLAST score 741 9.0e-79 E value Match length 176 79 % identity (AC009755) putative protein kinase [Arabidopsis thaliana] NCBI Description 411479 Seq. No. uC-osflcyp078e11a1 Seq. ID Method BLASTX NCBI GI g3193284 BLAST score 148 2.0e-10 E value 69 Match length 45 % identity (AF069298) No definition line found [Arabidopsis thaliana] NCBI Description 411480 Seq. No. uC-osflcyp078e11b1 Seq. ID Method BLASTX NCBI GI g3193284 BLAST score 449 2.0e-44E value Match length 181 % identity 51 NCBI Description (AF069298) No definition line found [Arabidopsis thaliana] Seq. No. 411481 uC-osflcyp078f01a1 Seq. ID Method BLASTX NCBI GI g3264605 BLAST score 166 2.0e-14 E value Match length 48 % identity 85 (AF061508) ribosomal protein L25 [Zea mays] NCBI Description 411482 Seq. No. Seq. ID uC-osflcyp078f01b1 Method BLASTX NCBI GI g585876 BLAST score 333 E value 5.0e-3194 Match length % identity 70 NCBI Description 60S RIBOSOMAL PROTEIN L23A (L25) >gi 1084424 pir S48026 ribosomal protein L25 - common tobacco >gi 310935 (L18908) 60S ribosomal protein L25 [Nicotiana tabacum] Seq. No. 411483 Seq. ID uC-osflcyp078f02a1

Method BLASTX
NCBI GI g1084455
BLAST score 248
E value 4.0e-21
Match length 49

```
% identity
 NCBI Description
                   peptidylprolyl isomerase (EC 5.2.1.8) Cyp2 - rice >gi 600767 (1.20460)
                    >gi_600767 (L29469) cyclophilin 2 [Oryza sativa]
 Seq. No.
                    411484
 Seq. ID
                    uC-osflcyp078f02b1
 Method
                    BLASTX
 NCBI GI
                    g1084455
 BLAST score
                   367
 E value
                   2.0e-70
Match length
                   134
 % identity
                   99
NCBI Description peptidylprolyl isomerase (EC 5.2.1.8) Cyp2 - rice
                   >gi_600767 (L29469) cyclophilin 2 [Oryza sativa]
Seq. No.
                   411485
Seq. ID
                   uC-osflcyp078f03a1
Method
                   BLASTX
NCBI GI
                   q2130069
BLAST score
                   179
E value
                   6.0e-13
Match length
                   39
% identity
                   90
NCBI Description catalase (EC 1.11.1.6) catA - rice
                   >gi_1261858_dbj_BAA06232_ (D29966) catalase [Oryza sativa]
Seq. No.
                   411486
Seq. ID
                   uC-osflcyp078f03b1
Method
                   BLASTX
NCBI GI
                   g2130069
BLAST score
                   452
E value
                   8.0e-45
Match length
                   97
% identity
                   89
NCBI Description
                   catalase (EC 1.11.1.6) catA - rice
                   >gi 1261858_dbj BAA06232 (D29966) catalase [Oryza sativa]
Seq. No.
                   411487
Seq. ID
                   uC-osflcyp078f06b1
Method
                   BLASTX
NCBI GI
                   g4185143
BLAST score
                   260
E value
                   2.0e-22
Match length
                   74
% identity
                   68
                   (AC005724) putative signal recognition particle receptor
NCBI Description
                   beta subunit [Arabidopsis thaliana]
Seq. No.
                   411488
Seq. ID
                   uC-osflcyp078f07b1
Method
                   BLASTX
NCBI GI
                   g1084455
BLAST score
                   444
E value
                   6.0e-44
Match length
                   110
% identity
NCBI Description peptidylprolyl isomerase (EC 5.2.1.8) Cyp2 - rice
```

% identity

94

cds



>gi 600767 (L29469) cyclophilin 2 [Oryza sativa]

Seq. No. 411489 Seq. ID uC-osflcyp078f08b1 Method BLASTX NCBI GI q3065835 BLAST score 319 2.0e-29 E value Match length 92 % identity 65 NCBI Description (AF058800) putative methyltransferase [Arabidopsis thaliana] 411490 Seq. No. Seq. ID uC-osflcyp078f09a1 Method BLASTX NCBI GI q1458106 BLAST score 144 3.0e-09 E value Match length 57 % identity 51 NCBI Description (U62554) 1-aminocyclopropane-1-carboxylic acid oxidase [Helianthus annuus] Seq. No. 411491 Seq. ID uC-osflcyp078f09b1 Method BLASTX NCBI GI q2952328 BLAST score 704 E value 2.0e-74Match length 135 % identity 99 NCBI Description (AF049889) 1-aminocyclopropane-1-carboxylate oxidase [Oryza sativa] Seq. No. 411492 Seq. ID uC-osflcyp078f10b1 Method BLASTX NCBI GI q2347100 BLAST score 628 E value 2.0e-65 Match length 191 % identity 62 NCBI Description (U76846) ubiquitin-specific protease [Arabidopsis thaliana] >gi 4567196 gb AAD23612.1 AC007168 3 (AC007168) putative ubiquitin-specific protease [Arabidopsis thaliana] Seq. No. 411493 Seq. ID uC-osflcyp078f11b1 Method BLASTN NCBI GI g2570510 BLAST score 57 E value 4.0e-23 Match length 81

53469

NCBI Description Oryza sativa chlorophyll a-b binding protein mRNA, complete

```
Seq. No.
                  411494
Seq. ID
                  uC-osflcyp078f12b1
Method
                  BLASTX
                  g1706082
NCBI GI
                  389
BLAST score
                  2.0e-37
E value
Match length
                  170
                  46
% identity
NCBI Description
                  SERINE CARBOXYPEPTIDASE II-3 PRECURSOR (CP-MII.3)
                  >gi_629787_pir__S44191 serine-type carboxypeptidase (EC
                  3.4.16.1) II-3 - barley >gi_619350_bbs_153536
                  CP-MII.3=serine carboxypeptidase [Hordeum vulgare=barley,
                  cv. Alexis, aleurone, Peptide, 516 aa]
                  >gi 474392 emb CAA55478.1 (X78877) serine carboxylase II-3
                  [Hordeum vulgare]
                  411495
Seq. No.
                  uC-osflcyp078g01a1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2130069
BLAST score
                  287
E value
                  2.0e-25
                  67
Match length
                  84
% identity
NCBI Description catalase (EC 1.11.1.6) catA - rice
                  >gi 1261858 dbj BAA06232 (D29966) catalase [Oryza sativa]
                  411496
Seq. No.
                  uC-osflcyp078g03b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q5080769
BLAST score
                  168
                  1.0e-11
E value
Match length
                  70
% identity
                  53
NCBI Description (AC007576) Unknown protein [Arabidopsis thaliana]
Seq. No.
                  411497
                  uC-osflcyp078q04b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2980806
BLAST score
                  445
E value
                   4.0e-44
Match length
                  166
% identity
NCBI Description (AL022197) putative protein [Arabidopsis thaliana]
Seq. No.
                   411498
Seq. ID
                  uC-osflcyp078g06b1
Method
                  BLASTX
NCBI GI
                  g5360230
BLAST score
                  747
E value
                  5.0e-88
Match length
                  160
                  98
% identity
NCBI Description (AB015287) Ran [Oryza sativa]
```

```
Seq. No.
                  411499
                  uC-osflcyp078g07b1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g487296
BLAST score
                  50
                  6.0e-19
E value
                  62
Match length
                  95
% identity
NCBI Description Rice mRNA EN251, partial sequence
Seq. No.
                  411500
                  uC-osflcyp078g08b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g602292
BLAST score
                  429
E value
                  3.0e-42
                  106
Match length
                  77
% identity
                 (U17987) RCH2 protein [Brassica napus]
NCBI Description
Seq. No.
                  411501
                  uC-osflcyp078g09a1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1170937
                  251
BLAST score
E value
                  2.0e-21
                  47
Match length
                  98
% identity
NCBI Description S-ADENOSYLMETHIONINE SYNTHETASE 1 (METHIONINE
                  ADENOSYLTRANSFERASE 1) (ADOMET SYNTHETASE 1)
                  >gi 450549 emb CAA81481 (Z26867) S-adenosyl methionine
                  synthetase [Oryza sativa]
Seq. No.
                  411502
Seq. ID
                  uC-osflcyp078g09b1
Method
                  BLASTX
NCBI GI
                  g1170937
BLAST score
                  672
E value
                  1.0e-70
Match length
                  134
% identity
                  96
                 S-ADENOSYLMETHIONINE SYNTHETASE 1 (METHIONINE
NCBI Description
                  ADENOSYLTRANSFERASE 1) (ADOMET SYNTHETASE 1)
                  >gi_450549_emb_CAA81481_ (Z26867) S-adenosyl methionine
                  synthetase [Oryza sativa]
Seq. No.
                  411503
Seq. ID
                  uC-osflcyp078g11b1
Method
                  BLASTX
NCBI GI
                  g5734721
BLAST score
                  482
E value
                  2.0e-48
Match length
                  165
% identity
                  59
NCBI Description
                  (AC008075) Similar to gb_AF023472 peptide transporter from
                  Hordeum vulgare and is a member of the PF 00854 Peptide
```

transporter family. ESTs gb_T41927 and gb_AA395024 come from this gene. [Arabidopsis thaliana]

Seq. No. 411504 uC-osflcyp078h01b1 Seq. ID BLASTX Method q1076670 NCBI GI 219 BLAST score E value 8.0e-18 43 Match length % identity 95 NADH dehydrogenase (EC 1.6.99.3) - potato NCBI Description >gi_668985_emb_CAA59062_ (X84319) NADH dehydrogenase [Solanum tuberosum] 411505 Seq. No. uC-osflcyp078h03b1 Seq. ID Method BLASTX q1076809 NCBI GI BLAST score 612 9.0e-64 E value Match length 145 82 % identity H+-transporting ATPase (EC 3.6.1.35) - maize NCBI Description >gi_758355_emb_CAA59800_ (X85805) H(+)-transporting ATPase [Zea mays] 411506 Seq. No. uC-osflcyp078h05b1 Seq. ID BLASTX Method NCBI GI g2497748 BLAST score 411 5.0e-40E value Match length 90 90 % identity NONSPECIFIC LIPID-TRANSFER PROTEIN 4 PRECURSOR (LTP 4) NCBI Description >gi 902058 (U29176) lipid transfer protein precursor [Oryza sativa] 411507 Seq. No. uC-osflcyp078h06b1 Seq. ID Method BLASTX g1184774 NCBI GI BLAST score 391 8.0e-38 E value Match length 103 75 % identity (U45856) cytosolic glyceroldehyde-3-phosphate dehydrogenase NCBI Description GAPC3 [Zea mays] 411508 Seq. No. Seq. ID uC-osflcyp078h07b1

53472

BLASTX

219

73

g129916

1.0e-19

Method

NCBI GI BLAST score

E value

Match length

% identity PHOSPHOGLYCERATE KINASE, CYTOSOLIC >gi_66911_pir__TVWTGY NCBI Description phosphoglycerate kinase (EC 2.7.2.3), cytosolic - wheat >gi_21835_emb_CAA33302_ (X15232) phosphoglycerate kinase (AA 1 - 401) [Triticum aestivum] 411509 Seq. No. uC-osflcyp078h09b1 Seq. ID BLASTX Method NCBI GI g2130069 699 BLAST score 6.0e-74E value 133 Match length 98 % identity catalase (EC 1.11.1.6) catA - rice NCBI Description >gi 1261858 dbj BAA06232_ (D29966) catalase [Oryza sativa] 411510 Seq. No. uC-osflcyp078h10b1 Seq. ID BLASTX Method NCBI GI g6006869 BLAST score 365 1.0e-34 E value 100 Match length 75 % identity (AC009540) putative cationic amino acid transporter NCBI Description [Arabidopsis thaliana] Seq. No. 411511 uC-osflcyp078h12b1 Seq. ID Method BLASTX NCBI GI g2285885 BLAST score 506 E value 3.0e-51158 Match length 63 % identity NCBI Description (D89631) sulfate transporter [Arabidopsis thaliana] 411512 Seq. No. Seq. ID uC-osflcyp079a12a1 Method BLASTX NCBI GI g3924606 BLAST score 255 7.0e-22 E value Match length 64 73 % identity NCBI Description (AF069442) hypothetical protein [Arabidopsis thaliana] Seq. No. 411513 uC-osflcyp079b01a1 Seq. ID Method BLASTX NCBI GI g5263329 BLAST score 157 E value 2.0e-10 Match length 42 % identity NCBI Description (AC007727) Contains PF_00646 F-box domain. ESTs gb Z37267, gb_R90412, gb_Z37268 and gb_T88189 come from this gene. [Arabidopsis thaliana]

Seq. No. 411514

Seq. ID uC-osflcyp079b02a1

Method BLASTX
NCBI GI g442693
BLAST score 569
E value 1.0e-58
Match length 120
% identity 83

NCBI Description Barwin, Basic Barley Seed Protein (Nmr, 20 Structures)

>gi_442694_pdb_1BW4_ Barwin, Basic Barley Seed Protein

(Nmr, 20 Structures)

Seq. No. 411515

Seq. ID uC-osflcyp079b06a1

Method BLASTX
NCBI GI 9729944
BLAST score 275
E value 3.0e-24
Match length 75
% identity 65

NCBI Description POLLEN ALLERGEN ZEA M 1 (ZEA M I) >gi_478272_pir__JC1524

major allergen mI protein - maize >gi_293902 (L14271) Zea

mI [Zea mays]

Seq. No. 411516

Seq. ID uC-osflcyp079b07a1

Method BLASTN
NCBI GI g1293783
BLAST score 98
E value 8.0e-48

Match length 202 % identity 87

NCBI Description Oryza sativa QM gene, complete cds

Seq. No. 411517

Seq. ID uC-osflcyp079b10a1

Method BLASTX
NCBI GI g4079798
BLAST score 190
E value 2.0e-14
Match length 66
% identity 58

NCBI Description (AF052203) 23 kDa polypeptide of photosystem II [Oryza

sativa]

Seq. No. 411518

Seq. ID uC-osflcyp079b11a1

Method BLASTX
NCBI GI g167097
BLAST score 199
E value 5.0e-28
Match length 77
% identity 83

NCBI Description (M55449) ribulose 1,5-bisphosphate carboxylase activase

% identity

NCBI Description

```
[Hordeum vulgare]
Seq. No.
                  411519
                  uC-osflcyp079c01a1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g21839
BLAST score
                  283
                   3.0e-25
E value
Match length
                  59
                   95
% identity
                  (X57952) phosphoribulokinase [Triticum aestivum]
NCBI Description
Seq. No.
                   411520
                  uC-osflcyp079c03a1
Seq. ID
Method
                   BLASTX
NCBI GI
                   q169661
BLAST score
                   200
E value
                   2.0e-15
Match length
                   40
                   95
% identity
                  (M62756) S-adenosylhomocysteine hydrolase [Petroselinum
NCBI Description
                   crispum]
                   411521
Seq. No.
                   uC-osflcyp079c05a1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g125606
BLAST score
                   239
E value
                   4.0e-20
                   59
Match length
                   83
% identity
                  PYRUVATE KINASE, CYTOSOLIC ISOZYME >gi_100463_pir__S12248
NCBI Description
                   pyruvate kinase (EC 2.7.1.40) - potato
                   >gi 22576 emb CAA37727 (X53688) pyruvate kinase [Solanum
                   tuberosum]
                   411522
Seq. No.
Seq. ID
                   uC-osflcyp079d10a1
Method
                   BLASTX
NCBI GI
                   q3915866
                   340
BLAST score
E value
                   8.0e-32
Match length
                   92
% identity
                   72
                   GLUTAMINYL-TRNA SYNTHETASE (GLUTAMINE--TRNA LIGASE) (GLNRS)
NCBI Description
                   >gi_2995455_emb_CAA62901_ (X91787) tRNA-glutamine
                   synthetase [Lupinus luteus]
                   411523
Seq. No.
                   uC-osflcyp079e11a1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g1870188
BLAST score
                   206
                   4.0e-16
E value
Match length
                   72
```

53475

(X87149) phosphoenolpyruvate-carboxylase [Vanilla

```
planifolia]
                                          19 -
                  411524
Seq. No.
                  uC-osflcyp079f01a1
Seq. ID
                  BLASTX
Method
                  q559005
NCBI GI
                  230
BLAST score
                  7.0e-19
E value
                  70
Match length
                   69
% identity
                  (U15933) ascorbate peroxidase [Nicotiana tabacum]
NCBI Description
                   411525
Seq. No.
                  uC-osflcyp079f02a1
Seq. ID
Method
                  BLASTN
                   g2570514
NCBI GI
                   77
BLAST score
                   4.0e-35
E value
                   274
Match length
                   82
% identity
                  Oryza sativa glycolate oxidase (GOX) mRNA, complete cds
NCBI Description
Seq. No.
                   411526
                   uC-osflcyp079f04a1
Seq. ID
                   BLASTN
Method
                   g20367
NCBI GI
                   260
BLAST score
E value
                   1.0e-144
                   365
Match length
                   99
% identity
NCBI Description Oryza sativa shoot GS1 mRNA for cytosolic glutamine
                   synthetase (EC 6.3.1.2) (clone lambda-GS28)
                   411527
Seq. No.
                   uC-osflcyp079f05a1
Seq. ID
                   BLASTX
Method
NCBI GI
                   q481477
BLAST score
                   443
                   6.0e-44
E value
                   89
Match length
                   17
% identity
NCBI Description
                   ubiquitin precursor - rice >gi 416038 emb CAA53665
                   (X76064) polyubiquitin [Oryza sativa] >gi 1574944 (U37687)
                   polyubiquitin [Oryza sativa]
                   >gi_6013289_gb_AAF01315.1_AF184279_1 (AF184279)
                   polyubiquitin [Oryza sativa]
                   >gi_6013291_gb_AAF01316.1_AF184280_1 (AF184280)
                   polyubiquitin [Oryza sativa]
                   411528
Seq. No.
                   uC-osflcyp079f10a1
Seq. ID
Method
                   BLASTN
NCBI GI
                   g20367
BLAST score
                   156
E value
                   3.0e-82
                   280
Match length
% identity
                   89
```

```
Oryza sativa shoot GS1 mRNA for cytosolic glutamine
NCBI Description
                  synthetase (EC 6.3.1.2) (clone lambda-GS28)
                  411529
Seq. No.
                  uC-osflcyp079g01a1
Seq. ID
                  BLASTN
Method
                  g20280
NCBI GI
                  90
BLAST score
                  4.0e-43
E value
                  226
Match length
                  85
% identity
NCBI Description Rice gene for phenylalanine ammonia-lyase (EC 4.3.1.5)
                  411530
Seq. No.
                  uC-osflcyp079g12a1
Seq. ID
Method
                  BLASTN
                  g20367
NCBI GI
BLAST score
                  163
                  2.0e-86
E value
                  263
Match length
                  90
% identity
                  Oryza sativa shoot GS1 mRNA for cytosolic glutamine
NCBI Description
                  synthetase (EC 6.3.1.2) (clone lambda-GS28)
                  411531
Seq. No.
                  uC-osflcyp079h09a1
Seq. ID
                  BLASTX
Method
NCBI GI
                  g82496
                  176
BLAST score
                  1.0e-12
E value
                  48
Match length
                  77
% identity
NCBI Description phenylalanine ammonia-lyase (EC 4.3.1.5) - rice
                  411532
Seq. No.
                  uC-osflcyp080a02b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q5453694
BLAST score
                  191
                   3.0e-14
E value
                   94
Match length
                   41
% identity
                  cell cycle-regulated factor (78 kDa) >gi 3201964 (AF068007)
NCBI Description
                   cell cycle-regulated factor p78 [Homo sapiens]
                   411533
Seq. No.
Seq. ID
                  uC-osflcyp080a05a1
Method
                  BLASTN
NCBI GI
                   q22651
BLAST score
                   35
                   5.0e-10
E value
Match length
                   71
% identity
                   87
NCBI Description H.vulgare mRNA for GRP94 homologue
Seq. No.
Seq. ID
                   uC-osflcyp080a05b1
```

Seq. ID

```
BLASTX
Method
NCBI GI
                  g544242
                  734
BLAST score
                  5.0e-78
E value
                  158
Match length
                  91
% identity
                  ENDOPLASMIN HOMOLOG PRECURSOR (GRP94 HOMOLOG)
NCBI Description
                  >gi 485498_pir__S33533 heat shock protein 90 homolog
                  precursor - barley >gi_22652_emb_CAA48143_ (X67960) GRP94
                  homologue [Hordeum vulgare]
                  411535
Seq. No.
                  uC-osflcyp080a06b1
Seq. ID
                  BLASTX
Method
                  q5823556
NCBI GI
BLAST score
                  513
                  3.0e-52
E value
Match length
                  120
                  88
% identity
                  (AF181096) ferric leghemoglobin reductase [Vigna
NCBI Description
                  unguiculata]
                   411536
Seq. No.
                  uC-osflcyp080a08a1
Seq. ID
                  BLASTX
Method
                  g4531444
NCBI GI
                  174
BLAST score
                  1.0e-12
E value
                   94
Match length
                   53
% identity
                  (AC006224) putative protein kinase [Arabidopsis thaliana]
NCBI Description
                   411537
Seq. No.
                   uC-osflcyp080a08b1
Seq. ID
                   BLASTX
Method
NCBI GI
                   g4531444
BLAST score
                   517
E value
                   2.0e-52
                   164
Match length
                   59
% identity
                  (AC006224) putative protein kinase [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   411538
                   uC-osflcyp080a09b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g1171008
BLAST score
                   354
E value
                   2.0e-33
Match length
                   88
% identity
                   65
                  POLLEN ALLERGEN PHL P 1 PRECURSOR (PHL P I)
NCBI Description
                   >gi 629812_pir__S44182 allergen Phl p I - common timothy
                   >gi_473360_emb_CAA55390_ (X78813) Phl p I allergen [Phleum
                   pratense]
                   411539
Seq. No.
```

53478

uC-osflcyp080a10b1

```
Method
                  BLASTX
                  g5690010
NCBI GI
BLAST score
                  237
                  1.0e-19
E value
Match length
                  111
                   47
% identity
                   (AJ132472) Family 3 Glycoside Hydrolase [Ruminococcus
NCBI Description
                  flavefaciens]
                   411540
Seq. No.
Seq. ID
                  uC-osflcyp080a12b1
                  BLASTX
Method
                   g5823556
NCBI GI
BLAST score
                   165
                   1.0e-11
E value
                   83
Match length
% identity
                   45
                  (AF181096) ferric leghemoglobin reductase [Vigna
NCBI Description
                   unguiculata]
Seq. No.
                   411541
Seq. ID
                   uC-osflcyp080b01a1
                   BLASTX
Method
NCBI GI
                   g226661
BLAST score
                   513
                   3.0e-52
E value
Match length
                   102
                   96
% identity
NCBI Description trnA intron ORF 109 [Oryza sativa]
                   411542
Seq. No.
                   uC-osflcyp080b01b1
Seq. ID
                   BLASTX
Method
NCBI GI
                   g320577
                   203
BLAST score
                   1.0e-15
E value
                   40
Match length
                   93
% identity
                   pvs protein 1 - kidney bean mitochondrion >gi_169320
NCBI Description
                   (M64246) ORF-98; putative [Phaseolus vulgaris]
                   411543
Seq. No.
                   uC-osflcyp080b02a1
Seq. ID
                   BLASTX
Method
                   g3915847
NCBI GI
                   145
BLAST score
                   5.0e-09
E value
                   77
Match length
                   45
% identity
NCBI Description 40S RIBOSOMAL PROTEIN S2 >gi_2335095 (AC002339) putative
                   40S ribosomal protein S2 [Arabidopsis thaliana]
                   411544
Seq. No.
                   uC-osflcyp080b02b1
Seq. ID
                   BLASTX
Method
                   g6094173
NCBI GI
```

53479

141

BLAST score

```
2.0e-09
E value
                  58
Match length
% identity
                  57
                  40S RIBOSOMAL PROTEIN S2 >gi 3687463_emb_CAA21187
NCBI Description
                   (AL031798) 40s ribosomal protein s2 [Schizosaccharomyces
                  pombe]
                   411545
Seq. No.
                  uC-osflcyp080b03b1
Seq. ID
                  BLASTX
Method
                   q1835731
NCBI GI
BLAST score
                   586
                   1.0e-60
E value
Match length
                   126
                   90
% identity
                  (U86018) photosystem II 10 kDa polypeptide [Oryza sativa]
NCBI Description
Seq. No.
                   411546
                   uC-osflcyp080b04a1
Seq. ID
                   BLASTX
Method
                   q3885892
NCBI GI
BLAST score
                   406
                   1.0e-39
E value
Match length
                   78
                   100
% identity
                  (AF093634) photosystem-1 F subunit precursor [Oryza sativa]
NCBI Description
Seq. No.
                   411547
                   uC-osflcyp080b04b1
Seq. ID
                   BLASTX
Method
                   q3885892
NCBI GI
                   268
BLAST score
                   2.0e-23
E value
Match length
                   114
                   50
% identity
                  (AF093634) photosystem-1 F subunit precursor [Oryza sativa]
NCBI Description
Seq. No.
                   411548
                   uC-osflcyp080b05a1
Seq. ID
                   BLASTN
Method
NCBI GI
                   q20321
                   139
BLAST score
                   3.0e-72
E value
                   220
Match length
                   90
% identity
NCBI Description Oryza sativa RAc1 mRNA for actin
Seq. No.
                   411549
                   uC-osflcyp080b05b1
Seq. ID
                   BLASTX
Method
                   q113222
NCBI GI
                   826
BLAST score
E value
                   9.0e-89
                   165
Match length
% identity
                   99
NCBI Description ACTIN 1 >gi 295885_emb_CAA33874_ (X15865) actin [Oryza
                   sativa]
```

NCBI GI

g517500

```
Seq. No.
                  411550
                  uC-osflcyp080b07a1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2244940
BLAST score
                  405
                  2.0e-39
E value
Match length
                  141
                   66
% identity
                  (Z97339) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                  411551
Seq. No.
Seq. ID
                  uC-osflcyp080b07b1
                  BLASTX
Method
                  q2244940
NCBI GI
                  229
BLAST score
E value
                  8.0e-19
                   55
Match length
% identity
                  73
                  (Z97339) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   411552
Seq. No.
Seq. ID
                   uC-osflcyp080b08a1
Method
                   BLASTX
NCBI GI
                   g5911363
BLAST score
                   312
                   1.0e-28
E value
Match length
                   70
% identity
                   84
                  (AF159699) putative host factor [Nicotiana tabacum]
NCBI Description
                   411553
Seq. No.
                   uC-osflcyp080b08b1
Seq. ID
Method
                   BLASTX
                   g4455180
NCBI GI
                   279
BLAST score
                   1.0e-33
E value
Match length
                   110
% identity
                   65
                  (AL035521) putative protein [Arabidopsis thaliana]
NCBI Description
                   411554
Seq. No.
                   uC-osflcyp080b09a1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g517500
                   271
BLAST score
                   6.0e-24
E value
Match length
                   68
                   81
% identity
                   (M87435) precursor of the oxygen evolving complex 17 kDa
NCBI Description
                   protein [Zea mays] >gi_444338_prf__1906386A photosystem II
                   OE17 protein [Pisum sativum]
                   411555
Seq. No.
                   uC-osflcyp080b09b1
Seq. ID
                   BLASTX
Method
```

BLAST score 333 6.0e-31 E value Match length 153 % identity 48 (M87435) precursor of the oxygen evolving complex 17 kDa NCBI Description protein [Zea mays] >gi_444338_prf__1906386A photosystem II OE17 protein [Pisum sativum] 411556 Seq. No. uC-osflcyp080b10a1 Seq. ID Method BLASTX NCBI GI g3860323 BLAST score 349 7.0e-33 E value Match length 77 83 % identity (AJ012688) hypothetical protein [Cicer arietinum] NCBI Description 411557 Seq. No. uC-osflcyp080b10b1 Seq. ID Method BLASTX g3860323 NCBI GI BLAST score 349 8.0e-33 E value Match length 77 83 % identity (AJ012688) hypothetical protein [Cicer arietinum] NCBI Description 411558 Seq. No. uC-osflcyp080b11b1 Seq. ID BLASTN Method g473996 NCBI GI 220 BLAST score 1.0e-120 E value 227 Match length 100 % identity NCBI Description Rice mRNA, partial homologous to ribosomal protein L7 gene 411559 Seq. No. uC-osflcyp080b12b1 Seq. ID Method BLASTX NCBI GI q1531758 BLAST score 231 6.0e-19 E value 75 Match length 60 % identity (X98772) AUX1 [Arabidopsis thaliana] >gi 3335360 (AC003028) NCBI Description unknown protein [Arabidopsis thaliana] Seq. No. 411560 uC-osflcyp080c01a1 Seq. ID Method BLASTX g2911042 NCBI GI 254 BLAST score 4.0e-23 E value Match length 87 % identity 71

(AL021961) Phosphoglycerate dehydrogenase - like protein NCBI Description [Arabidopsis thaliana] 411561 Seq. No. Seq. ID uC-osflcyp080c01b1 Method BLASTX g2911042 NCBI GI BLAST score 300 2.0e-35 E value 143 Match length 58 % identity (AL021961) Phosphoglycerate dehydrogenase - like protein NCBI Description [Arabidopsis thaliana] 411562 Seq. No. uC-osflcyp080c02a1 Seq. ID Method BLASTX NCBI GI q3695403 BLAST score 267 3.0e-23 E value Match length 75 % identity (AF096373) contains similarity to the pfkB family of NCBI Description carbohydrate kinases (Pfam: PF00294, E=1.6e-75) [Arabidopsis thaliana] >gi 4538955 emb CAB39779.1 (AL049488) fructokinase-like protein [Arabidopsis thaliana] 411563 Seq. No. Seq. ID uC-osflcyp080c02b1 Method BLASTX q3695403 NCBI GI BLAST score 413 2.0e-40 E value Match length 104 % identity 78 (AF096373) contains similarity to the pfkB family of NCBI Description carbohydrate kinases (Pfam: PF00294, E=1.6e-75) [Arabidopsis thaliana] >gi_4538955_emb_CAB39779.1 (ALO49488) fructokinase-like protein [Arabidopsis thaliana] Seq. No. 411564 uC-osflcyp080c03b1 Seq. ID Method BLASTX q3885888 NCBI GI BLAST score 316 6.0e-29 E value 107 Match length 65 % identity (AF093632) high mobility group protein [Oryza sativa] NCBI Description

Seq. No. 411565

Seq. ID uC-osflcyp080c04a1

Method BLASTX
NCBI GI g1172813
BLAST score 294
E value 1.0e-26
Match length 61

% identity 89 60S RIBOSOMAL PROTEIN L10-2 (PUTATIVE TUMOR SUPRESSOR SG12) NCBI Description >gi_1076752_pir__S49596 ribosomal protein L10.e, cytosolic - rice >qi 575357 emb CAA57340 (X81692) putative tumor supressor [Oryza sativa] 411566 Seq. No. uC-osflcyp080c04b1 Seq. ID BLASTX Method g4836948 NCBI GI BLAST score 176 1.0e-12 E value Match length 60 58 % identity (AC006085) Similar to human CGI-33 protein [Arabidopsis NCBI Description thaliana] 411567 Seq. No. uC-osflcyp080c05a1 Seq. ID BLASTX Method q3258575 NCBI GI 160 BLAST score 8.0e-11 E value Match length 45 67 % identity (U89959) Hypothetical protein [Arabidopsis thaliana] NCBI Description 411568 Seq. No. Seq. ID uC-osflcyp080c06a1 Method BLASTX NCBI GI q543711 217 BLAST score 2.0e-17 E value Match length 41 100 % identity 14-3-3-LIKE PROTEIN S94 >gi_419796_pir__S30927 14-3-3 protein homolog - rice >gi_303859_dbj_BAA03711_ (D16140) NCBI Description brain specific protein [Oryza sativa] 411569 Seq. No. uC-osflcyp080c06b1 Seq. ID BLASTX Method g543711 NCBI GI 464 BLAST score 2.0e-46 E value 97 Match length 98 % identity 14-3-3-LIKE PROTEIN S94 >gi_419796_pir__S30927 14-3-3 protein homolog - rice >gi_303859_dbj_BAA03711_ (D16140) NCBI Description brain specific protein [Oryza satīva] Seq. No. 411570 uC-osflcyp080c07b1 Seq. ID BLASTX Method NCBI GI q125271

53484

182

5.0e-28

BLAST score

E value

Match length 80 % identity 84 CASEIN KINASE II, ALPHA CHAIN (CK II) (CK2-ALPHA) NCBI Description >gi_100860_pir__S19726 casein kinase II (EC 2.7.1.-) alpha chain - maize >gi 3318993 pdb 1A60 Protein Kinase Ck2 (Catalytic Subunit) From Zea Mays >gi_22117_emb_CAA43659_ (X61387) casein kinase II alpha subunit [Zea mays] 411571 Seq. No. Seq. ID uC-osflcyp080c10b1 Method BLASTX g2500353 NCBI GI BLAST score 808 1.0e-86 E value 151 Match length 100 % identity 60S RIBOSOMAL PROTEIN L10-3 (QM/R22) >gi 1293784 (U55048) NCBI Description similar to human QM protein, a putative tumor supressor, and to maize ubiquinol-cytochrome C reductase complex subunit VI requiring protein SC34 [Oryza sativa] 411572 Seq. No. uC-osflcyp080c11a1 Seq. ID Method BLASTN q303858 NCBI GI 265 BLAST score 1.0e-147 E value 321 Match length % identity 96 Rice mRNA for brain specific protein (S94 gene), complete NCBI Description 411573 Seq. No. uC-osflcyp080c11b1 Seq. ID Method BLASTX g3258575 NCBI GI 281 BLAST score 7.0e-25 E value Match length 76 % identity 68 (U89959) Hypothetical protein [Arabidopsis thaliana] NCBI Description 411574 Seq. No. uC-osflcyp080c12b1 Seq. ID Method BLASTX g2224901 NCBI GI BLAST score 149 2.0e-09 E value Match length 44 % identity (U67134) PcMYB1 protein [Petroselinum crispum] NCBI Description 411575 Seq. No. Seq. ID uC-osflcyp080d01a1 Method BLASTX q3128168 NCBI GI

53485

182

BLAST score

Match length

% identity

47 74

```
3.0e-13
E value
                  46
Match length
% identity
                  61
                   (AC004521) putative carboxyl-terminal peptidase
NCBI Description
                   [Arabidopsis thaliana]
                  411576
Seq. No.
                  uC-osflcyp080d01b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3128168
BLAST score
                  462
E value
                  3.0e-46
Match length
                  120
% identity
                   64
                   (AC004521) putative carboxyl-terminal peptidase
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                  411577
                  uC-osflcyp080d02a1
Seq. ID
Method
                  BLASTX
                  q5107819
NCBI GI
BLAST score
                  150
E value
                   8.0e-11
                   90
Match length
                   50
% identity
                  (AF149413) contains similarity to arabinosidase
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                   411578
                   uC-osflcyp080d03a1
Seq. ID
Method
                   BLASTN
                   g2913890
NCBI GI
                   93
BLAST score
                   1.0e-44
E value
                   327
Match length
                   85
% identity
NCBI Description Oryza sativa mRNA for LIP9, partial cds
                   411579
Seq. No.
                   uC-osflcyp080d03b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g1657843
BLAST score
                   199
                   3.0e-15
E value
                   130
Match length
                   40
% identity
                  (U73210) cold acclimation protein WCOR410b [Triticum
NCBI Description
                   aestivum]
Seq. No.
                   411580
                   uC-osflcyp080d04b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   q3341691
                   190
BLAST score
                   3.0e-14
E value
```

(AC003672) putative heterogeneous nuclear ribonucleoprotein NCBI Description Al [Arabidopsis thaliana] 411581 Seq. No. Seq. ID uC-osflcyp080d05b1 BLASTN Method g2645161 NCBI GI BLAST score 180 E value 1.0e-96 252 Match length 93 % identity NCBI Description Oryza sativa mRNA, similar to protein kinase 411582 Seq. No. uC-osflcyp080d06b1 Seq. ID BLASTN Method NCBI GI q2286112 BLAST score 55 E value 1.0e-22 59 Match length 98 % identity NCBI Description Oryza sativa MADS box protein (OsMADS8) mRNA, complete cds Seq. No. 411583 uC-osflcyp080d07b1 Seq. ID Method BLASTX q3763933 NCBI GI 315 BLAST score E value 1.0e-34 Match length 145 % identity 56 NCBI Description (AC004450) unknown protein [Arabidopsis thaliana] Seq. No. 411584 uC-osflcyp080d11b1 Seq. ID Method BLASTX NCBI GI g1168537 BLAST score 447 E value 2.0e-44 Match length 136 % identity 62 ASPARTIC PROTEINASE PRECURSOR >gi 82458 pir JS0732 NCBI Description aspartic proteinase (EC 3.4.23.-) - rice >gi 218143 dbj BAA02242 (D12777) aspartic proteinase [Oryza sativa] 411585 Seq. No. uC-osflcyp080e01a1 Seq. ID BLASTN Method g1574943 NCBI GI BLAST score 135 1.0e-69 E value 266 Match length 88 % identity NCBI Description Oryza sativa polyubiquitin (Rubq1) mRNA, complete cds

53487

411586

Seq. No.

```
Seq. ID
                  uC-osflcyp080e03b1
Method
                  BLASTX
NCBI GI
                  q131225
                  507
BLAST score
                  6.0e-53
E value
                  159
Match length
                  74
% identity
                  PHOTOSYSTEM I REACTION CENTRE SUBUNIT XI PRECURSOR (SUBUNIT
NCBI Description
                  V) (PSI-L) >gi_100605_pir_ A39759 photosystem I 18K protein
                  precursor - barley >gi 167087 (M61146) photosystem I
                  hydrophobic protein [Hordeum vulgare]
                  411587
Seq. No.
                  uC-osflcyp080e06a1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g5734616
                  40
BLAST score
                  4.0e-13
E value
                  60
Match length
                  92
% identity
NCBI Description Oryza sativa genomic DNA, chromosome 6, clone:P0538C01
Seq. No.
                  411588
                  uC-osflcyp080e08b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3913426
BLAST score
                  492
E value
                  4.0e-62
Match length
                  129
                  98
% identity
                  S-ADENOSYLMETHIONINE DECARBOXYLASE PROENZYME (ADOMETDC)
NCBI Description
                  (SAMDC) >qi 1532048 emb CAA69074 (Y07766)
                  S-adenosylmethionine decarboxylase [Oryza sativa]
                  411589
Seq. No.
                  uC-osflcyp080e09b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4755193
BLAST score
                  489
                  3.0e-49
E value
Match length
                  117
% identity
                  (AC007018) putative ribosomal protein S17 [Arabidopsis
NCBI Description
                  thaliana]
                  411590
Seq. No.
Seq. ID
                  uC-osflcyp080e10b1
Method
                  BLASTX
NCBI GI
                  q2499488
BLAST score
                  622
                  7.0e-65
E value
                  166
Match length
% identity
                  67
                  PYROPHOSPHATE--FRUCTOSE 6-PHOSPHATE 1-PHOSPHOTRANSFERASE
NCBI Description
                  ALPHA SUBUNIT (PFP) (6-PHOSPHOFRUCTOKINASE (PYROPHOSPHATE))
                   (PYROPHOSPHATE-DEPENDENT 6-PHOSPHOFRUCTOSE-1-KINASE)
```

(PPI-PFK) >gi_483547_emb_CAA83682_ (Z32849) 53488

% identity

NCBI Description

```
pyrophosphate-dependent phosphofructokinase alpha subunit
                  [Ricinus communis]
                  411591
Seq. No.
                  uC-osflcyp080e12a1
Seq. ID
                  BLASTN
Method
NCBI GI
                  q5803242
BLAST score
                  60
                  7.0e-25
E value
                  100
Match length
                  59
% identity
                  Oryza sativa genomic DNA, chromosome 6, clone:P0535G04
NCBI Description
                  411592
Seq. No.
                  uC-osflcyp080e12b1
Seq. ID
                  BLASTN
Method
                  g5679837
NCBI GI
BLAST score
                  39
                  2.0e-12
E value
Match length
                  47
                  96
% identity
                  Oryza sativa chromosome 4 BAC 11332 genomic sequences
NCBI Description
Seq. No.
                   411593
                  uC-osflcyp080f02b1
Seq. ID
                  BLASTX
Method
                   g3885894
NCBI GI
BLAST score
                   239
E value
                   2.0e-32
                   97
Match length
                   80
% identity
                  (AF093635) photosystem-1 H subunit GOS5 [Oryza sativa]
NCBI Description
                   411594
Seq. No.
                   uC-osflcyp080f03b1
Seq. ID
                   BLASTX
Method
                   g1168654
NCBI GI
                   291
BLAST score
                   3.0e-26
E value
                   73
Match length
                   67
% identity
                  BETA-GALACTOSIDASE PRECURSOR (LACTASE)
NCBI Description
                   >gi_542198_pir__S41889 beta-galactosidase (EC 3.2.1.23) -
                   garden asparagus >gi_452712_emb_CAA54525_ (X77319)
                   beta-galactosidase [Asparagus officinalis]
                   411595
Seq. No.
                   uC-osflcyp080f04a1
Seq. ID
Method
                   BLASTN
NCBI GI
                   q1311478
                   199
BLAST score
                   1.0e-108
E value
                   259
Match length
```

Oryza sativa DNA for sucrose phosphate synthase, complete

```
Seq. No.
                  411596
                  uC-osflcyp080f04b1
Seq. ID
Method
                  BLASTX
                  g1311479
NCBI GI
BLAST score
                  574
                  2.0e-59
E value
Match length
                  118
% identity
                  91
                  (D45890) sucrose phosphate synthase [Oryza sativa]
NCBI Description
                  411597
Seq. No.
Seq. ID
                  uC-osflcyp080f05a1
Method
                  BLASTX
NCBI GI
                  g129591
BLAST score
                  219
                  1.0e-17
E value
Match length
                  46
                  89
% identity
                  PHENYLALANINE AMMONIA-LYASE >gi 295824 emb CAA34226
NCBI Description
                   (X16099) phenylalanine ammonia-lyase [Oryza sativa]
                  411598
Seq. No.
Seq. ID
                  uC-osflcyp080f05b1
Method
                  BLASTX
NCBI GI
                  g129591
BLAST score
                  430
                  2.0e-42
E value
Match length
                  103
                  82
% identity
                  PHENYLALANINE AMMONIA-LYASE >gi 295824 emb CAA34226_
NCBI Description
                   (X16099) phenylalanine ammonia-lyase [Oryza sativa]
Seq. No.
                   411599
                   uC-osflcyp080f06a1
Seq. ID
                   BLASTX
Method
                   g5816996
NCBI GI
                   280
BLAST score
E value
                   1.0e-41
                   101
Match length
                   84
% identity
                  (AL110123) ribosomal protein L32-like protein [Arabidopsis
NCBI Description
                   thaliana]
                   411600
Seq. No.
                   uC-osflcyp080f06b1
Seq. ID
                   BLASTX
Method
NCBI GI
                   q5816996
BLAST score
                   405
                   4.0e-47
E value
Match length
                   130
                   76
% identity
                   (AL110123) ribosomal protein L32-like protein [Arabidopsis
NCBI Description
                   thaliana]
                   411601
Seq. No.
                   uC-osflcyp080f09a1
Seq. ID
                   BLASTX
Method
```

```
g3789940
NCBI GI
BLAST score
                   331
                   9.0e-31
E value
Match length
                   71
% identity
                   24
                   (AF093504) tetra-ubiquitin [Saccharum hybrid cultivar
NCBI Description
                   H32-8560]
                   411602
Seq. No.
                   uC-osflcyp080f09b1
Seq. ID
                   BLASTX
Method
                   g1800281
NCBI GI
BLAST score
                   553
                   9.0e-57
E value
                   145
Match length
                   19
% identity
                   (U82086) polyubiquitin [Fragaria x ananassa]
NCBI Description
Seq. No.
                   411603
                   uC-osflcyp080f12a1
Seq. ID
                   BLASTX
Method
                   g126386
NCBI GI
                   186
BLAST score
                   9.0e-14
E value
                   65
Match length
                   49
% identity
                   POLLEN ALLERGEN LOL P 2-A (LOL P II-A)
NCBI Description
                   >gi_82449_pir__A34291 pollen allergen Lol p IIA - perennial
                   ryegrass
                   411604
Seq. No.
                   uC-osflcyp080f12b1
Seq. ID
                   BLASTX
Method
NCBI GI
                   g126386
                   196
BLAST score
                   7.0e-15
E value
                   90
Match length
                   43
% identity
                   POLLEN ALLERGEN LOL P 2-A (LOL P II-A)
NCBI Description
                   >gi_82449_pir__A34291 pollen allergen Lol p IIA - perennial
                   ryegrass
                   411605
Seq. No.
                   uC-osflcyp080g04b1
Seq. ID
                   BLASTX
Method
                   g2293480
NCBI GI
                   357
BLAST score
                   4.0e-34
E value
                   73
Match length
                   96
 % identity
                   (AF011331) glycine-rich protein [Oryza sativa]
NCBI Description
                   411606
 Seq. No.
                   uC-osflcyp080g06a1
 Seq. ID
                   BLASTX
Method
 NCBI GI
                   q2696221
                   384
 BLAST score
```

```
4.0e-37
E value
                  105
Match length
% identity
                  71
                  (D55708) chitinase [Oryza sativa]
NCBI Description
Seq. No.
                  411607
                  uC-osflcyp080g06b1
Seq. ID
                  BLASTX
Method
NCBI GI
                  g2696221
                  333
BLAST score
                  4.0e-31
E value
                  89
Match length
                  75
% identity
                  (D55708) chitinase [Oryza sativa]
NCBI Description
Seq. No.
                  411608
                  uC-osflcyp080g07b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4522009
BLAST score
                  453
                  5.0e-45
E value
Match length
                  161
                  54
% identity
                  (AC007069) unknown protein [Arabidopsis thaliana]
NCBI Description
                  411609
Seq. No.
                  uC-osflcyp080g09b1
Seq. ID
Method
                  BLASTX
                  g5669924
NCBI GI
                  279
BLAST score
                  1.0e-24
E value
Match length
                  78
                  67
% identity
NCBI Description
                  (AF149116) soluble inorganic pyrophosphatase [Populus
                  tremula x Populus tremuloides]
Seq. No.
                  411610
                  uC-osflcyp080g12b1
Seq. ID
Method
                  BLASTN
                  g5006854
NCBI GI
BLAST score
                  104
E value
                  3.0e-51
Match length
                  282
                  93
% identity
NCBI Description Oryza sativa homeodomain leucine zipper protein (hox5)
                  mRNA, complete cds
Seq. No.
                  411611
Seq. ID
                  uC-osflcyp080h02a1
Method
                  BLASTX
NCBI GI
                  q4262174
BLAST score
                  174
E value
                  2.0e-12
Match length
                  51
% identity
                   65
NCBI Description (AC005508) 9058 [Arabidopsis thaliana]
```

411612 Seq. No. Seq. ID uC-osflcyp080h04a1 Method BLASTX NCBI GI g1170937 365 BLAST score 1.0e-34 E value 67 Match length 100 % identity S-ADENOSYLMETHIONINE SYNTHETASE 1 (METHIONINE NCBI Description ADENOSYLTRANSFERASE 1) (ADOMET SYNTHETASE 1) >gi_450549_emb_CAA81481_ (Z26867) S-adenosyl methionine synthetase [Oryza sativa] 411613 Seq. No. Seq. ID uC-osflcyp080h04b1 BLASTX Method NCBI GI g1170937 BLAST score 691 E value 6.0e-73Match length 134 98 % identity S-ADENOSYLMETHIONINE SYNTHETASE 1 (METHIONINE NCBI Description ADENOSYLTRANSFERASE 1) (ADOMET SYNTHETASE 1) $>gi_450549_emb_CAA81481_ (Z26867)$ S-adenosyl methionine synthetase [Oryza sativa] 411614 Seq. No. Seq. ID uC-osflcyp080h05b1 Method BLASTX NCBI GI g4544408 475 BLAST score 1.0e-47 E value 110 Match length % identity 78 NCBI Description (AC006955) unknown protein [Arabidopsis thaliana] 411615 Seq. No. Seq. ID uC-osflcyp080h06a1 Method BLASTN NCBI GI g4105124 BLAST score 47 3.0e-17 E value Match length 141 % identity 92 NCBI Description Zea mays cell wall invertase (incw4) gene, complete cds Seq. No. 411616 uC-osflcyp080h08b1 Seq. ID Method BLASTX NCBI GI g2708532 186 BLAST score 2.0e-14 E value 70 Match length 49 % identity (AF029351) putative RNA binding protein [Nicotiana tabacum] NCBI Description 411617 Seq. No.



Seq. ID uC-osflcyp080h10a1 Method BLASTX NCBI GI q2984709 BLAST score 167 E value 2.0e-11 Match length 48 75 % identity (AF053468) DnaJ-related protein ZMDJ1 [Zea mays] NCBI Description Seq. No. 411618 uC-osflcyp080h10b1 Seq. ID Method BLASTX NCBI GI g2984709 BLAST score 522 E value 4.0e-53 Match length 121 % identity 85 NCBI Description (AF053468) DnaJ-related protein ZMDJ1 [Zea mays] Seq. No. 411619 Seq. ID uC-osflcyp081a04b1 Method BLASTX NCBI GI g5262201 BLAST score 232 2.0e-19 E value Match length 76 59 % identity NCBI Description (AL080252) putative protein [Arabidopsis thaliana] Seq. No. 411620 uC-osflcyp081a05b1 Seq. ID Method BLASTX g2501189 NCBI GI BLAST score 454 3.0e-45E value 129 Match length 74 % identity NCBI Description THIAMINE BIOSYNTHETIC ENZYME 1-1 PRECURSOR >gi_2130146_pir__S61419 thiamine biosynthetic enzyme thi1-1 - maize >gi 596078 (U17350) thiamine biosynthetic enzyme [Zea mays] 411621 Seq. No. uC-osflcyp081a06b1 Seq. ID Method BLASTX NCBI GI g2961176 BLAST score 263 E value 4.0e-23 Match length 82 % identity 68 NCBI Description (AF050674) ribosomal protein L27 precursor [Oryza sativa]

Seq. No. 411622

Seq. ID uC-osflcyp081a07b1

Method BLASTX NCBI GI g3789952 BLAST score 522

% identity

```
E value
                   4.0e-53
Match length
                  100
                   96
% identity
                  (AF094775) chlorophyll a/b-binding protein presursor [Oryza
NCBI Description
                   sativa]
                   411623
Seq. No.
                  uC-osflcyp081a09b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1346109
BLAST score
                   493
E value
                   4.0e-58
Match length
                  134
% identity
                  85
NCBI Description
                  GUANINE NUCLEOTIDE-BINDING PROTEIN BETA SUBUNIT-LIKE
                   PROTEIN (GPB-LR) (RWD) >gi 540535 dbj BAA07404 (D38231)
                  RWD [Oryza sativa]
Seq. No.
                   411624
                  uC-osflcyp081a12b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2384760
                  559
BLAST score
                  2.0e-57
E value
Match length
                  135
                  79
% identity
NCBI Description
                  (AF016897) GDP dissociation inhibitor protein OsGDI2 [Oryza
                   sativa]
                   411625
Seq. No.
                  uC-osflcyp081b01b1
Seq. ID
Method
                  BLASTX
                  g3885882
NCBI GI
BLAST score
                   382
                   8.0e-37
E value
Match length
                  88
% identity
                   77
NCBI Description (AF093629) inorganic pyrophosphatase [Oryza sativa]
Seq. No.
                  411626
                  uC-osflcyp081b03b1
Seq. ID
Method
                  BLASTX
NCBI GI
                   q3668069
BLAST score
                  512
E value
                   6.0e-52
Match length
                  130
% identity
                   74
NCBI Description (U28007) Pto kinase interactor 1 [Lycopersicon esculentum]
Seq. No.
                  411627
Seq. ID
                  uC-osflcyp081b07b1
Method
                  BLASTX
NCBI GI
                  q2454182
BLAST score
                  639
E value
                  6.0e-67
Match length
                  149
```

Match length

% identity

112

```
NCBI Description
                   (U80185) pyruvate dehydrogenase E1 alpha subunit
                   [Arabidopsis thaliana]
Seq. No.
                   411628
Seq. ID
                  uC-osflcyp081b10b1
Method
                  BLASTX
NCBI GI
                  g3522956
BLAST score
                   229
                  7.0e-19
E value
Match length
                  81
% identity
                  54
NCBI Description
                 (AC004411) putative pectinacetylesterase precursor
                   [Arabidopsis thaliana]
Seq. No.
                   411629
Seq. ID
                  uC-osflcyp081b12b1
Method
                  BLASTX
NCBI GI
                  g1632822
BLAST score
                  480
E value
                  2.0e-48
                  96
Match length
% identity
                  96
                  (Y08962) transmembrane protein [Oryza sativa] >gi 1667594
NCBI Description
                   (U77297) transmembrane protein [Oryza sativa]
Seq. No.
                  411630
Seq. ID
                  uC-osflcyp081c01b1
Method
                  BLASTX
NCBI GI
                  g2443329
BLAST score
                  614
E value
                  6.0e-64
Match length
                  140
% identity
                  79
NCBI Description (D86122) Mei2-like protein [Arabidopsis thaliana]
Seq. No.
                  411631
Seq. ID
                  uC-osflcyp081c03b1
Method
                  BLASTX
NCBI GI
                  g2501189
BLAST score
                  544
E value
                  1.0e-55
Match length
                  150
% identity
                  74
NCBI Description
                  THIAMINE BIOSYNTHETIC ENZYME 1-1 PRECURSOR
                  >gi_2130146_pir__S61419 thiamine biosynthetic enzyme thi1-1
                   maize >gi_596078 (U17350) thiamine biosynthetic enzyme
                  [Zea mays]
Seq. No.
                  411632
Seq. ID
                  uC-osflcyp081c04b1
Method
                  BLASTX
NCBI GI
                  g1172635
BLAST score
                  473
E value
                  2.0e-47
```

53496

NCBI Description 26S PROTEASE REGULATORY SUBUNIT 4 HOMOLOG (TAT-BINDING

PROTEIN HOMOLOG 2) >gi_556558_dbj_BAA04615_ (D17789) rice homologue of Tat binding protein [Oryza sativa]

Seq. No. 411633

Seq. ID uC-osflcyp081c08b1

Method BLASTX
NCBI GI g4115379
BLAST score 279
E value 1.0e-24
Match length 136
% identity 46

NCBI Description (AC005967) putative carbonyl reductase [Arabidopsis

thaliana]

Seq. No. 411634

Seq. ID uC-osflcyp081c09b1

Method BLASTN
NCBI GI g459268
BLAST score 84
E value 3.0e-39
Match length 166
% identity 88

NCBI Description Z.mays mRNA Transcribed Sequence

Seq. No. 411635

Seq. ID uC-osflcyp081c11b1

Method BLASTX
NCBI GI g6094303
BLAST score 217
E value 7.0e-21
Match length 82
% identity 65

NCBI Description SELENOCYSTEINE METHYLTRANSFERASE (SECYS-METHYLTRANSFERASE)

(SECYS-MT) >gi_4006848_emb_CAA10368_ (AJ131433)

selenocysteine methyltransferase [Astragalus bisulcatus]

Seq. No. 411636

Seq. ID uC-osflcyp081c12b1

Method BLASTX
NCBI GI g4544438
BLAST score 161
E value 7.0e-11
Match length 79
% identity 44

NCBI Description (AC006592) hypothetical protein [Arabidopsis thaliana]

Seq. No. 411637

Seq. ID uC-osflcyp081d01b1

Method BLASTX
NCBI GI g2501189
BLAST score 436
E value 4.0e-43
Match length 124
% identity 70

NCBI Description THIAMINE BIOSYNTHETIC ENZYME 1-1 PRECURSOR

>gi_2130146_pir__S61419 thiamine biosynthetic enzyme thi1-1
- maize >gi_596078 (U17350) thiamine biosynthetic enzyme

```
[Zea mays]
Seq. No.
                  411638
Seq. ID
                  uC-osflcyp081d02b1
Method
                  BLASTX
NCBI GI
                  q3882355
BLAST score
                  635
E value
                  2.0e-66
Match length
                  155
                  76
% identity
NCBI Description
                  (U92460) 12-oxophytodienoate reductase OPR1 [Arabidopsis
                  thaliana]
                  411639
Seq. No.
Seq. ID
                  uC-osflcyp081d03b1
                  BLASTX
Method
NCBI GI
                  q4126809
BLAST score
                  771
E value
                  2.0e-82
Match length
                  145
                  54
% identity
NCBI Description (AB017042) glyoxalase I [Oryza sativa]
Seq. No.
                  411640
                  uC-osflcyp081d04b1
Seq. ID
                  BLASTX
Method
NCBI GI
                  q1684857
BLAST score
                  368
E value
                  2.0e-35
Match length
                  80
% identity
                  35
NCBI Description (U77940) polyubiquitin [Phaseolus vulgaris]
Seq. No.
                  411641
                  uC-osflcyp081d06b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2626753
BLAST score
                  141
E value
                  6.0e-18
Match length
                  89
% identity
                   60
                  (AB008782) sulfate transporter [Arabidopsis thaliana]
NCBI Description
                  411642
Seq. No.
                  uC-osflcyp081d07b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2773154
BLAST score
                  352
E value
                  3.0e-33
Match length
                  138
% identity
                  52
                  (AF039573) abscisic acid- and stress-inducible protein
NCBI Description
                   [Oryza sativa]
```

Seq. No. 411643

Seq. ID uC-osflcyp081d11b1

Method BLASTX



```
q4586117
NCBI GI
BLAST score
                  336
                  3.0e-31
E value
                  116
Match length
                  54
% identity
                 (AL049638) putative protein [Arabidopsis thaliana]
NCBI Description
                  411644
Seq. No.
Seq. ID
                  uC-osflcyp081d12b1
                  BLASTN
Method
NCBI GI
                  g415314
BLAST score
                  259
                  1.0e-143
E value
Match length
                  363
                  97
% identity
NCBI Description Rice mRNA for NADP dependent malic enzyme, complete cds
                  411645
Seq. No.
Seq. ID
                  uC-osflcyp081e02b1
Method
                  BLASTX
NCBI GI
                  q4539335
BLAST score
                  147
                  4.0e-09
E value
                  54
Match length
                  50
% identity
NCBI Description (AL035539) putative protein [Arabidopsis thaliana]
                  411646
Seq. No.
Seq. ID
                  uC-osflcyp081e04b1
Method
                  BLASTX
NCBI GI
                  q2565436
BLAST score
                  324
E value
                  7.0e-30
Match length
                  69
                  93
% identity
NCBI Description (AF028842) DegP protease precursor [Arabidopsis thaliana]
                  411647
Seq. No.
Seq. ID
                  uC-osflcyp081e07b1
Method
                  BLASTX
NCBI GI
                  q4539335
                   774
BLAST score
                  1.0e-82
E value
Match length
                  177
                  76
% identity
NCBI Description (AL035539) putative protein [Arabidopsis thaliana]
                   411648
Seq. No.
                  uC-osflcyp081e08b1
Seq. ID
```

Method BLASTX
NCBI GI g5824783
BLAST score 199
E value 3.0e-15
Match length 141
% identity 35

NCBI Description (AL110487) Y39E4B.7 [Caenorhabditis elegans]

```
Seq. No.
                   411649
                  uC-osflcyp081e09b1
Seq. ID
                   BLASTX
Method
NCBI GI
                  q4309697
BLAST score
                  240
                   5.0e-20
E value
                  106
Match length
% identity
                   47
                   (AC006266) putative DNA-directed RNA polymerase subunit
NCBI Description
                   [Arabidopsis thaliana]
                   411650
Seq. No.
Seq. ID
                   uC-osflcyp081e12b1
                   BLASTX
Method
                   q3885343
NCBI GI
                   172
BLAST score
E value
                   3.0e-12
Match length
                   63
% identity
                  (AC005623) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   411651
                   uC-osflcyp081f01b1
Seq. ID
Method
                   BLASTX
                   g3063708
NCBI GI
                   216
BLAST score
                   3.0e-17
E value
                   136
Match length
% identity
                   40
                  (AL022537) putative protein [Arabidopsis thaliana]
NCBI Description
                   411652
Seq. No.
                   uC-osflcyp081f03b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g1710521
BLAST score
                   560
                   1.0e-57
E value
Match length
                   112
% identity
                   96
                   60S RIBOSOMAL PROTEIN L24 >gi 1154859_emb_CAA63960_
NCBI Description
                   (X94296) L24 ribosomal protein [Hordeum vulgare]
                   411653
Seq. No.
                   uC-osflcyp081f05b1
Seq. ID
Method
                   BLASTX
                   g4959461
NCBI GI
                   810
BLAST score
                   7.0e-87
E value
Match length
                   155
                   99
% identity
                  (AF126053) RACB small GTP binding protein [Zea mays]
NCBI Description
                   411654
Seq. No.
                   uC-osflcyp081f07b1
Seq. ID
Method
                   BLASTX
                   g3023713
NCBI GI
```

53500

766

BLAST score

```
E value
                   1.0e-81
Match length
                   158
                   93
% identity
                  ENOLASE (2-PHOSPHOGLYCERATE DEHYDRATASE)
NCBI Description
                   (2-PHOSPHO-D-GLYCERATE HYDRO-LYASE) (OSE1) >gi 780372
                   (U09450) enolase [Oryza sativa]
Seq. No.
                   411655
Seq. ID
                  uC-osflcyp081f08b1
                  BLASTX
Method
NCBI GI
                  g1076800
BLAST score
                   686
E value
                  2.0e-72
                  151
Match length
% identity
                  84
                  L-ascorbate peroxidase (EC 1.11.1.11), cytosolic isozyme -
NCBI Description
                  maize >gi_600116_emb_CAA84406_ (Z34934) cytosolic ascorbate
                  peroxidase [Zea mays] >gi_1096503_prf__2111423A ascorbate
                  peroxidase [Zea mays]
Seq. No.
                   411656
Seq. ID
                  uC-osflcyp081f09b1
Method
                  BLASTX
NCBI GI
                  g1136120
BLAST score
                  588
                  6.0e-61
E value
Match length
                  109
                  99
% identity
NCBI Description (X91806) alpha-tubulin [Oryza sativa]
Seq. No.
                  411657
Seq. ID
                  uC-osflcyp081f10b1
Method
                  BLASTX
NCBI GI
                  g131225
BLAST score
                  533
E value
                  1.0e-54
Match length
                  113
% identity
                  92
NCBI Description
                  PHOTOSYSTEM I REACTION CENTRE SUBUNIT XI PRECURSOR (SUBUNIT
                  V) (PSI-L) >gi_100605 pir A39759 photosystem I 18K protein
                  precursor - barley >gi 167087 (M61146) photosystem I
                  hydrophobic protein [Hordeum vulgare]
Seq. No.
                  411658
Seq. ID
                  uC-osflcyp081f11b1
Method
                  BLASTX
NCBI GI
                  g639722
BLAST score
                  658
E value
                  4.0e-69
Match length
                  155
% identity
                  82
NCBI Description
                  (L27484) calcium-dependent protein kinase [Zea mays]
```

Seq. No. 411659

Seq. ID uC-osflcyp081g03b1

Method BLASTX NCBI GI g4138343

```
BLAST score
                   467
E value
                   1.0e-46
Match length
                  163
% identity
                  60
NCBI Description (AJ011979) RNA-directed RNA polymerase [Petunia x hybrida]
Seq. No.
                  411660
                  uC-osflcyp081g07b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3894158
BLAST score
                  216
E value
                  3.0e-17
Match length
                  158
% identity
                  39
NCBI Description (AC005312) similar to phloem-specific lectin [Arabidopsis
                  thaliana]
Seq. No.
                  411661
Seq. ID
                  uC-osflcyp081g08b1
Method
                  BLASTX
NCBI GI
                  g2642446
BLAST score
                  274
E value
                  4.0e-24
                  92
Match length
% identity
                  61
NCBI Description (AC002391) similar to auxin-responsive GH3 protein
                  [Arabidopsis thaliana]
Seq. No.
                  411662
                  uC-osflcyp081g11b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1518540
BLAST score
                  554
E value
                  2.0e-58
Match length
                  132
% identity
NCBI Description (U53418) UDP-glucose dehydrogenase [Glycine max]
Seq. No.
                  411663
Seq. ID
                  uC-osflcyp081g12b1
Method
                  BLASTX
NCBI GI
                  g6056199
BLAST score
                  263
E value
                  7.0e-23
Match length
                  100
% identity
NCBI Description (AC009400) unknown protein [Arabidopsis thaliana]
```

Seq. No. 411664

Seq. ID uC-osflcyp081h02b1

Method BLASTX NCBI GI g1084454 BLAST score 519 E value 6.0e-53Match length 107 % identity 91

NCBI Description peptidylprolyl isomerase (EC 5.2.1.8) Cyp1 - rice

>gi_600765 (L29471) cyclophilin 1 [Oryza sativa] Seq. No. 411665 Seq. ID uC-osflcyp081h04b1 Method BLASTX NCBI GI g4850330 BLAST score 332 E value 7.0e-31 Match length 63 % identity 100 NCBI Description (AB027123) cytochrome c oxidase subunit 5c [Oryza sativa] Seq. No. 411666 uC-osflcyp081h09b1 Seq. ID Method BLASTX NCBI GI g2257756 BLAST score 430 E value 2.0e-42 Match length 108 % identity 80 NCBI Description (U82815) nucleolar histone deacetylase HD2-p39 [Zea mays] >gi_3650466 (AF026917) histone deacetylase HD2-p39 [Zea mays] Seq. No. 411667 Seq. ID uC-osflcyp081h10b1 Method BLASTN NCBI GI g473996 BLAST score 237 E value 1.0e-130 Match length 272 % identity 98 NCBI Description Rice mRNA, partial homologous to ribosomal protein L7 gene 411668 Seq. No. Seq. ID uC-osflcyp081h11b1 Method BLASTX NCBI GI q2407281 BLAST score 691 E value 5.0e-73 Match length 129 99 % identity NCBI Description (AF017363) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa] Seq. No. 411669 uC-osflcyp082a01a1 Seq. ID

Method BLASTN NCBI GI g1261857 BLAST score 47 E value 3.0e-17 Match length 86 % identity 91

NCBI Description Rice CatA gene for catalase, complete cds

Seq. No. 411670

Seq. ID uC-osflcyp082a01b1

BLAST score

E value

9.0e-45

```
BLASTX
Method
NCBI GI
                  g2130069
                  182
BLAST score
                  5.0e-17
E value
Match length
                  84
                  67
% identity
                  catalase (EC 1.11.1.6) catA - rice
NCBI Description
                  >gi 1261858_dbj_BAA06232_ (D29966) catalase [Oryza sativa]
                  411671
Seq. No.
                  uC-osflcyp082a05b1
Seq. ID
                  BLASTX
Method
NCBI GI
                  q1272410
                  346
BLAST score
                  8.0e-35
E value
                  106
Match length
                  71
% identity
NCBI Description (U52045) immunophilin precursor [Vicia faba]
Seq. No.
                  411672
                  uC-osflcyp082a06a1
Seq. ID
                  BLASTX
Method
                  q3075488
NCBI GI
BLAST score
                  242
                  2.0e-20
E value
                  49
Match length
                  96
% identity
NCBI Description (AF058796) chlorophyll a/b-binding protein [Oryza sativa]
Seq. No.
                   411673
Seq. ID
                   uC-osflcyp082a06b1
                   BLASTN
Method
                   g3075487
NCBI GI
BLAST score
                   41
E value
                   6.0e-14
                   57
Match length
                   93
% identity
NCBI Description Oryza sativa chlorophyll a/b-binding protein (RCABP69)
                   mRNA, complete cds
Seq. No.
                   411674
                   uC-osflcyp082a07a1
Seq. ID
                   BLASTX
Method
NCBI GI
                   g2130069
BLAST score
                   408
                   9.0e-40
E value
Match length
                   86
                   92
% identity
                  catalase (EC 1.11.1.6) catA - rice
NCBI Description
                   >gi 1261858 dbj_BAA06232_ (D29966) catalase [Oryza sativa]
                   411675
Seq. No.
                   uC-osflcyp082a08b1
Seq. ID
Method
                   BLASTX
                   g2271477
NCBI GI
                   448
```



Match length 93 % identity 90

NCBI Description (AF009631) AP47/50p [Arabidopsis thaliana]

Seq. No. 411676

Seq. ID uC-osflcyp082a10b1

Method BLASTN
NCBI GI g20181
BLAST score 73
E value 7.0e-33
Match length 105
% identity 93

NCBI Description Rice cab2R gene for light harvesting chlorophyll

a/b-binding protein

Seq. No. 411677

Seq. ID uC-osflcyp082a12a1

Method BLASTN
NCBI GI g3075487
BLAST score 50
E value 4.0e-19
Match length 78
% identity 91

NCBI Description Oryza sativa chlorophyll a/b-binding protein (RCABP69)

mRNA, complete cds

Seq. No. 411678

Seq. ID uC-osflcyp082a12b1

Method BLASTX
NCBI GI g5565981
BLAST score 276
E value 2.0e-24
Match length 88
% identity 70

NCBI Description (AF152600) unknown [Zea mays]

Seq. No. 411679

Seq. ID uC-osflcyp082b02a1

Method BLASTX
NCBI GI g3360289
BLAST score 158
E value 1.0e-10
Match length 39
% identity 90

NCBI Description (AF023164) leucine-rich repeat transmembrane protein kinase

1 [Zea mays]

Seq. No. 411680

Seq. ID uC-osflcyp082b03a1

Method BLASTN
NCBI GI g3859567
BLAST score 55
E value 2.0e-22
Match length 127
% identity 87

NCBI Description Oryza sativa clone FIL1 unknown mRNA

Method

NCBI GI

BLASTX

g3287695

```
411681
Seq. No.
Seq. ID
                  uC-osflcyp082b05a1
Method
                  BLASTX
NCBI GI
                  g5262760
BLAST score
                  276
E value
                  2.0e-24
Match length
                  67
                  85
% identity
NCBI Description (AL080283) Beta-COP-like protein [Arabidopsis thaliana]
                  411682
Seq. No.
                  uC-osflcyp082b05b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g5262759
BLAST score
                  448
                  2.0e-44
E value
                  110
Match length
                  77
% identity
NCBI Description (AL080283) putative protein [Arabidopsis thaliana]
                  411683
Seq. No.
                  uC-osflcyp082b06b1
Seq. ID
                  BLASTX
Method
                  g1076660
NCBI GI
                  161
BLAST score
                  2.0e-11
E value
                  52
Match length
                  60
% identity
                  D13F(MYBST1) protein - potato >gi 786426_bbs_159122
NCBI Description
                   (S74753) MybSt1=Myb-related transcriptional activator
                   {DNA-binding domain repeats} [Solanum tuberosum=potatoes,
                  leaf, Peptide, 342 aa] [Solanum tuberosum]
                  411684
Seq. No.
Seq. ID
                  uC-osflcyp082b07a1
Method
                  BLASTN
                  q218221
NCBI GI
                   69
BLAST score
                  3.0e-30
E value
Match length
                   97
                   93
% identity
NCBI Description Oryza sativa p-SINE1-r6 gene, repeat sequence
                   411685
Seq. No.
                  uC-osflcyp082b08b1
Seq. ID
Method
                   BLASTN
NCBI GI
                   g3859567
BLAST score
                   65
                   4.0e-28
E value
Match length
                  219
% identity
                   88
NCBI Description Oryza sativa clone FIL1 unknown mRNA
Seq. No.
                   411686
                   uC-osflcyp082b10a1
Seq. ID
```



222 BLAST score 6.0e-18 E value 91 Match length 54 % identity (AC003979) Similar to hypothetical protein C34B7.2 NCBI Description gb 1729503 from C. elegans cosmid gb_Z83220. [Arabidopsis thaliana] 411687 Seq. No. uC-osflcyp082b11a1 Seq. ID Method BLASTX g6015059 288 BLAST score 9.0e - 26E value

NCBI GI Match length 60 92 % identity

ELONGATION FACTOR 1-ALPHA (EF-1-ALPHA) >gi 2996096 NCBI Description (AF030517) translation elongation factor-1 alpha; EF-1

alpha [Oryza sativa]

411688 Seq. No.

uC-osflcyp082b11b1 Seq. ID

Method BLASTX NCBI GI g2662343 BLAST score 190 6.0e-15 E value 40 Match length 95 % identity

NCBI Description (D63581) EF-1 alpha [Oryza sativa]

411689 Seq. No.

uC-osflcyp082b12a1 Seq. ID

Method BLASTX NCBI GI g6056209 318 BLAST score 3.0e-29 E value 71 Match length 82 % identity

NCBI Description (AC009400) unknown protein [Arabidopsis thaliana]

411690 Seq. No.

uC-osflcyp082c01a1 Seq. ID

BLASTX Method NCBI GI g3047103 160 BLAST score 1.0e-10 E value 83 Match length 52 % identity

NCBI Description (AF058919) regions of weak similarity to 1-asparaginase

[Arabidopsis thaliana]

Seq. No. 411691

uC-osflcyp082c06b1 Seq. ID

BLASTX Method NCBI GI g3023816 554 BLAST score 5.0e-57 E value

Method

NCBI GI

BLASTX

g4586117

```
106
Match length
% identity
                  100
                  GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC
NCBI Description
                  >qi 968996 (U31676) glyceraldehyde-3-phosphate
                  dehydrogenase [Oryza sativa]
                  411692
Seq. No.
Seq. ID
                  uC-osflcyp082c07a1
Method
                  BLASTX
NCBI GI
                  q4103987
BLAST score
                  403
                  3.0e-39
E value
Match length
                  101
% identity
                  77
                  (AF030516) 5,10-methylenetetrahydrofolate
NCBI Description
                  dehydrogenase-5,10-methenyltetrahydrofolate cyclohydrolase
                  [Pisum sativum] >gi 6002383 emb CAB56756.1 (AJ011589)
                  5,10-methylenetetrahydrofolate dehydrogenase:
                  5,10-methenyltetrahydrofolate cyclohydrolase [Pisum
                  sativum]
                  411693
Seq. No.
Seq. ID
                  uC-osflcyp082c08b1
                  BLASTN
Method
                  q4336204
NCBI GI
                  46
BLAST score
                  2.0e-16
E value
                  166
Match length
                  83
% identity
NCBI Description Zea mays cytochrome b5 reductase (NFR) mRNA, complete cds
                  411694
Seq. No.
                  uC-osflcyp082c12a1
Seq. ID
                  BLASTX
Method
NCBI GI
                  g82263
BLAST score
                  227
                  1.0e-18
E value
Match length
                  57
                  79
% identity
                  ubiquinol--cytochrome-c reductase (EC 1.10.2.2) cytochrome
NCBI Description
                  c1 precursor (clone pC(1)3II) - potato
                   411695
Seq. No.
                  uC-osflcyp082c12b1
Seq. ID
Method
                  BLASTX
                   g82263
NCBI GI
                   746
BLAST score
                   2.0e-79
E value
                   151
Match length
                   93
% identity
                  ubiquinol--cytochrome-c reductase (EC 1.10.2.2) cytochrome
NCBI Description
                   c1 precursor (clone pC(1)3II) - potato
                   411696
Seq. No.
                  uC-osflcyp082d05b1
Seq. ID
```

BLAST score 266 E value 4.0e-23 Match length 94 % identity 53

NCBI Description (AL049638) putative protein [Arabidopsis thaliana]

Seq. No. 411697

Seq. ID uC-osflcyp082d12a1

Method BLASTN
NCBI GI g2443401
BLAST score 182
E value 6.0e-98
Match length 190
% identity 99

NCBI Description Oryza sativa mRNA for orthophosphate dikinase, complete cds

Seq. No. 411698

Seq. ID uC-osflcyp082d12b1

Method BLASTX
NCBI GI g2443402
BLAST score 402
E value 5.0e-53
Match length 120
% identity 92

NCBI Description (D87745) orthophosphate dikinase [Oryza sativa]

>gi_2443405_dbj_BAA22420_ (D87952) orthophosphate dikinase

[Oryza sativa]

Seq. No. 411699

Seq. ID uC-osflcyp082e01a1

Method BLASTX
NCBI GI g3087888
BLAST score 184
E value 2.0e-13
Match length 57
% identity 63

NCBI Description (X94302) hexokinase [Solanum tuberosum]

Seq. No. 411700

Seq. ID uC-osflcyp082e01b1

Method BLASTX
NCBI GI g2833378
BLAST score 165
E value 6.0e-12
Match length 49
% identity 65

NCBI Description HEXOKINASE >gi 619928 (U18754) hexokinase [Arabidopsis

thaliana] >gi 1582383 prf__2118367A hexokinase [Arabidopsis

thaliana]

Seq. No. 411701

Seq. ID uC-osflcyp082e03a1

Method BLASTX
NCBI GI g2342676
BLAST score 444
E value 5.0e-44
Match length 116

% identity 69

NCBI Description (AC000106) Strong similarity to Oryza NADPH oxidase

(gb X93301). [Arabidopsis thaliana]

Seq. No. 411702

Seq. ID uC-osflcyp082e04b1

Method BLASTX
NCBI GI g2959781
BLAST score 706
E value 1.0e-74
Match length 159
% identity 82

NCBI Description (AJ223508) Zwille protein [Arabidopsis thaliana]

Seq. No. 411703

Seq. ID uC-osflcyp082e05a1

Method BLASTN
NCBI GI g3287498
BLAST score 59
E value 3.0e-24
Match length 59
% identity 100

NCBI Description Oryza sativa gene for importin alpha, complete cds

Seq. No. 411704

Seq. ID uC-osflcyp082e05b1

Method BLASTX
NCBI GI g1174745
BLAST score 607
E value 4.0e-63
Match length 130
% identity 90

NCBI Description TRIOSEPHO

I Description TRIOSEPHOSPHATE ISOMERASE, CHLOROPLAST PRECURSOR (TIM)

>gi_1363523_pir__S53761 triose-phosphate isomerase (EC

5.3.1.1) precursor, chloroplast - rye

>gi_609262_emb_CAA83533_ (Z32521) triosephosphate isomerase [Secale cereale] >gi_1095494_prf__2109226B triosephosphate

isomerase [Secale cereale]

Seq. No. 411705

Seq. ID uC-osflcyp082e09b1

Method BLASTX
NCBI GI g2129727
BLAST score 255
E value 3.0e-22
Match length 84
% identity 56

NCBI Description RNA-binding protein 37 - Arabidopsis thaliana >gi 1174153

(U44134) RNA-binding protein [Arabidopsis thaliana]

Seq. No. 411706

Seq. ID uC-osflcyp082f03a1

Method BLASTN
NCBI GI g3885891
BLAST score 84
E value 2.0e-39
Match length 184

Seq. ID

```
% identity
NCBI Description
                   Oryza sativa photosystem-1 F subunit precursor (PSI-F)
                   mRNA, complete cds
Seq. No.
                   411707
                   uC-osflcyp082f03b1
Seq. ID
Method
                   BLASTN
NCBI GI
                   q3885891
BLAST score
                   183
E value
                   1.0e-98
Match length
                   211
                   97
% identity
                  Oryza sativa photosystem-1 F subunit precursor (PSI-F)
NCBI Description
                   mRNA, complete cds
Seq. No.
                   411708
Seq. ID
                   uC-osflcyp082f04a1
Method
                   BLASTX
NCBI GI
                   q4539314
BLAST score
                   232
E value
                   4.0e-19
Match length
                   100
% identity
                   49
NCBI Description
                  (AL035679) kinesin like protein [Arabidopsis thaliana]
Seq. No.
                   411709
Seq. ID
                   uC-osflcyp082f08b1
Method
                   BLASTX
NCBI GI
                   g3789948
BLAST score
                   677
E value
                   2.0e-71
Match length
                  131
% identity
                   98
NCBI Description
                  (AF094773) translation initiation factor 5A [Oryza sativa]
Seq. No.
                   411710
Seq. ID
                  uC-osflcyp082g01b1
Method
                  BLASTX
NCBI GI
                  g3482977
BLAST score
                   614
E value
                   6.0e-64
Match length
                  153
% identity
                   77
NCBI Description
                  (AL031369) putative protein [Arabidopsis thaliana]
Seq. No.
                  411711
Seq. ID
                  uC-osflcyp082g02b1
Method
                  BLASTX
NCBI GI
                  g1777921
BLAST score
                  595
E value
                  2.0e-75
Match length
                  162
% identity
                  90
                  (U54774) glutamate decarboxylase [Nicotiana tabacum]
NCBI Description
Seq. No.
                  411712
```

53511

uC-osflcyp082g04a1

```
Method
                  BLASTX
NCBI GI
                  q1305525
BLAST score
                  372
E value
                  1.0e-35
Match length
                  73
                  100
% identity
                  (U55212) Wilms' tumor-related protein QM [Oryza sativa]
NCBI Description
                  411713
Seq. No.
                  uC-osflcyp082g04b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2129608
BLAST score
                  289
                   5.0e-36
E value
                  131
Match length
% identity
                  66
                  GTP-binding protein, 68K - Arabidopsis thaliana >gi 807577
NCBI Description
                   (L38614) GTP-binding protein [Arabidopsis thaliana]
Seq. No.
                  411714
                  uC-osflcyp082g06b1
Seq. ID
Method
                  BLASTX
                  q100525
NCBI GI
BLAST score
                  577
                  8.0e-60
E value
Match length
                  125
% identity
                  24
                  ubiquitin precursor UbB2 - common sunflower (fragment)
NCBI Description
                  >gi_18803_emb_CAA40323_ (X57003) polyubiquitin protein
                   [Helianthus annuus]
Seq. No.
                  411715
                  uC-osflcyp082g08a1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1813595
BLAST score
                  186
                  9.0e-14
E value
Match length
                  67
% identity
                  51
NCBI Description
                  (U73749) xylan endohydrolase isoenzyme X-I [Hordeum
                  vulgare]
                  411716
Seq. No.
Seq. ID
                  uC-osflcyp082g08b1
Method
                  BLASTX
NCBI GI
                  g1718238
BLAST score
                  261
E value
                  2.0e-22
Match length
                  72
                  65
% identity
NCBI Description
                   (U59313) (1,4)-beta-xylan endohydrolase, isoenzyme X-II
                   [Hordeum vulgare]
Seq. No.
                  411717
Seq. ID
                  uC-osflcyp082g09a1
Method
                  BLASTN
NCBI GI
                  g2306980
```

BLAST score 203 1.0e-110 E value Match length 260 95 % identity NCBI Description Oryza sativa photosystem I antenna protein (Lhca) mRNA, complete cds Seq. No. 411718 Seq. ID uC-osflcyp082g09b1 Method BLASTX NCBI GI g1076724 BLAST score 142 E value 4.0e-18 Match length 86 % identity 67 NCBI Description LHCI-680, photosystem I antenna protein - barley >gi 666054 emb CAA59049 (X84308) LHCI-680, photosystem I antenna protein [Hordeum vulgare] Seq. No. 411719 uC-osflcyp082g10a1 Seq. ID Method BLASTX NCBI GI g2129826 BLAST score 184 2.0e-13 E value Match length 65 55 % identity NCBI Description dynamin-like protein phragmoplastin 5 - soybean >gi 1218004 (U36430) SDL5A [Glycine max] Seq. No. 411720 uC-osflcyp082g12a1 Seq. ID Method BLASTX NCBI GI g481477 BLAST score 376 4.0e-36 E value Match length 81 % identity 16 NCBI Description ubiquitin precursor - rice >gi 416038 emb CAA53665 (X76064) polyubiquitin [Oryza sativa] >gi_1574944 (U37687) polyubiquitin [Oryza sativa] >gi_6013289_gb_AAF01315.1 AF184279 1 (AF184279) polyubiquitin [Oryza sativa] >gi_6013291_gb_AAF01316.1 AF184280 1 (AF184280) polyubiquitin [Oryza sativa] Seq. No. 411721 Seq. ID uC-osflcyp082g12b1 Method BLASTX NCBI GI q5668645

Method BLASTX
NCBI GI g5668645
BLAST score 395
E value 2.0e-38
Match length 111
% identity 75

NCBI Description (AL109619) putative protein [Arabidopsis thaliana]

Seq. No. 411722

Seq. No.

Seq. ID

411727

uC-osflcyp082h12b1

```
Seq. ID
                  uC-osflcyp082h03a1
                  BLASTX
Method
NCBI GI
                  g1351270
BLAST score
                  246
                  8.0e-21
E value
                  57
Match length
                  88
% identity
NCBI Description
                  TRIOSEPHOSPHATE ISOMERASE, CYTOSOLIC (TIM)
                  >gi 478410 pir JQ2255 triose-phosphate isomerase (EC
                  5.3.1.1) - rice >gi 169821 (M87064) triosephosphate
                  isomerase [Oryza sativa]
                  411723
Seq. No.
                  uC-osflcyp082h03b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1351279
BLAST score
                  248
E value
                  8.0e-26
Match length
                  105
% identity
                  61
                  TRIOSEPHOSPHATE ISOMERASE, CYTOSOLIC (TIM)
NCBI Description
                  >gi 602590 emb CAA58230 (X83227) triosephosphate isomerase
                  [Petunia x hybrida]
Seq. No.
                  411724
                  uC-osflcyp082h08a1
Seq. ID
Method
                  BLASTN
NCBI GI
                  q4884525
BLAST score
                  247
                  1.0e-136
E value
                  255
Match length
                  99
% identity
NCBI Description Oryza sativa mRNA for beta 1,3-glucanase, complete cds,
                  clone:E1149
                  411725
Seq. No.
Seq. ID
                  uC-osflcyp082h08b1
Method
                  BLASTX
NCBI GI
                  q4884526
BLAST score
                  432
E value
                  6.0e-43
Match length
                  95
% identity
                  95
NCBI Description (AB027428) beta 1,3-glucanase [Oryza sativa]
                  411726
Seq. No.
Seq. ID
                  uC-osflcyp082h11b1
Method
                  BLASTX
NCBI GI
                  g2431771
BLAST score
                  255
                  8.0e-22
E value
Match length
                  111
% identity
                  50
NCBI Description
                 (U62753) acidic ribosomal protein P2b [Zea mays]
```

Method BLASTX
NCBI GI g1172811
BLAST score 692
E value 3.0e-74
Match length 146
% identity 95

NCBI Description 60S RIBOSOMAL PROTEIN L10-1 (PUTATIVE TUMOR SUPRESSOR SC34) >gi 1076751 pir S49575 ribosomal protein L10.e, cytosolic

- rice >gi 575355 emb CAA57339 (X81691) putative tumor

suppresser [Oryza satīva]

Seq. No. 411728

Seq. ID uC-osflcyp083a02a1

Method BLASTX
NCBI GI g3342804
BLAST score 215
E value 3.0e-17
Match length 63
% identity 81

NCBI Description (AF061839) putative 6-phosphogluconate dehydrogenase [Zea

mays]

Seq. No. 411729

Seq. ID uC-osflcyp083a09a1

Method BLASTX
NCBI GI g3559805
BLAST score 258
E value 4.0e-22
Match length 53
% identity 77

NCBI Description (AJ006787) putative phytochelatin synthetase [Arabidopsis

thaliana]

Seq. No. 411730

Seq. ID uC-osflcyp083a10a1

Method BLASTN
NCBI GI g218209
BLAST score 105
E value 4.0e-52
Match length 149
% identity 94

NCBI Description Oryza sativa mRNA for the small subunit of

ribulose-1,5-bisphosphate carboxylase, complete cds, clone

pOSSS2106

Seq. No. 411731

Seq. ID uC-osflcyp083b02a1

Method BLASTN
NCBI GI g3859567
BLAST score 320
E value 1.0e-180
Match length 351
% identity 97

NCBI Description Oryza sativa clone FIL1 unknown mRNA

Seq. No. 411732

Seq. ID uC-osflcyp083b03a1

E value

Match length

% identity

4.0e-46

93 17

Method BLASTX NCBI GI g2865177 BLAST score 313 1.0e-28 E value Match length 77 % identity 75 NCBI Description (AB010946) AtRer1B [Arabidopsis thaliana] Seq. No. 411733 Seq. ID uC-osflcyp083c01a1 Method BLASTX NCBI GI g5802606 BLAST score 477 E value 8.0e-48 Match length 100 % identity (AF174486) methylenetetrahydrofolate reductase [Zea mays] NCBI Description Seq. No. 411734 Seq. ID uC-osflcyp083c06a1 Method BLASTN NCBI GI g4959460 BLAST score 43 E value 8.0e-15 Match length 108 % identity 94 NCBI Description Zea mays RACB small GTP binding protein mRNA, complete cds Seq. No. 411735 uC-osflcyp083c07a1 Seq. ID Method BLASTX NCBI GI g5802606 BLAST score 281 E value 7.0e-25 Match length 63 78 % identity NCBI Description (AF174486) methylenetetrahydrofolate reductase [Zea mays] Seq. No. 411736 Seq. ID uC-osflcyp083c09a1 Method BLASTX NCBI GI g100598 BLAST score 472 E value 2.0e-47 Match length 117 79 % identity ubiquitin / ribosomal protein S27a-1 - barley >gi 167073 NCBI Description (M60175) ubiquitin [Hordeum vulgare] Seq. No. 411737 uC-osflcyp083d02a1 Seq. ID Method BLASTX NCBI GI q481477 BLAST score 462

```
NCBI Description ubiquitin precursor - rice >gi 416038 emb CAA53665
                   (X76064) polyubiquitin [Oryza sativa] >gi_1574944 (U37687)
                  polyubiquitin [Oryza sativa]
                  >gi_6013289 gb AAF01315.1 AF184279 1 (AF184279)
                  polyubiquitin [Oryza sativa]
                  >gi_6013291 gb AAF01316.1 AF184280 1 (AF184280)
                  polyubiquitin [Oryza sativa]
Seq. No.
                  411738
Seq. ID
                  uC-osflcyp083d08a1
Method
                  BLASTX
NCBI GI
                  q4582456
BLAST score
                  191
E value
                  3.0e-14
                  58
Match length
                  67
% identity
NCBI Description
                  (AC007071) putative trithorax protein [Arabidopsis
                  thaliana]
Seq. No.
                  411739
Seq. ID
                  uC-osflcyp083d10a1
Method
                  BLASTX
NCBI GI
                  q5002357
BLAST score
                  172
E value
                  4.0e-12
Match length
                  54
                  63
% identity
NCBI Description (AF150957) heat-shock protein ClpP [Azospirillum
                  brasilense]
Seq. No.
                  411740
Seq. ID
                  uC-osflcyp083e03a1
Method
                  BLASTN
NCBI GI
                  g4406131
BLAST score
                  179
E value
                  6.0e-96
Match length
                  304
% identity
                  94
NCBI Description Oryza sativa MADS box protein (MADS16) mRNA, complete cds
Seq. No.
                  411741
Seq. ID
                  uC-osflcyp083e04a1
Method
                  BLASTX
NCBI GI
                  g2493650
BLAST score
                  202
E value
                  9.0e-16
Match length
                  47
                  79
% identity
NCBI Description RUBISCO SUBUNIT BINDING-PROTEIN BETA SUBUNIT (60 KD
                  CHAPERONIN BETA SUBUNIT) (CPN-60 BETA)
                  >gi_1167858_emb_CAA93139 (Z68903) chaperonin [Secale
                  cereale]
Seq. No.
                  411742
Seq. ID
                  uC-osflcyp083e06a1
Method
                  BLASTX
NCBI GI
                  g5734739
```

```
BLAST score
                   240
E value
                   1.0e-20
Match length
                   100
% identity
                   61
NCBI Description
                  (AC007259) Similar to syntaxin [Arabidopsis thaliana]
Seq. No.
                   411743
Seq. ID
                  uC-osflcyp083e08a1
Method
                  BLASTX
NCBI GI
                  g347451
BLAST score
                   304
                  1.0e-27
E value
Match length
                  59
% identity
                   98
NCBI Description
                  (L22155) ribulose 1,5-bisphosphate carboxylase [Oryza
                  sativa]
                  411744
Seq. No.
Seq. ID
                  uC-osflcyp083e09a1
Method
                  BLASTN
NCBI GI
                  g4159705
BLAST score
                  36
E value
                  1.0e-10
                  76
Match length
                  87
% identity
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
                  MGD8, complete sequence
Seq. No.
                  411745
Seq. ID
                  uC-osflcyp083e10a1
Method
                  BLASTX
NCBI GI
                  g1872521
BLAST score
                  183
E value
                  2.0e-13
Match length
                  62
% identity
                  61
NCBI Description
                  (U87833) zinc-finger protein Lsd1 [Arabidopsis thaliana]
                  >gi 1872523 (U87834) zinc-finger protein Lsd1 [Arabidopsis
                  thaliana] >gi 5262161_emb CAB45804.1_ (AL080253)
                  zinc-finger protein Lsd1 [Arabidopsis thaliana]
Seq. No.
                  411746
Seq. ID
                  uC-osflcyp083e11a1
Method
                  BLASTX
NCBI GI
                  q3056601
BLAST score
                  320
E value
                  2.0e-29
Match length
                  114
% identity
                  61
NCBI Description
                  (AC004255) T1F9.22 [Arabidopsis thaliana]
                  411747
Seq. No.
Seq. ID
                  uC-osflcyp083f03a1
Method
                  BLASTX
NCBI GI
                  q2340166
BLAST score
                  153
E value
                  6.0e-10
```

Match length 45 % identity (AF008124) glutathione S-conjugate transporting ATPase NCBI Description [Arabidopsis thaliana] >gi 2459949 (AF008125) multidrug resistance-associated protein homolog [Arabidopsis thaliana] Seq. No. 411748 Seq. ID uC-osflcyp083f04a1 Method BLASTX NCBI GI g4406782 BLAST score 159 E value 1.0e-10 47 Match length % identity 66 NCBI Description (AC006532) hypothetical protein [Arabidopsis thaliana] Seq. No. 411749 Seq. ID uC-osflcyp083f06a1 Method BLASTX NCBI GI q2286113 BLAST score 197 E value 5.0e-15 Match length 36 100 % identity NCBI Description (U78892) MADS box protein [Oryza sativa] Seq. No. 411750 Seq. ID uC-osflcyp083f08a1 Method BLASTX NCBI GI g1737492 BLAST score 293 E value 3.0e-26Match length 75 77 % identity NCBI Description (U81318) poly(A)-binding protein [Triticum aestivum] Seq. No. 411751 Seq. ID uC-osflcyp083f09a1 Method BLASTX NCBI GI g1621465 BLAST score 212 E value 6.0e-17 Match length 53

75 % identity

NCBI Description (U73105) laccase [Liriodendron tulipifera]

Seq. No. 411752

uC-osflcyp083f11a1 Seq. ID

BLASTN Method NCBI GI g607894 BLAST score 218 E value 1.0e-119 Match length 282 % identity 95

NCBI Description Oryza sativa IR54 anther specific (RTS2) gene, complete cds

Seq. ID

```
Seq. No.
                  411753
Seq. ID
                  uC-osflcyp083g10a1
Method
                  BLASTX
                  g2827711
NCBI GI
BLAST score
                  182
                  3.0e-13
E value
                  53
Match length
                  70
% identity
                  (AL021684) oxoglutarate dehydrogenase - like protein
NCBI Description
                   [Arabidopsis thaliana]
                  411754
Seq. No.
                  uC-osflcyp083g11a1
Seq. ID
                  BLASTX
Method
NCBI GI
                  q5031275
BLAST score
                  173
E value
                  3.0e-12
                  46
Match length
                  67
% identity
                 (AF139496) unknown [Prunus armeniaca]
NCBI Description
                  411755
Seq. No.
                  uC-osflcyp083h04a1
Seq. ID
                  BLASTN
Method
                  g2668745
NCBI GI
                  47
BLAST score
E value
                  3.0e-17
Match length
                  71
                  92
% identity
NCBI Description Zea mays inorganic pyrophosphatase (IPP) mRNA, complete cds
Seq. No.
                  411756
                  uC-osflcyp083h11a1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g6015059
BLAST score
                  420
E value
                   3.0e-41
                  83
Match length
% identity
                  100
                  ELONGATION FACTOR 1-ALPHA (EF-1-ALPHA) >gi_2996096
NCBI Description
                   (AF030517) translation elongation factor-1 alpha; EF-1
                  alpha [Oryza sativa]
                   411757
Seq. No.
                  uC-osflcyp083h12a1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1076746
BLAST score
                  270
E value
                  1.0e-23
Match length
                  92
                   64
% identity
                  heat shock protein 70 - rice (fragment)
NCBI Description
                  >gi_763160_emb_CAA47948_ (X67711) heat shock protein 70
                   [Oryza sativa]
                   411758
Seq. No.
```

uC-osflcyp084e01a1



```
BLASTN
Method
NCBI GI
                  g218144
                  49
BLAST score
                  6.0e-19
E value
                  95
Match length
                  91
% identity
NCBI Description Rice mRNA for ATP/ADP translocator, complete cds
                  411759
Seq. No.
Seq. ID
                  uC-osflcyp084e11a1
                  BLASTN
Method
                  g6006355
NCBI GI
BLAST score
                  87
                  2.0e-41
E value
                  95
Match length
                  99
% identity
NCBI Description Oryza sativa genomic DNA, chromosome 6, clone:P0493C11
Seq. No.
                  411760
                  uC-osflcyp084f02a1
Seq. ID
                  BLASTN
Method
                  q5295983
NCBI GI
                  109
BLAST score
                  1.0e-54
E value
                  136
Match length
                  97
% identity
NCBI Description Oryza sativa mRNA for MADS box-like protein, complete cds,
                  clone:E31864
Seq. No.
                  411761
Seq. ID
                  uC-osflcyp084f05a1
                  BLASTN
Method
                  q2913892
NCBI GI
                  46
BLAST score
E value
                  3.0e-17
Match length
                  70
                  91
% identity
NCBI Description Oryza sativa mRNA for LIP5, complete cds
Seq. No.
                  411762
                  uC-osflcyp084g04a1
Seq. ID
Method
                  BLASTN
                  g1399912
NCBI GI
BLAST score
                  138
                  1.0e-71
E value
                  154
Match length
                  99
% identity
NCBI Description Oryza sativa dehydrin mRNA, complete cds
Seq. No.
                  411763
                  uC-osflcyp084g07a1
Seq. ID
```

seq. in ac ostroypoorgovar

Method BLASTN
NCBI GI g343208
BLAST score 81
E value 7.0e-38
Match length 89
% identity 99

```
NCBI Description Rice chloroplast apocytochrome b6 (petB) gene, complete cds
                  411764
Seq. No.
                  uC-osflcyp084g08a1
Seq. ID
                  BLASTN
Method
                  q4079797
NCBI GI
                  73
BLAST score
                  2.0e-33
E value
                  97
Match length
                   97
% identity
                  Oryza sativa 23 kDa polypeptide of photosystem II mRNA,
NCBI Description
                  complete cds
                   411765
Seq. No.
                  uC-osflcyp085a01b1
Seq. ID
                  BLASTX
Method
                   g1781115
NCBI GI
                   158
BLAST score
                   2.0e-10
E value
                   74
Match length
% identity
                   42
NCBI Description (Z83864) glpQ1 [Mycobacterium tuberculosis]
                   411766
Seq. No.
                   uC-osflcyp085a02a1
Seq. ID
                   BLASTX
Method
                   g1076820
NCBI GI
                   285
BLAST score
                   2.0e-25
E value
                   58
Match length
                   93
% identity
NCBI Description phosphoglycerate mutase (EC 5.4.2.1) - maize
                   411767
Seq. No.
                   uC-osflcyp085a02b1
Seq. ID
                   BLASTX
Method
                   q400803
NCBI GI
                   730
BLAST score
                   2.0e-77
E value
                   150
Match length
                   90
 % identity
NCBI Description 2,3-BISPHOSPHOGLYCERATE-INDEPENDENT PHOSPHOGLYCERATE MUTASE
                   (PHOSPHOGLYCEROMUTASE) (BPG-INDEPENDENT PGAM) (PGAM-I)
                   >qi 283033 pir A42807 phosphoglycerate mutase (EC
                   5.4.2.1), \overline{2}, 3-bisphosphoglycerate-independent - maize
                   >gi 168588 (M80912) 2,3-bisphosphoglycerate-independent
                   phosphoglycerate mutase [Zea mays]
                   411768
 Seq. No.
 Seq. ID
                   uC-osflcyp085a05b1
 Method
                   BLASTX
                   g4006978
 NCBI GI
 BLAST score
                   150
                   2.0e-09
 E value
                   90
 Match length
                   36
 % identity
 NCBI Description (AJ131335) pollen allergen (group II) [Cynodon dactylon]
```

411769 Seq. No. Seq. ID uC-osflcyp085a06b1 BLASTX Method g1669341 NCBI GI BLAST score 379 2.0e-36 E value 100 Match length 68 % identity (D45066) AOBP (ascorbate oxidase promoter-binding protein) NCBI Description [Cucurbita maxima] 411770 Seq. No. Seq. ID uC-osflcyp085a08a1 BLASTX Method g3914470 NCBI GI BLAST score 409 6.0e-40E value Match length 87 % identity 84 PHOTOSYSTEM II 10 KD POLYPEPTIDE PRECURSOR NCBI Description >gi 1321868 emb CAA66373 (X97771) 10kD PSII protein [Hordeum vulgare] Seq. No. 411771 Seq. ID uC-osflcyp085a08b1 BLASTX Method NCBI GI g3914470 BLAST score 507 2.0e-51 E value 133 Match length % identity 72 PHOTOSYSTEM II 10 KD POLYPEPTIDE PRECURSOR NCBI Description >gi 1321868 emb CAA66373 (X97771) 10kD PSII protein [Hordeum vulgare] 411772 Seq. No. Seq. ID uC-osflcyp085a11a1 Method BLASTN NCBI GI g2773153 BLAST score 427 0.0e+00E value Match length 443 99 % identity NCBI Description Oryza sativa abscisic acid- and stress-inducible protein (Asr1) mRNA, complete cds

Seq. No. 411773

uC-osflcyp085a11b1 Seq. ID

Method BLASTN NCBI GI g2773153 BLAST score 366 0.0e + 00E value Match length 478 95 % identity

NCBI Description Oryza sativa abscisic acid- and stress-inducible protein

(Asr1) mRNA, complete cds

```
Seq. No.
                  411774
Seq. ID
                  uC-osflcyp085a12a1
Method
                  BLASTN
NCBI GI
                  g2773153
BLAST score
                  43
                   3.0e-15
E value
Match length
                   95
                  87
% identity
                  Oryza sativa abscisic acid- and stress-inducible protein
NCBI Description
                   (Asr1) mRNA, complete cds
Seq. No.
                   411775
Seq. ID
                   uC-osflcyp085a12b1
                   BLASTN
Method
                  g2773153
NCBI GI
BLAST score
                   48
                   8.0e-18
E value
Match length
                   56
% identity
                   96
                  Oryza sativa abscisic acid- and stress-inducible protein
NCBI Description
                   (Asr1) mRNA, complete cds
Seq. No.
                   411776
Seq. ID
                   uC-osflcyp085b02b1
                   BLASTX
Method
NCBI GI
                   q4589961
BLAST score
                   561
E value
                   9.0e-58
Match length
                   147
                   70
% identity
                  (AC007169) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   411777
                   uC-osflcyp085b04a1
Seq. ID
                   BLASTX
Method
                   g3176686
NCBI GI
BLAST score
                   152
E value
                   8.0e-10
Match length
                   44
% identity
                   66
NCBI Description
                   (AC003671) Similar to high affinity potassium transporter,
                   HAK1 protein gb U22945 from Schwanniomyces occidentalis.
                   [Arabidopsis thaliana]
Seq. No.
                   411778
                   uC-osflcyp085b04b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3176686
BLAST score
                   429
E value
                   3.0e-42
Match length
                   176
                   51
% identity
                  (AC003671) Similar to high affinity potassium transporter,
NCBI Description
                   HAK1 protein gb U22945 from Schwanniomyces occidentalis.
                   [Arabidopsis thaliana]
```



411779 Seq. No. Seq. ID uC-osflcyp085b05a1 Method BLASTX NCBI GI g3176723 BLAST score 153 7.0e-10 E value 108 Match length 37 % identity (AC002392) putative protein kinase [Arabidopsis thaliana] NCBI Description 411780 Seq. No. Seq. ID uC-osflcyp085b05b1 Method BLASTX q4519671 NCBI GI 251 BLAST score 3.0e-21 E value Match length 120 % identity 42 NCBI Description (AB017693) transfactor [Nicotiana tabacum] 411781 Seq. No. uC-osflcyp085b06b1 Seq. ID Method BLASTX NCBI GI g2130069 BLAST score 829 4.0e-89 E value Match length 159 96 % identity NCBI Description catalase (EC 1.11.1.6) catA - rice >gi_1261858_dbj_BAA06232_ (D29966) catalase [Oryza sativa] Seq. No. 411782 uC-osflcyp085b08a1 Seq. ID Method BLASTX NCBI GI g1835731 BLAST score 187 6.0e-14 E value Match length 47 % identity 79 NCBI Description (U86018) photosystem II 10 kDa polypeptide [Oryza sativa] 411783 Seq. No. uC-osflcyp085b08b1 Seq. ID BLASTX Method NCBI GI q1835731 BLAST score 362 1.0e-34 E value 98 Match length 74 % identity

NCBI Description (U86018) photosystem II 10 kDa polypeptide [Oryza sativa]

Seq. No. 411784

Seq. ID uC-osflcyp085b11a1

Method BLASTN
NCBI GI g20181
BLAST score 85
E value 6.0e-40

```
217
Match length
% identity
                  Rice cab2R gene for light harvesting chlorophyll
NCBI Description
                  a/b-binding protein
                  411785
Seq. No.
                  uC-osflcyp085b11b1
Seq. ID
                  BLASTX
Method
NCBI GI
                  q320618
                  672
BLAST score
                  9.0e-71
E value
                  144
Match length
                  91
% identity
                  chlorophyll a/b-binding protein I precursor - rice
NCBI Description
                  >gi 218172 dbj BAA00536_ (D00641) type I light-harvesting
                  chlorophyll a/b-binding protein [Oryza sativa]
                  >gi 227611 prf 1707316A chlorophyll a/b binding protein 1
                   [Oryza sativa]
                  411786
Seq. No.
                  uC-osflcyp085b12b1
Seq. ID
                  BLASTX
Method
                  q2290528
NCBI GI
                   464
BLAST score
                   2.0e-46
E value
                  125
Match length
                   73
% identity
                  (U94746) ATAN11 [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   411787
Seq. ID
                   uC-osflcyp085c02a1
                   BLASTX
Method
                   q2078350
NCBI GI
                   179
BLAST score
E value
                   5.0e-13
                   47
Match length
                   77
% identity
                  (U95923) transaldolase [Solanum tuberosum]
NCBI Description
Seq. No.
                   411788
                   uC-osflcyp085c02b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2078350
BLAST score
                   646
                   1.0e-67
E value
Match length
                   139
                   91
% identity
NCBI Description (U95923) transaldolase [Solanum tuberosum]
Seq. No.
                   411789
                   uC-osflcyp085c04b1
Seq. ID
                   BLASTN
Method
NCBI GI
                   g1808687
                   122
BLAST score
                   7.0e-62
E value
                   270
Match length
                   87
% identity
```

Seq. ID

Method

BLASTN

```
411790
Seq. No.
Seq. ID
                  uC-osflcyp085c12b1
                  BLASTX
Method
                  g2213867
NCBI GI
                  625
BLAST score
                  3.0e-65
E value
                  152
Match length
                  82
% identity
                  (AF003124) fructose-biphosphate aldolase [Mesembryanthemum
NCBI Description
                  crystallinum]
                  411791
Seq. No.
Seq. ID
                  uC-osflcyp085d03a1
Method
                  BLASTX
                  g3413706
NCBI GI
BLAST score
                  482
E value
                  2.0e-48
Match length
                  139
% identity
                  55
NCBI Description (AC004747) hypothetical protein [Arabidopsis thaliana]
                  411792
Seq. No.
Seq. ID
                  uC-osflcyp085d03b1
Method
                  BLASTX
                  g3413706
NCBI GI
BLAST score
                  209
                  2.0e-16
E value
Match length
                  66
% identity
                  58
NCBI Description (AC004747) hypothetical protein [Arabidopsis thaliana]
                  411793
Seq. No.
Seq. ID
                  uC-osflcyp085d04b1
Method
                  BLASTX
                  g2275199
NCBI GI
BLAST score
                  403
                  3.0e-39
E value
Match length
                  154
                  62
% identity
NCBI Description (AC002337) hypothetical protein [Arabidopsis thaliana]
                  411794
Seq. No.
Seq. ID
                  uC-osflcyp085d12b1
Method
                  BLASTX
NCBI GI
                  g322854
BLAST score
                  626
E value
                  2.0e-65
Match length
                  124
% identity
                  98
NCBI Description pollen-specific protein - rice >gi 20310 emb CAA78897
                  (Z16402) pollen specific gene [Oryza sativa]
                  411795
Seq. No.
                  uC-osflcyp085e01b1
```

NCBI Description S.stapfianus pSD.13 mRNA

NCBI GI g471330 BLAST score 69 E value 3.0e-31 Match length 69 % identity 100

NCBI Description O.sativa Adhl gene, 5' flanking region

Seq. No. 411796

Seq. ID uC-osflcyp085e02a1

Method BLASTN
NCBI GI g5912298
BLAST score 127
E value 7.0e-65
Match length 141
% identity 98

NCBI Description Oryza sativa mRNA for gigantea homologue, partial

Seq. No. 411797

Seq. ID uC-osflcyp085e02b1

Method BLASTX
NCBI GI g5912299
BLAST score 830
E value 3.0e-89
Match length 165
% identity 99

NCBI Description (AJ133787) gigantea homologue [Oryza sativa]

Seq. No. 411798

Seq. ID uC-osflcyp085e04a1

Method BLASTX
NCBI GI g2499819
BLAST score 461
E value 4.0e-46
Match length 99
% identity 84

NCBI Description ASPARTIC PROTEINASE ORYZASIN 1 PRECURSOR

>gi_2130068_pir__S66516 aspartic proteinase 1 precursor rice >gi_1030715_dbj_BAA06876_ (D32165) aspartic protease
[Oryza sativa] >gi_1711289_dbj_BAA06875_ (D32144) aspartic

protease [Oryza sativa]

Seq. No. 411799

Seq. ID uC-osflcyp085e04b1

Method BLASTX
NCBI GI g2499819
BLAST score 545
E value 6.0e-56
Match length 136
% identity 75

NCBI Description ASPARTIC PROTEINASE ORYZASIN 1 PRECURSOR

>gi_2130068_pir__S66516 aspartic proteinase 1 precursor rice >gi_1030715_dbj_BAA06876_ (D32165) aspartic protease
[Oryza sativa] >gi_1711289_dbj_BAA06875_ (D32144) aspartic

protease [Oryza sativa]

Seq. No. 411800

Seq. ID uC-osflcyp085f01a1

Seq. No.

```
Method
                  BLASTX
NCBI GI
                  g1345809
BLAST score
                  183
                  4.0e-14
E value
Match length
                  49
% identity
                  76
NCBI Description
                  CHALCONE SYNTHASE (NAREGENIN-CHALCONE SYNTHASE)
                  >gi 2117713 pir S58190 naringenin-chalcone synthase (EC
                  2.3.1.74) - rice >qi 927491 emb CAA61955 (X89859)
                  naringenin-chalcone synthase [Oryza sativa]
Seq. No.
                  411801
                  uC-osflcyp085f01b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1816444
BLAST score
                  197
E value
                  5.0e-19
Match length
                  52
% identity
                  96
NCBI Description (AB000801) chalcone synthase [Oryza sativa]
Seq. No.
                  411802
Seq. ID
                  uC-osflcyp085f02b1
Method
                  BLASTX
NCBI GI
                  g4321401
BLAST score
                  299
E value
                  4.0e-27
Match length
                  72
% identity
                  35
NCBI Description (AF047353) LIM domain protein PLIM-2 [Helianthus annuus]
Seq. No.
                  411803
Seq. ID
                  uC-osflcyp085f04b1
Method
                  BLASTX
NCBI GI
                  g1173347
BLAST score
                  914
E value
                  5.0e-99
Match length
                  175
% identity
                  95
NCBI Description SEDOHEPTULOSE-1,7-BISPHOSPHATASE, CHLOROPLAST PRECURSOR
                  (SEDOHEPTULOSE-BISPHOSPHATASE) (SBPASE) (SED(1,7)P2ASE)
                  >gi 100803 pir S23452 sedoheptulose-bisphosphatase (EC
                  3.1.3.37) precursor - wheat >gi 14265 emb CAA46507
                  (X65540) sedoheptulose-1,7-bisphosphatase [Triticum
                  aestivum]
Seq. No.
                  411804
Seq. ID
                  uC-osflcyp085f11b1
Method
                  BLASTX
NCBI GI
                  g553107
BLAST score
                  394
E value
                  2.0e-38
                  97
Match length
                  80
% identity
NCBI Description
                 (L04967) triosephosphate isomerase [Oryza sativa]
```

Seq. No.

Seq. ID

411810

uC-osflcyp085h03b1

```
uC-osflcyp085g02a1
Seq. ID
Method
                  BLASTN
                  q5441876
NCBI GI
BLAST score
                  36
E value
                  1.0e-10
                  40
Match length
                  97
% identity
NCBI Description
                  Oryza sativa genomic DNA, chromosome 2, clone:P0437H03
                   (contig b)
                  411806
Seq. No.
                  uC-osflcyp085g03b1
Seq. ID
Method
                  BLASTX
                  g2317725
NCBI GI
BLAST score
                  364
                  1.0e-34
E value
Match length
                  164
% identity
                   44
NCBI Description
                  (AF015811) putative lysophosphatidic acid acyltransferase
                   [Mus musculus]
                   411807
Seq. No.
                  uC-osflcyp085g04b1
Seq. ID
Method
                  BLASTX
                  q3850588
NCBI GI
BLAST score
                   630
                   9.0e-66
E value
                  179
Match length
                   69
% identity
NCBI Description
                  (AC005278) Contains similarity to gb AB011110 KIAA0538
                  protein from Homo sapiens brain and to phospholipid-binding
                  domain C2 PF 00168. ESTs gb AA585988 and gb T04384 come
                   from this gene. [Arabidopsis thaliana]
Seq. No.
                   411808
                   uC-osflcyp085g11b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g439586
BLAST score
                  172
E value
                   3.0e-12
Match length
                  74
% identity
                   46
                  (L27348) calreticulin [Hordeum vulgare]
NCBI Description
Seq. No.
                   411809
                   uC-osflcyp085h01b1
Seq. ID
Method
                   BLASTN
                   g455499
NCBI GI
                   58
BLAST score
E value
                   1.0e-23
                   58
Match length
                   100
% identity
                  Rice mRNA for ubiquitin-conjugating enzyme, partial
NCBI Description
                   sequence
```



Method BLASTX
NCBI GI g2132267
BLAST score 182
E value 2.0e-13
Match length 109
% identity 35

NCBI Description hypothetical protein YPR082c - yeast (Saccharomyces

cerevisiae) >gi_1230688 (U51033) Weak similarity to

hypothetical E. coli protein (PIR accession number S47687)

[Saccharomyces cerevisiae]

Seq. No. 411811

Seq. ID uC-osflcyp085h04a1

Method BLASTX
NCBI GI g3913426
BLAST score 234
E value 2.0e-19
Match length 46
% identity 93

NCBI Description S-ADENOSYLMETHIONINE DECARBOXYLASE PROENZYME (ADOMETDC)

(SAMDC) >gi 1532048 emb CAA69074 (Y07766)

S-adenosylmethionine decarboxylase [Oryza sativa]

Seq. No. 411812

Seq. ID uC-osflcyp085h05a1

Method BLASTX
NCBI GI g729103
BLAST score 157
E value 7.0e-11
Match length 73
% identity 52

NCBI Description CHALCONE--FLAVONONE ISOMERASE (CHALCONE ISOMERASE)

>gi_542181_pir__S41570 chalcone isomerase (EC 5.5.1.6) - maize >gi_396149_emb_CAA80441_ (Z22760) chalcone flavonone

isomerase [Zea mays]

Seq. No. 411813

Seq. ID uC-osflcyp085h05b1

Method BLASTX
NCBI GI g4006818
BLAST score 357
E value 9.0e-34
Match length 138
% identity 51

NCBI Description (AC005970) putative translation initiation factor eIF-2B,

alpha subunit [Arabidopsis thaliana]

Seq. No. 411814

Seq. ID uC-osflcyp085h07b1

Method BLASTX
NCBI GI g131225
BLAST score 544
E value 7.0e-56
Match length 115
% identity 92

NCBI Description PHOTOSYSTEM I REACTION CENTRE SUBUNIT XI PRECURSOR (SUBUNIT

```
precursor - barley >gi 167087 (M61146) photosystem I
                  hydrophobic protein [Hordeum vulgare]
                  411815
Seq. No.
Seq. ID
                  uC-osflcyp085h09b1
Method
                  BLASTX
NCBI GI
                  q548770
BLAST score
                  717
                  8.0e-77
E value
                  142
Match length
                  99
% identity
```

NCBI Description 60S RIBOSOMAL PROTEIN L3 >gi_481228_pir_S38359 ribosomal protein L3 - rice >gi_303853_dbj_BAA02155_ (D12630)

ribosomal protein L3 [Oryza sativa]

Seq. No. 411816

Seq. ID uC-osflcyp085h12b1

Method BLASTX
NCBI GI g5051781
BLAST score 416
E value 9.0e-41
Match length 145
% identity 56

NCBI Description (AL078637) transport inhibitor response-like protein

[Arabidopsis thaliana]

Seq. No. 411817

Seq. ID uC-osflcyp086a01a1

Method BLASTX
NCBI GI g133806
BLAST score 384
E value 5.0e-37
Match length 77
% identity 97

NCBI Description CHLOROPLAST 30S RIBOSOMAL PROTEIN S16

>gi_282999_pir__S28766 ribosomal protein S16 - barley chloroplast >gi 11603 emb CAA36973_ (X52765) ribosomal

protein rps16 [Hordeum vulgare]

Seq. No. 411818

Seq. ID uC-osflcyp086a01b1

Method BLASTN
NCBI GI g11957
BLAST score 245
E value 1.0e-135
Match length 430
% identity 100

NCBI Description Rice complete chloroplast genome

Seq. No. 411819

Seq. ID uC-osflcyp086a04b1

Method BLASTX
NCBI GI g1362086
BLAST score 165
E value 6.0e-12
Match length 48
% identity 71

Seq. ID

```
5-methyltetrahydropteroyltriglutamate--homocysteine
NCBI Description
                  S-methyltransferase (EC 2.1.1.14) - Madagascar periwinkle
                  >gi 2129919 pir S65957
                  5-methyltetrahydropteroyltriglutamate--homocysteine
                  S-methyltransferase (EC 2.1.1.14) - Madagascar periwinkle
                  >gi_886471_emb_CAA58474_ (X83499) methionine synthase
                  [Catharanthus roseus]
                  411820
Seq. No.
Seq. ID
                  uC-osflcyp086a07a1
Method
                  BLASTX
                  q2952328
NCBI GI
BLAST score
                  584
                  2.0e-60
E value
Match length
                  131
                  88
% identity
                  (AF049889) 1-aminocyclopropane-1-carboxylate oxidase [Oryza
NCBI Description
                  sativa]
Seq. No.
                  411821
Seq. ID
                  uC-osflcyp086a07b1
                  BLASTX
Method
NCBI GI
                  q2952328
BLAST score
                  408
E value
                  1.0e-39
Match length
                  76
                  100
% identity
NCBI Description (AF049889) 1-aminocyclopropane-1-carboxylate oxidase [Oryza
                  sativa]
                  411822
Seq. No.
                  uC-osflcyp086a09b1
Seq. ID
                  BLASTX
Method
NCBI GI
                  q3860333
BLAST score
                  290
                  5.0e-26
E value
Match length
                  79
% identity
NCBI Description (AJ012693) basic blue copper protein [Cicer arietinum]
Seq. No.
                  411823
                  uC-osflcyp086a11b1
Seq. ID
Method
                  BLASTX
                  q3122933
NCBI GI
BLAST score
                  296
                  1.0e-26
E value
                  97
Match length
                  57
% identity
NCBI Description PUTATIVE QUEUINE TRNA-RIBOSYLTRANSFERASE (TRNA-GUANINE
                  TRANSGLYCOSYLASE) (GUANINE INSERTION ENZYME)
                  >gi 3881825 emb CAA98076.1 (Z73899) Similarity to
                  Haemophilus Queuine tRNA-ribosyltransferase (SW:TGT HAEIN);
                  cDNA EST yk673g6.3 comes from this gene [Caenorhabditis
                  elegans]
                  411824
Seq. No.
```

53533

uC-osflcyp086b03b1

Method

NCBI GI

BLAST score

BLASTX

340

g3319353

Method BLASTX NCBI GI g1431622 BLAST score 729 E value 2.0e-77 Match length 157 86 % identity NCBI Description (X99100) protein kinase [Trifolium repens] Seq. No. 411825 uC-osflcyp086b04a1 Seq. ID Method BLASTX NCBI GI g1632831 BLAST score 254 E value 9.0e-22 Match length 55 91 % identity NCBI Description (Z49698) orf [Ricinus communis] Seq. No. 411826 Seq. ID uC-osflcyp086b04b1 Method BLASTX NCBI GI g4512684 BLAST score 369 3.0e-35 E value 97 Match length 74 % identity NCBI Description (AC006931) unknown protein [Arabidopsis thaliana] >gi 4559324 gb AAD22986.1 AC007087 5 (AC007087) unknown protein [Arabidopsis thaliana] 411827 Seq. No. uC-osflcyp086b06a1 Seq. ID Method BLASTX NCBI GI g3298541 187 BLAST score 7.0e-14 E value Match length 125 % identity 39 NCBI Description (AC004681) putative cellulose synthase [Arabidopsis thaliana] 411828 Seq. No. Seq. ID uC-osflcyp086b06b1 Method BLASTX NCBI GI g3298541 BLAST score 201 E value 2.0e-15 Match length 139 37 % identity NCBI Description (AC004681) putative cellulose synthase [Arabidopsis thaliana] Seq. No. 411829 uC-osflcyp086b07b1 Seq. ID

E value 6.0e-32 Match length 101 % identity 55

NCBI Description (AF077407) contains similarity to copper-binding proteins

[Arabidopsis thaliana]

Seq. No. 411830

Seq. ID uC-osflcyp086b09a1

Method BLASTX
NCBI GI g5821138
BLAST score 190
E value 3.0e-14
Match length 72
% identity 54

NCBI Description (AB014484) heat shock factor [Nicotiana tabacum]

Seq. No. 411831

Seq. ID uC-osflcyp086b11b1

Method BLASTX
NCBI GI g5354158
BLAST score 578
E value 1.0e-59
Match length 152
% identity 68

NCBI Description (AF149841) digalactosyldiacylglycerol synthase [Arabidopsis

thaliana] >gi_5354160_gb_AAD42379.1_AF149842_1 (AF149842) digalactosyldiacylglycerol synthase [Arabidopsis thaliana]

>gi_6041825_gb_AAF02140.1_AC009918 12 (AC009918)

digalactosyldiacylglycerol synthase [Arabidopsis thaliana]

Seq. No. 411832

Seq. ID uC-osflcyp086b12b1

Method BLASTX
NCBI GI g131225
BLAST score 384
E value 4.0e-37
Match length 103
% identity 76

NCBI Description PHOTOSYSTEM I REACTION CENTRE SUBUNIT XI PRECURSOR (SUBUNIT

V) (PSI-L) >gi 100605 pir A39759 photosystem I 18K protein

precursor - barley >gi_167087 (M61146) photosystem I

hydrophobic protein [Hordeum vulgare]

Seq. No. 411833

Seq. ID uC-osflcyp086c01a1

Method BLASTX
NCBI GI g3420055
BLAST score 468
E value 7.0e-47
Match length 101
% identity 86

NCBI Description (AC004680) cyclophilin [Arabidopsis thaliana]

Seq. No. 411834

Seq. ID uC-osflcyp086c01b1

Method BLASTX NCBI GI g3420055

```
BLAST score
                  369
E value
                  3.0e-35
Match length
                  118
                  64
% identity
NCBI Description (AC004680) cyclophilin [Arabidopsis thaliana]
Seq. No.
                  411835
Seq. ID
                  uC-osflcyp086c02a1
Method
                  BLASTX
NCBI GI
                  q4105782
BLAST score
                  158
E value
                  1.0e-10
Match length
                  32
% identity
                  81
NCBI Description (AF049922) PGP169-12 [Petunia x hybrida]
                  411836
Seq. No.
Seq. ID
                  uC-osflcyp086c02b1
Method
                  BLASTX
NCBI GI
                  q4105782
BLAST score
                  635
E value
                  2.0e-66
Match length
                  155
% identity
                  80
NCBI Description (AF049922) PGP169-12 [Petunia x hybrida]
Seq. No.
                  411837
Seq. ID
                  uC-osflcyp086c04a1
Method
                  BLASTX
NCBI GI
                  g1632831
BLAST score
                  256
E value
                  5.0e-22
Match length
                  56
% identity
NCBI Description (Z49698) orf [Ricinus communis]
Seq. No.
                  411838
Seq. ID
                  uC-osflcyp086c04b1
Method
                  BLASTX
NCBI GI
                  g1632831
BLAST score
                  559
E value
                  2.0e-57
Match length
                  139
% identity
                  78
NCBI Description (Z49698) orf [Ricinus communis]
Seq. No.
                  411839
                  uC-osflcyp086c05a1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2446981
BLAST score
                  295
E value
                  1.0e-26
Match length
                  76
% identity
                  71
```

NCBI Description (AB005560) AtGDI2 [Arabidopsis thaliana]

>gi_2569936_emb_CAA04727_ (AJ001397) GDI2 [Arabidopsis thaliana]

```
411840
Seq. No.
Seq. ID
                  uC-osflcyp086c05b1
                  BLASTX
Method
                  g2501850
NCBI GI
BLAST score
                  671
                  2.0e-70
E value
Match length
                  151
                  83
% identity
NCBI Description (AF012823) GDP dissociation inhibitor [Nicotiana tabacum]
                  411841
Seq. No.
Seq. ID
                  uC-osflcyp086c06a1
Method
                  BLASTX
NCBI GI
                  g3043426
BLAST score
                  373
                  1.0e-35
E value
Match length
                  113
                  64
% identity
NCBI Description (AJ005345) hypothetical protein [Cicer arietinum]
                  411842
Seq. No.
Seq. ID
                  uC-osflcyp086c06b1
Method
                  BLASTX
NCBI GI
                  g1621268
BLAST score
                  715
E value
                  1.0e-75
Match length
                  173
% identity
                  75
NCBI Description (Z81012) unknown [Ricinus communis]
Seq. No.
                  411843
                  uC-osflcyp086c08a1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1170937
BLAST score
                  242
                  2.0e-20
E value
Match length
                  44
                  98
% identity
NCBI Description S-ADENOSYLMETHIONINE SYNTHETASE 1 (METHIONINE
                  ADENOSYLTRANSFERASE 1) (ADOMET SYNTHETASE 1)
                  >qi 450549 emb CAA81481 (Z26867) S-adenosyl methionine
                  synthetase [Oryza sativa]
Seq. No.
                  411844
                  uC-osflcyp086c08b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1170937
BLAST score
                  804
E value
                  4.0e-86
Match length
                  172
% identity
                  92
NCBI Description
                 S-ADENOSYLMETHIONINE SYNTHETASE 1 (METHIONINE
                  ADENOSYLTRANSFERASE 1) (ADOMET SYNTHETASE 1)
                  >qi 450549 emb CAA81481 (Z26867) S-adenosyl methionine
```

synthetase [Oryza sativa]

411845 Seq. No. Seq. ID uC-osflcyp086c11a1 BLASTX Method NCBI GI g3128168 173 BLAST score 3.0e-12 E value Match length 45 58 % identity (AC004521) putative carboxyl-terminal peptidase NCBI Description [Arabidopsis thaliana] 411846 Seq. No. Seq. ID uC-osflcyp086d01a1 BLASTX Method NCBI GI g2493045 177 BLAST score

NCBI GI g2493045
BLAST score 177
E value 8.0e-13
Match length 55
% identity 65

NCBI Description ATP SYNTHASE DELTA' CHAIN, MITOCHONDRIAL PRECURSOR

>gi_1655484_dbj_BAA13601_ (D88376) delta-prime subunit of

mitochondrial F1-ATPase [Arabidopsis thaliana]

Seq. No. 411847

Seq. ID uC-osflcyp086d02a1

Method BLASTX
NCBI GI g115787
BLAST score 432
E value 1.0e-42
Match length 82
% identity 100

NCBI Description CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I

CAB-2) (LHCP) >gi_82461_pir__S03706 chlorophyll a/b-binding

protein 2R precursor - rice >gi 20182 emb CAA32109

(X13909) chlorophyll a/b-binding preprotein (AA -28 to 235)

[Oryza sativa]

Seq. No. 411848

Seq. ID uC-osflcyp086d02b1

Method BLASTX
NCBI GI g320618
BLAST score 793
E value 7.0e-85
Match length 169
% identity 91

NCBI Description chlorophyll a/b-binding protein I precursor - rice

>gi_218172_dbj_BAA00536_ (D00641) type I light-harvesting

chlorophyll a/b-binding protein [Oryza sativa]

>gi_227611_prf__1707316A chlorophyll a/b binding protein 1

[Oryza sativa]

Seq. No. 411849

Seq. ID uC-osflcyp086d05b1

Method BLASTX
NCBI GI g3643598
BLAST score 187
E value 9.0e-14

Match length 60 % identity 52

NCBI Description (AC005395) putative poly(A) polymerase [Arabidopsis

thaliana]

Seq. No. 411850

Seq. ID uC-osflcyp086d06a1

Method BLASTN
NCBI GI g2331132
BLAST score 174
E value 6.0e-93
Match length 366
% identity 98

NCBI Description Oryza sativa glycine-rich protein (OSGRP2) mRNA, complete

cds

Seq. No. 411851

Seq. ID uC-osflcyp086d06b1

Method BLASTX
NCBI GI g2293480
BLAST score 428
E value 2.0e-42
Match length 83
% identity 100

NCBI Description (AF011331) glycine-rich protein [Oryza sativa]

Seq. No. 411852

Seq. ID uC-osflcyp086d07a1

Method BLASTX
NCBI GI g115787
BLAST score 399
E value 8.0e-39
Match length 78
% identity 97

NCBI Description CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I

CAB-2) (LHCP) >gi_82461_pir__S03706 chlorophyll a/b-binding

protein 2R precursor - rice >gi 20182 emb CAA32109

(X13909) chlorophyll a/b-binding preprotein (AA -28 to 235)

[Oryza sativa]

Seq. No. 411853

Seq. ID uC-osflcyp086d07b1

Method BLASTX
NCBI GI g320618
BLAST score 806
E value 2.0e-86
Match length 173
% identity 90

NCBI Description chlorophyll a/b-binding protein I precursor - rice

>gi_218172_dbj_BAA00536_ (D00641) type I light-harvesting

chlorophyll a/b-binding protein [Oryza sativa]

>gi 227611 prf 1707316A chlorophyll a/b binding protein 1

[Oryza sativa]

Seq. No. 411854

Seq. ID uC-osflcyp086d08a1

Method BLASTN

```
g2267005
NCBI GI
BLAST score
                  266
                  1.0e-148
E value
                  368
Match length
                  97
% identity
NCBI Description
                  Oryza sativa endosperm lumenal binding protein (BiP) mRNA,
                  complete cds
                  411855
Seq. No.
                  uC-osflcyp086d08b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2267006
BLAST score
                  863
E value
                  4.0e-93
Match length
                  172
% identity
                  99
NCBI Description (AF006825) endosperm lumenal binding protein [Oryza sativa]
Seq. No.
                  411856
                  uC-osflcyp086d09b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g5813796
BLAST score
                  146
                  4.0e-09
E value
Match length
                  81
% identity
                  40
NCBI Description (AF082862) unknown [Pisum sativum]
Seq. No.
                  411857
                  uC-osflcyp086d11b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3367582
BLAST score
                  232
                  5.0e-19
E value
                  89
Match length
                  52
% identity
NCBI Description (AL031135) putative protein [Arabidopsis thaliana]
                  411858
Seq. No.
                  uC-osflcyp086d12b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4455274
BLAST score
                  270
E value
                  2.0e-23
Match length
                  116
                  50
% identity
NCBI Description
                  (AL035527) spliceosome associated protein-like [Arabidopsis
                  thaliana]
                  411859
Seq. No.
                  uC-osflcyp086e01b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1777312
BLAST score
                  292
E value
                  1.0e-35
Match length
                  119
```

53540

67

% identity

```
NCBI Description
                  (D30622) novel serine/threonine protein kinase [Arabidopsis
                  thaliana]
Seq. No.
                  411860
Seq. ID
                  uC-osflcyp086e02a1
                  BLASTX
Method
                  q3721942
NCBI GI
BLAST score
                  291
                  4.0e-26
E value
                  69
Match length
% identity
                  84
NCBI Description (AB018248) chitinase [Oryza sativa]
                  411861
Seq. No.
                  uC-osflcyp086e04b1
Seq. ID
                  BLASTN
Method
NCBI GI
                  q5734616
BLAST score
                  126
E value
                  3.0e-64
                  524
Match length
                  99
% identity
NCBI Description Oryza sativa genomic DNA, chromosome 6, clone:P0538C01
Seq. No.
                  411862
                  uC-osflcyp086e05a1
Seq. ID
Method
                  BLASTX
                  g2130069
NCBI GI
BLAST score
                  373
E value
                  9.0e-36
Match length
                  80
                  91
% identity
NCBI Description catalase (EC 1.11.1.6) catA - rice
                  >gi 1261858 dbj BAA06232 (D29966) catalase [Oryza sativa]
                  411863
Seq. No.
                  uC-osflcyp086e05b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2130069
BLAST score
                  900
                  2.0e-97
E value
Match length
                  166
                  100
% identity
                  catalase (EC 1.11.1.6) catA - rice
NCBI Description
                  >gi 1261858 dbj BAA06232 (D29966) catalase [Oryza sativa]
Seq. No.
                  411864
Seq. ID
                  uC-osflcyp086e07b1
Method
                  BLASTX
NCBI GI
                  g1684855
                  439
BLAST score
E value
                  2.0e-43
                  88
Match length
% identity
                  25
NCBI Description (U77939) ubiquitin-like protein [Phaseolus vulgaris]
Seq. No.
                  411865
                  uC-osflcyp086e08a1
Seq. ID
```

Method BLASTX g3935169 NCBI GI BLAST score 275 3.0e-24E value Match length 67 82 % identity NCBI Description (AC004557) F17L21.12 [Arabidopsis thaliana] Seq. No. 411866 uC-osflcyp086e08b1 Seq. ID Method BLASTX NCBI GI g3935169 BLAST score 291 5.0e-26 E value Match length 68 84 % identity NCBI Description (AC004557) F17L21.12 [Arabidopsis thaliana] Seq. No. 411867 uC-osflcyp086e09b1 Seq. ID BLASTX Method q6006848 NCBI GI BLAST score 609 E value 6.0e-64179 Match length 69 % identity NCBI Description (AC009540) unknown protein, 5' partial [Arabidopsis thaliana] Seq. No. 411868 Seq. ID uC-osflcyp086e10a1 Method BLASTN NCBI GI g6041757 BLAST score 146 2.0e-76 E value 326 Match length % identity 86 NCBI Description Genomic Sequence For Oryza sativa Clone 10P20, Lemont Strain, Complete Sequence, complete sequence Seq. No. 411869 uC-osflcyp086e10b1 Seq. ID Method BLASTX NCBI GI q2055230 BLAST score 222 7.0e-18 E value 137 Match length % identity 40 NCBI Description (AB000130) SRC2 [Glycine max]

Seq. No. 411870

Seq. ID uC-osflcyp086e11a1

Method BLASTX
NCBI GI 9439879
BLAST score 156
E value 2.0e-10
Match length 39

```
% identity
                  (L15194) [Golden delicious apple fruit expressed mRNA,
NCBI Description
                  complete cds.], gene product [Malus domestica]
                  411871
Seq. No.
                  uC-osflcyp086e11b1
Seq. ID
Method
                  BLASTX
                  g2995990
NCBI GI
                  298
BLAST score
                  8.0e-27
E value
Match length
                  125
                  50
% identity
                  (AF053746) dormancy-associated protein [Arabidopsis
NCBI Description
                  thaliana] >gi 2995992 (AF053747) dormancy-associated
                  protein [Arabidopsis thaliana]
                  411872
Seq. No.
                  uC-osflcyp086e12b1
Seq. ID
Method
                  BLASTX
                  g2827711
NCBI GI
BLAST score
                  822
                  3.0e-88
E value
Match length
                  177
% identity
                  88
                  (AL021684) oxoglutarate dehydrogenase - like protein
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                   411873
                  uC-osflcyp086f01a1
Seq. ID
                  BLASTX
Method
                  g3559805
NCBI GI
                   258
BLAST score
                   2.0e-30
E value
                   89
Match length
                   70
% identity
                  (AJ006787) putative phytochelatin synthetase [Arabidopsis
NCBI Description
                   thaliana]
                   411874
Seq. No.
                   uC-osflcyp086f01b1
Seq. ID
Method
                   BLASTX
                   g3559805
NCBI GI
BLAST score
                   322
                   9.0e-30
E value
                   86
Match length
                   64
% identity
                  (AJ006787) putative phytochelatin synthetase [Arabidopsis
NCBI Description
                   thaliana]
                   411875
Seq. No.
                   uC-osflcyp086f03b1
Seq. ID
                   BLASTX
Method
NCBI GI
                   g2117937
BLAST score
                   480
                   3.0e-48
E value
Match length
                   135
                   71
% identity
```

```
UTP--qlucose-1-phosphate uridylyltransferase (EC 2.7.7.9) -
NCBI Description
                  barley >gi_1212996_emb_CAA62689_ (X91347) UDP-glucose
                  pyrophosphorylase [Hordeum vulgare]
                  411876
Seq. No.
                  uC-osflcyp086f04b1
Seq. ID
Method
                  BLASTX
                  g4432861
NCBI GI
                  237
BLAST score
                  1.0e-19
E value
                  71
Match length
                  58
% identity
                  (AC006300) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   411877
Seq. No.
                  uC-osflcyp086f05b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2072555
BLAST score
                   237
                   9.0e-20
E value
Match length
                   44
                   100
% identity
                  (AF001396) metallothionein-like protein [Oryza sativa]
NCBI Description
                   >gi 6103441 gb AAF03603.1_ (AF147786) metallothionein-like
                   protein [Oryza sativa]
                   411878
Seq. No.
Seq. ID
                   uC-osflcyp086f06a1
Method
                   BLASTX
                   g1835731
NCBI GI
                   160
BLAST score
                   8.0e-11
E value
                   72
Match length
% identity
                   50
                  (U86018) photosystem II 10 kDa polypeptide [Oryza sativa]
NCBI Description
                   411879
Seq. No.
                   uC-osflcyp086f06b1
Seq. ID
Method
                   BLASTN
                   q1835730
NCBI GI
                   106
BLAST score
                   2.0e-52
E value
                   194
Match length
                   89
% identity
                  Oryza sativa photosystem II 10 kDa polypeptide mRNA,
NCBI Description
                   complete cds
                   411880
Seq. No.
                   uC-osflcyp086f07b1
Seq. ID
                   BLASTX
Method
                   g4314378
NCBI GI
BLAST score
                   218
                   1.0e-17
E value
                   86
Match length
```

(AC006232) putative lipase [Arabidopsis thaliana]

>gi_5306262_gb_AAD41994.1_AC006233_5 (AC006233) putative

50

% identity

NCBI Description

BLAST score

161

lipase [Arabidopsis thaliana]

Seq. No. 411881 Seq. ID uC-osflcyp086f08b1 Method BLASTX NCBI GI q4680685 BLAST score 240 E value 5.0e-20 Match length 146 % identity NCBI Description (AF132957) CGI-23 protein [Homo sapiens] Seq. No. 411882 uC-osflcyp086f09b1 Seq. ID Method BLASTX q2739375 NCBI GI BLAST score 163 6.0e-11 E value Match length 119 37 % identity NCBI Description (AC002505) unknown protein [Arabidopsis thaliana] 411883 Seq. No. Seq. ID uC-osflcyp086f10a1 Method BLASTX q100490 NCBI GI BLAST score 296 1.0e-26 E value Match length 60 % identity NCBI Description polyubiquitin - garden snapdragon (fragment) >gi 16071 emb CAA48140 (X67957) ubiquitin [Antirrhinum majus] Seq. No. 411884 uC-osflcyp086f10b1 Seq. ID Method BLASTX NCBI GI g1076708 BLAST score 798 E value 2.0e-85 Match length 165 % identity 28 NCBI Description seed tetraubiquitin - common sunflower >gi_303901_dbj_BAA03764_ (D16248) ubiquitin [Glycine max] >gi_456714_dbj_BAA05670_ (D28123) Ubiquitin [Glycine max] >gi 556688 emb CAA84440 (Z34988) seed tetraubiquitin [Helianthus annuus] >gi 994785 dbj BAA05085 (D26092) Ubiquitin [Glycine max] >gi 4263514 gb AAD15340 (AC004044) putative polyubiquitin [Arabidopsis thaliana] >gi_1096513_prf 2111434A tetraubiquitin [Helianthus annuus] 411885 Seq. No. uC-osflcyp086f11a1 Seq. ID Method BLASTX NCBI GI q1389654

```
7.0e-11
E value
                 50
Match length
                 68
% identity
NCBI Description (D85912) cytosolic ascorbate peroxidase [Nicotiana tabacum]
                 411886
Seq. No.
                 uC-osflcyp086f11b1
Seq. ID
                 BLASTX
Method
NCBI GI
                 q1076800
BLAST score
                 813
                 3.0e-87
E value
                 173
Match length
                 86
% identity
NCBI Description L-ascorbate per (EC 1.11.1.11), cytosolic isozyme -
                 peroxidase [Zea mays] >
                                                               ascorbate
                 peroxidase [Zea mays]
                 411887
Seq. No.
                 uC-osflcyp086g02a1
Seq. ID
Method
                 BLASTX
NCBI GI
                 q2934902
                 361
BLAST score
                 9.0e-36
E value
                 109
Match length
                 77
% identity
NCBI Description (AF039304) cpSer [Zea ma ]
                 411888
Seq. No.
                 uC-osflcyp∪36g02b1
Seq. ID
                BLASTX
Method
NCBI GI
                 g2934902
                 695
BLAST score
                 2.0e-73
E value
                 146
Match length
                95
% identity
NCBI Description (AF039304) cpSecY [Zea mays]
                 411889
Seq. No.
Seq. ID
                 uC-osflcyp086g03a1
Method
                BLASTX
NCBI GI
                 g5802955
BLAST score
                 187
E value
                 5.0e-14
                 60
Match length
                 62
% identity
NCBI Description (AF178990) stress related protein [Vitis riparia]
                 411890
Seq. No.
Seq. ID
                 uC-osflcyp086g05a1
Method
                 BLASTX
                g4886756
NCBI GI
BLAST score
                227
E value
                 9.0e-19
Match length
                52
% identity
NCBI Description (AF088917) cellulose synthase catalytic subunit
```

[Arabidopsis thaliana]

```
Seq. No.
                  411891
Seq. ID
                  uC-osflcyp086g05b1
                  BLASTX
Method
NCBI GI
                  g5230423
BLAST score
                  761
                  4.0e-81
E value
Match length
                  167
% identity
                  83
                  (AF091713) cellulose synthase catalytic subunit
NCBI Description
                  [Arabidopsis thaliana]
                  411892
Seq. No.
Seq. ID
                  uC-osflcyp086g06a1
                  BLASTX
Method
                  g3738338
NCBI GI
BLAST score
                  159
E value
                  9.0e-11
Match length
                  83
                  45
% identity
                  (AC005170) putative polygalacturonase [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  411893
                  uC-osflcyp086g06b1
Seq. ID
                  BLASTX
Method
                  g3738338
NCBI GI
                  510
BLAST score
E value
                  9.0e-52
Match length
                  151
% identity
NCBI Description (AC005170) putative polygalacturonase [Arabidopsis
                  thaliana]
                  411894
Seq. No.
                  uC-osflcyp086g07b1
Seq. ID
                  BLASTX
Method
NCBI GI
                  q4538920
BLAST score
                  394
E value
                  4.0e-38
Match length
                  115
                  70
% identity
NCBI Description (AL049483) nitrogen fixation like protein [Arabidopsis
                  thaliana]
                  411895
Seq. No.
                  uC-osflcyp086g08b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3402718
BLAST score
                  152
                  1.0e-09
E value
Match length
                  110
% identity
NCBI Description (AC004261) hypothetical protein [Arabidopsis thaliana]
```

53547

411896

Seq. No.

```
Seq. ID
                  uC-osflcyp086g11b1
Method
                  BLASTX
NCBI GI
                  q4455246
BLAST score
                  160
E value
                  1.0e-10
                  71
Match length
                  55
% identity
NCBI Description
                 (AL035523) putative protein [Arabidopsis thaliana]
                  411897
Seq. No.
Seq. ID
                  uC-osflcyp086g12b1
                  BLASTX
Method
NCBI GI
                  q1483563
BLAST score
                  808
                  1.0e-86
E value
                  168
Match length
% identity
                  92
NCBI Description (X99825) leucine aminopeptidase [Petroselinum crispum]
                  411898
Seq. No.
                  uC-osflcyp086h01a1
Seq. ID
                  BLASTX
Method
NCBI GI
                  q6041808
BLAST score
                  273
                  6.0e-26
E value
                  81
Match length
% identity
                  68
NCBI Description (AC009755) unknown protein [Arabidopsis thaliana]
Seq. No.
                  411899
                  uC-osflcyp086h01b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g6041808
BLAST score
                  218
                  9.0e-18
E value
                  69
Match length
                  57
% identity
NCBI Description (AC009755) unknown protein [Arabidopsis thaliana]
Seq. No.
                  411900
                  uC-osflcyp086h02a1
Seq. ID
                  BLASTN
Method
NCBI GI
                  g11957
BLAST score
                  42
                  2.0e-14
E value
                  58
Match length
                  93
% identity
NCBI Description Rice complete chloroplast genome
                  411901
Seq. No.
                  uC-osflcyp086h02b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1171027
BLAST score
                  429
                  3.0e-42
E value
                  144
Match length
```

53548

58

% identity

.

MALE STERILITY PROTEIN 2 >gi 421835 pir S33804 gene MS2 NCBI Description protein - Arabidopsis thaliana >gi 396835 emb CAA52019 (X73652) male sterility 2 (MS2) protein [Arabidopsis thaliana] >qi 448297 prf 1916413A male sterility 2 gene [Arabidopsis thaliana] 411902 Seq. No. Seq. ID uC-osflcyp086h05b1 Method BLASTX NCBI GI q6065749 338 BLAST score 1.0e-31 E value 133 Match length 50 % identity NCBI Description (AJ250341) beta-amylase enzyme [Arabidopsis thaliana] 411903 Seq. No. Seq. ID uC-osflcyp086h07a1 Method BLASTX NCBI GI q134022 467 BLAST score 8.0e-47E value 101 Match length 92 % identity NCBI Description CHLOROPLAST 30S RIBOSOMAL PROTEIN S8 >gi 70914 pir_ R3RZ8 ribosomal protein S8 - rice chloroplast >qi 12022 emb CAA33931 (X15901) ribosomal protein S8 [Oryza sativa] >gi 226643 prf 1603356BT ribosomal protein S8 [Oryza sativa] 411904 Seq. No. uC-osflcyp086h07b1 Seq. ID Method BLASTX q132712 NCBI GI BLAST score 693 3.0e-73E value 134 Match length 99 % identity NCBI Description CHLOROPLAST 50S RIBOSOMAL PROTEIN L16 >gi_71250_pir__R5RZ16 ribosomal protein L16 - rice chloroplast >qi 669084 emb CAA33933 (X15901) ribosomal protein L16 [Oryza sativa] >gi 226645 prf 1603356BV ribosomal protein L16 [Oryza sativa] Seq. No. 411905 uC-osflcyp086h08b1 Seq. ID Method BLASTX NCBI GI g4581139 BLAST score 386 E value 3.0e-37 Match length 125 % identity NCBI Description (AC006919) putative ABC transporter [Arabidopsis thaliana]

Seq. No. 411906

Seq. ID uC-osflcyp086h09b1

Method BLASTX

```
q3264767
NCBI GI
BLAST score
                  275
                  4.0e-24
E value
Match length
                  161
                  43
% identity
NCBI Description (AF071893) AP2 domain containing protein [Prunus armeniaca]
                  411907
Seq. No.
Seq. ID
                  uC-osflcyp086h11a1
                  BLASTX
Method
NCBI GI
                  g1351017
BLAST score
                  192
E value
                  2.0e-14
Match length
                  44
                  80
% identity
                 40S RIBOSOMAL PROTEIN S9 (S4) >gi 629697 pir S45375
NCBI Description
                  ribosomal protein S4 - common tobacco (fragment)
                  >gi_443960_emb_CAA78463_ (Z14085) RIBOSOMAL PROTEIN S4
                  [Nicotiana tabacum]
                  411908
Seq. No.
Seq. ID
                  uC-osflcyp086h11b1
                  BLASTX
Method
NCBI GI
                  g131770
BLAST score
                  531
                  3.0e-54
E value
Match length
                  146
                  68
% identity
NCBI Description
                  40S RIBOSOMAL PROTEIN S9 (40S RIBOSOMAL PROTEIN 1024)
                  (VEGETATIVE SPECIFIC PROTEIN V12) >qi 70880 pir R3DO24
                  ribosomal protein S9.e - slime mold (Dictyostelium
                  discoideum) >qi 7353 emb CAA29844 (X06636) rp1024 protein
                  [Dictyostelium discoideum]
Seq. No.
                  411909
                  uC-osflcyp086h12b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1491712
BLAST score
                  211
E value
                  1.0e-16
Match length
                  111
% identity
                  44
NCBI Description (X99961) unknown [Homo sapiens]
Seq. No.
                  411910
                  uC-osflcyp087a03a1
Seq. ID
                  BLASTX
Method
NCBI GI
                  g131225
BLAST score
                  221
                  5.0e-26
E value
Match length
                  111
                  59
% identity
NCBI Description PHOTOSYSTEM I REACTION CENTRE SUBUNIT XI PRECURSOR (SUBUNIT
```

hydrophobic protein [Hordeum vulgare]

V) (PSI-L) >gi_100605_pir__A39759 photosystem I 18K protein

precursor - barley >gi_167087 (M61146) photosystem I

```
Seq. No.
                   411911
Seq. ID
                  uC-osflcyp087a06a1
Method
                  BLASTN
NCBI GI
                  g6006309
BLAST score
                   93
                   3.0e-45
E value
                  113
Match length
% identity
                  Oryza sativa mRNA for nonphototrophic hypocotyl 1b,
NCBI Description
                  complete cds
                   411912
Seq. No.
Seq. ID
                  uC-osflcyp087a07a1
Method
                  BLASTX
NCBI GI
                   g1346883
                   286
BLAST score
                  1.0e-25
E value
                  73
Match length
                   73
% identity
NCBI Description PHYTOENE SYNTHASE PRECURSOR >gi 2130144 pir S68307
                  phytoene synthase - maize >gi_1098665 (U32636) phytoene
                   synthase [Zea mays]
                   411913
Seq. No.
                   uC-osflcyp087a10a1
Seq. ID
Method
                   BLASTN
                   q493709
NCBI GI
BLAST score
                   356
E value
                   0.0e + 00
Match length
                   380
                   98
% identity
NCBI Description Rice mRNA for beta-tubulin, complete cds
Seq. No.
                   411914
                   uC-osflcyp087b02a1
Seq. ID
Method
                   BLASTN
NCBI GI
                   g1261857
BLAST score
                   56
E value
                   7.0e-23
Match length
                   160
% identity
                   84
NCBI Description Rice CatA gene for catalase, complete cds
Seq. No.
                   411915
Seq. ID
                   uC-osflcyp087b06a1
Method
                   BLASTN
                   g5257255
NCBI GI
BLAST score
                   134
                   3.0e-69
E value
Match length
                   230
                   91
% identity
NCBI Description Oryza sativa genomic DNA, chromosome 8, clone:P0026F07
```

Seq. No. 411916

Seq. ID uC-osflcyp087c07a1

Method BLASTN NCBI GI g1658312

68 BLAST score 1.0e-29 E value 80 Match length 57 % identity NCBI Description O.sativa osr40g2 gene 411917 Seq. No. uC-osflcyp087c08a1 Seq. ID Method BLASTN q218209 NCBI GI BLAST score 87 4.0e-41 E value Match length 259 85 % identity Oryza sativa mRNA for the sn 11 subuni NCBI Description $\verb|ribulose-1,5-bisphosphate carboxylase, comp_{\bot}|\\$ cds, clone posss2106 411918 Seq. No. uC-osflcyp087c10a1 Seq. ID Method BLASTN NCBI GI g1132482 102 BLAST score 5.0e-50 E value 254 Match length 91 % identity NCBI Description Rice mRNA for ADP-ribosylation factor, complete cds 411919 Seq. No. uC-osflcyp087d04a1 Seq. ID BLASTN Method NCBI GI g1616658 BLAST score 61 1.0e-25 E value 200 Match length 85 % identity NCBI Description Triticum aestivum adenylosuccinate synthetase mRNA, partial cds >gi_3011202_gb_I75061_I75061 Sequence 5 from patent US 411920 Seq. No. Seq. ID uC-osflcyp087d09a1 BLASTX Method NCBI GI g3738261 BLAST score 332 6.0e-31 E value 78 Match length 88 % identity NCBI Description (AB018412) chloroplast phosphoglycerate kinase [Populus nigra] 411921 Seq. No. uC-osflcyp087d11a1 Seq. ID

BLASTX Method NCBI GI g6014938 BLAST score 245 1.0e-20 E value Match length 50

```
92
% identity
                 UROPORPHYRINOGEN DECARBOXYLASE PRECURSOR (UPD) >gi 3420233
NCBI Description
                  (AF058763) uroporphyrinogen decarboxylase [Zea mays]
Seq. No.
                  411922
                  uC-osflcyp087e01a1
Seq. ID
                  BLASTX
Method
                  q3204108
NCBI GI
BLAST score
                  402
                  4.0e-39
E value
Match length
                  89
% identity
                  84
                 (AJ006764) putative deoxycytidylate deaminase [Cicer
NCBI Description
                  arietinum]
Seq. No.
                  411923
                  uC-osflcyp087e03a1
Seq. ID
                  BLASTN
Method
                  q2331130
NCBI GI
BLAST score
                  151
E value
                  3.0e-79
Match length
                  275
                  93
% identity
NCBI Dear stion Oryza active alycino-rich protein (OSGRP1) mRNA, complete
Seq. No.
                  411924
                  uC-osflcyp087e08a1
Seq. ID
                  BLASTN
Method
                  g331 1/14
NCBI G
BLAST
E vo
                   ,Je−176
Match length
                  430
                  96
% identity
NCBI Description Oryza sativa mRNA for mitoc. ...
                                                                  cansporter,
                  complete cds
                  411925
Seq. No.
Seq. ID
                  uC-osflcyp087f01a1
                  BLASTN
Method
NCBI GI
                  q303858
BLAST score
                  307
E value
                  1.0e-172
Match length
                  367
                  96
% identity
NCBI Description Rice mRNA for brain specific protein (S94 gene), complete
                  cds
                  411926
Seq. No.
Seq. ID
                  uC-osflcyp087f04a1
Method
                  BLASTX
                  g5802606
NCBI GI
                  157
BLAST score
E value
                  1.0e-10
Match length
                  35
% identity
NCBI Description (AF174486) methylenetetrahydrofolate reductase [Zea mays]
```

```
Seq. No.
                  411927
                  uC-osflcyp087f10a1
Seq. ID
Method
                  BLASTN
                  g2149018
NCBI GI
BLAST score
                  45
                  6.0e-16
E value
Match length
                  69
% identity
                  91
                  Oryza sativa putative ADP-glucose pyrophosphorylase subunit
NCBI Description
                  SH2 and putative NADPH-dependent reductase A1 genes,
                  complete cds
                  411928
Seq. No.
                  uC-osflcyp087f11a1
Seq. ID
Method
                  BLASTX
                  q2109293
NCBI GI
BLAST score
                  240
E value
                  4.0e-20
                  74
Match length
% identity
                  69
                  (U97568) serine/threonine protein kinase [Arabidopsis
NCBI Description
                  thaliana]
                  411929
Seq. No.
                  uC-osflcyp087g05a1
Seq. ID
                  BLASTX
Method
                  g3641837
NCBI GI
BLAST score
                  281
E value
                  6.0e-25
Match length
                  87
% identity
                  (AL023094) Nonclathrin coat protein gamma-like protein
NCBI Description
                  [Arabidopsis thaliana]
Seq. No.
                  411930
Seq. ID
                  uC-osflcyp087g09a1
Method
                  BLASTX
NCBI GI
                  g2088643
BLAST score
                  369
E value
                  3.0e-35
Match length
                  74
% identity
                  46
                  (AF002109) transcription factor SF3 isolog [Arabidopsis
NCBI Description
                  thaliana]
                  411931
Seq. No.
                  uC-osflcyp087g10a1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3024657
BLAST score
                  169
                  9.0e-12
E value
                  56
Match length
                  62
% identity
                  PROTEIN TRANSLATION FACTOR SUI1 HOMOLOG (GOS2 PROTEIN)
NCBI Description
                  >gi 2668740 (AF034944) translation initiation factor; GOS2
```

[Zea mays]

NCBI GI

```
411932
Seq. No.
                  uC-osflcyp087h01a1
Seq. ID
                  BLASTX
Method
NCBI GI
                  g3183079
                  352
BLAST score
                  3.0e - 33
E value
                  87
Match length
                  77
% identity
NCBI Description MALATE DEHYDROGENASE, GLYOXYSOMAL PRECURSOR
                  >gi_1375075_dbj_BAA12870.1_ (D85763) glyoxysomal malate
                  dehydrogenase [Oryza sativa]
                  411933
Seq. No.
Seq. ID
                  uC-osflcyp087h02a1
Method
                  BLASTN
NCBI GI
                  g20191
                  375
BLAST score
                  0.0e+00
E value
                  394
Match length
% identity
                  99
NCBI Description O.sativa mRNA for catalase
                  411934
Seq. No.
                  uC-osflcyp087h03a1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g2662309
BLAST score
                   74
                  3.0e-33
E value
                  98
Match length
                  94
% identity
NCBI Description Hordeum vulgare mRNA for bpw1, complete cds
                   411935
Seq. No.
                  uC-osflcyp087h05a1
Seq. ID
                  BLASTN
Method
                  g5257255
NCBI GI
                   124
BLAST score
                  4.0e-63
E value
                  214
Match length
                   91
% identity
NCBI Description Oryza sativa genomic DNA, chromosome 8, clone:P0026F07
                   411936
Seq. No.
Seq. ID
                   uC-osflcyp087h06a1
                  BLASTX
Method
NCBI GI
                  q5051771
                   306
BLAST score
                   7.0e-28
E value
                  73
Match length
                   77
% identity
NCBI Description (AL078637) putative protein [Arabidopsis thaliana]
                   411937
Seq. No.
Seq. ID
                   uC-osflcyp087h11a1
                   BLASTX
Method
```

53555

g1172977



BLAST score 392 E value 6.0e-38 Match length 86 % identity 86

NCBI Description 60S RIBOSOMAL PROTEIN L18 >gi 606970 (U15741) cytoplasmic

ribosomal protein L18 [Arabidopsis thaliana]

Seq. No. 411938

Seq. ID uC-osflcyp088a01a1

Method BLASTX
NCBI GI g3294467
BLAST score 305
E value 9.0e-28
Match length 63
% identity 98

NCBI Description (U89341) phosphoglucomutase 1 [Zea mays]

Seq. No. 411939

Seq. ID uC-osflcyp088a01b1

Method BLASTX
NCBI GI g3294467
BLAST score 814
E value 6.0e-87
Match length 170
% identity 97

NCBI Description (U89341) phosphoglucomutase 1 [Zea mays]

Seq. No. 411940

Seq. ID uC-osflcyp088a08b1

Method BLASTX
NCBI GI g2864624
BLAST score 278
E value 2.0e-24
Match length 185
% identity 34

NCBI Description (AL021811) putative protein [Arabidopsis thaliana]

Seq. No. 411941

Seq. ID uC-osflcyp088a09b1

Method BLASTX
NCBI GI g3193330
BLAST score 412
E value 3.0e-40
Match length 124
% identity 66

NCBI Description (AF069299) contains similarity to Medicago sativa corC

(GB:L22305) [Arabidopsis thaliana]

Seq. No. 411942

Seq. ID uC-osflcyp088a10b1

Method BLASTX
NCBI GI g4204268
BLAST score 554
E value 6.0e-57
Match length 119
% identity 84

NCBI Description (AC005223) 62134 [Arabidopsis thaliana]

Seq. No.

```
411943
Seq. No.
                  uC-osflcyp088a11b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4314378
BLAST score
                  249
                  2.0e-23
E value
                  135
Match length
% identity
                  (AC006232) putative lipase [Arabidopsis thaliana]
NCBI Description
                  >gi_5306262_gb_AAD41994.1_AC006233_5 (AC006233) putative
                  lipase [Arabidopsis thaliana]
                  411944
Seq. No.
Seq. ID
                  uC-osflcyp088b01a1
                  BLASTX
Method
NCBI GI
                  g2895866
                  313
BLAST score
                  9.0e-29
E value
Match length
                  80
                  79
% identity
                 (AF045770) methylmalonate semi-aldehyde dehydrogenase
NCBI Description
                  [Oryza sativa]
                  411945
Seq. No.
                  uC-osflcyp088b01b1
Seq. ID
                  BLASTX
Method
NCBI GI
                  q2895866
                  378
BLAST score
                  2.0e-36
E value
                  104
Match length
                  75
% identity
NCBI Description (AF045770) methylmalonate semi-aldehyde dehydrogenase
                  [Oryza sativa]
                  411946
Seq. No.
                  uC-osflcyp088b11b1
Seq. ID
Method
                  BLASTX
                  q2739044
NCBI GI
                  657
BLAST score
                  6.0e-69
E value
                  175
Match length
% identity
                  70
                  (AF024651) polyphosphoinositide binding protein Sshlp
NCBI Description
                   [Glycine max]
                   411947
Seq. No.
Seq. ID
                  uC-osflcyp088b12b1
Method
                  BLASTN
                  q5257255
NCBI GI
                  79
BLAST score
                  3.0e-36
E value
                  94
Match length
                   97
% identity
NCBI Description Oryza sativa genomic DNA, chromosome 8, clone:P0026F07
```

BLAST score

514

```
Seq. ID
                  uC-osflcyp088c11a1
Method
                  BLASTX
NCBI GI
                  g82517
BLAST score
                  363
E value
                  1.0e-34
Match length
                  68
                  100
% identity
NCBI Description hypothetical 12K protein (trnA intron) - rice chloroplast
                  411949
Seq. No.
Seq. ID
                  uC-osflcyp088c11b1
Method
                  BLASTX
                  g320577
NCBI GI
                  197
BLAST score
E value
                  6.0e-15
Match length
                  40
                  90
% identity
                  pvs protein 1 - kidney bean mitochondrion >gi 169320
NCBI Description
                   (M64246) ORF-98; putative [Phaseolus vulgaris]
                  411950
Seq. No.
                  uC-osflcyp088c12a1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1084455
BLAST score
                  252
                  1.0e-21
E value
Match length
                  48
% identity
                  100
                  peptidylprolyl isomerase (EC 5.2.1.8) Cyp2 - rice
NCBI Description
                  >gi 600767 (L29469) cyclophilin 2 [Oryza sativa]
Seq. No.
                  411951
Seq. ID
                  uC-osflcyp088c12b1
Method
                  BLASTX
NCBI GI
                  g1084455
BLAST score
                  488
E value
                  4.0e-49
Match length
                  106
% identity
                  88
NCBI Description
                  peptidylprolyl isomerase (EC 5.2.1.8) Cyp2 - rice
                  >gi_600767 (L29469) cyclophilin 2 [Oryza sativa]
                  411952
Seq. No.
Seq. ID
                  uC-osflcyp088d01a1
Method
                  BLASTX
NCBI GI
                  q4585992
BLAST score
                  229
E value
                  5.0e-19
Match length
                  66
% identity
NCBI Description
                  (AC005287) Hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  411953
Seq. ID
                  uC-osflcyp088d02b1
Method
                  BLASTX
NCBI GI
                  g586038
```

E value 9.0e-63 Match length 157 % identity 84

NCBI Description SIGNAL RECOGNITION PARTICLE 54 KD PROTEIN, CHLOROPLAST PRECURSOR (SRP54) (54 CHLOROPLAST PROTEIN) (54CP) (FFC)

PRECURSOR (SRP54) (54 CHLOROPLAST PROTEIN) (54CP) (FFC) >gi 480296 pir S36637 signal recognition particle 54CP

protein precursor - Arabidopsis thaliana

>gi_396701_emb_CAA79981.1_ (Z21970) 54CP [Arabidopsis

thaliana]

Seq. No. 411954

Seq. ID uC-osflcyp088d11a1

Method BLASTN
NCBI GI g3273244
BLAST score 71
E value 1.0e-31
Match length 187

% identity 84

NCBI Description Oryza sativa DNA for NLS receptor, complete cds

Seq. No. 411955

Seq. ID uC-osflcyp088e02a1

Method BLASTX
NCBI GI g3892058
BLAST score 309
E value 3.0e-28
Match length 96
% identity 55

NCBI Description (AC002330) putative glutamate-/aspartate-binding peptide

[Arabidopsis thaliana]

Seq. No. 411956

Seq. ID uC-osflcyp088e02b1

Method BLASTX
NCBI GI g2244904
BLAST score 151
E value 1.0e-09
Match length 80
% identity 49

NCBI Description (Z97339) hypothetical protein [Arabidopsis thaliana]

Seq. No. 411957

Seq. ID uC-osflcyp088e11b1

Method BLASTX
NCBI GI g115787
BLAST score 681
E value 9.0e-72
Match length 152
% identity 89

NCBI Description CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I

CAB-2) (LHCP) $>gi_82461_pir_S03706$ chlorophyll a/b-binding

protein 2R precursor - rice >gi_20182_emb_CAA32109_

(X13909) chlorophyll a/b-binding preprotein (AA -28 to 235)

[Oryza sativa]

Seq. No. 411958

Seq. ID uC-osflcyp088e12a1

Method

BLASTX

```
BLASTN
Method
NCBI GI
                  g1261857
                  48
BLAST score
                  8.0e-19
E value
Match length
                  52
                  98
% identity
                  Rice CatA gene for catalase, complete cds
NCBI Description
                  411959
Seq. No.
                  uC-osflcyp088e12b1
Seq. ID
Method
                  BLASTX
                  q2829886
NCBI GI
BLAST score
                  270
                  2.0e-23
E value
                  162
Match length
% identity
                  (AC002396) Hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  411960
                  uC-osflcyp088f01b1
Seq. ID
                  BLASTX
Method
NCBI GI
                  g119150
                  920
BLAST score
E value
                  1.0e-100
                  176
Match length
                  98
% identity
                  ELONGATION FACTOR 1-ALPHA (EF-1-ALPHA)
NCBI Description
                  >gi_82081_pir__S10507 translation elongation factor eEF-1
                  alpha chain - tomato >gi_19273_emb_CAA32618_ (X14449) EF
                  1-alpha (AA 1-448) [Lycopersicon esculentum]
                  >qi 295810 emb CAA37212 (X53043) elongation factor 1-alpha
                   [Lycopersicon esculentum]
Seq. No.
                  411961
                  uC-osflcyp088f02b1
Seq. ID
Method
                  BLASTX
                  g2352084
NCBI GI
                  546
BLAST score
E value
                  5.0e-56
Match length
                  108
                  94
% identity
NCBI Description (U96613) serine/threonine kinase [Arabidopsis thaliana]
                  411962
Seq. No.
                  uC-osflcyp088f03a1
Seq. ID
                  BLASTX
Method
                  g6015065
NCBI GI
                  390
BLAST score
                  1.0e-37
E value
Match length
                  82
                   90
% identity
NCBI Description ELONGATION FACTOR 2 (EF-2) >gi_2369714_emb_CAB09900_
                   (Z97178) elongation factor 2 [Beta vulgaris]
                   411963
Seq. No.
                  uC-osflcyp088f03b1
Seq. ID
```

```
NCBI GI
                  g6015065
BLAST score
                  739
                  1.0e-78
E value
Match length
                  152
% identity
                  92
NCBI Description ELONGATION FACTOR 2 (EF-2) >gi 2369714 emb CAB09900
                  (Z97178) elongation factor 2 [Beta vulgaris]
                  411964
Seq. No.
Seq. ID
                  uC-osflcyp088f06a1
                  BLASTN
Method
NCBI GI
                  g20191
BLAST score
                  114
                  2.0e-57
E value
                  146
Match length
                  95
% identity
NCBI Description O.sativa mRNA for catalase
Seq. No.
                  411965
                  uC-osflcyp088f10b1
Seq. ID
                  BLASTX
Method
NCBI GI
                  g3426041
BLAST score
                  370
E value
                  3.0e-35
Match length
                  152
% identity
NCBI Description (AC005168) unknown protein [Arabidopsis thaliana]
Seq. No.
                  411966
                  uC-osflcyp088f11b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2924792
BLAST score
                  362
E value
                  3.0e-34
                  142
Match length
                  50
% identity
NCBI Description (AC002334) similar to synaptobrevin [Arabidopsis thaliana]
                  411967
Seq. No.
                  uC-osflcyp088f12a1
Seq. ID
Method
                  BLASTX
                  g2130069
NCBI GI
                  200
BLAST score
                  2.0e-15
E value
                  39
Match length
                  97
% identity
NCBI Description catalase (EC 1.11.1.6) catA - rice
                  >gi_1261858_dbj_BAA06232_ (D29966) catalase [Oryza sativa]
                   411968
Seq. No.
                  uC-osflcyp088f12b1
Seq. ID
Method
                  BLASTX
                  g2130069
NCBI GI
BLAST score
                  861
                  4.0e-97
E value
Match length
                  174
```

53561

99

% identity

NCBI Description catalase (EC 1.11.1.6) catA - rice >gi 1261858 dbj BAA06232 (D29966) catalase [Oryza sativa]

Seq. No.

Seq. ID uC-osflcyp088g01b1

BLASTX Method q1076800 NCBI GI BLAST score 261 8.0e-47E value 123 Match length 71 % identity

L-ascorbate peroxidase (EC 1.11.1.11), cytosolic isozyme -NCBI Description

maize >gi 600116 emb CAA84406 (Z34934) cytosolic ascorbate peroxidase [Zea mays] >gi 1096503 prf 2111423A ascorbate

peroxidase [Zea mays]

Seq. No. 411970

uC-osflcyp088g02b1 Seq. ID

Method BLASTX q4914452 NCBI GI BLAST score 179 5.0e-13 E value 124 Match length % identity

NCBI Description

(AL050398) putative protein [Arabidopsis thaliana]

411971 Seq. No.

uC-osflcyp088g09b1 Seq. ID

Method BLASTX NCBI GI q3874563 BLAST score 316 6.0e-29 E value Match length 132 44 % identity

(Z81042) similar to Yeast hypothetical protein YEY6 like; NCBI Description

cDNA EST yk206h5.3 comes from this gene; cDNA EST yk206h5.5 comes from this gene; cDNA EST yk303h1.3 comes from this gene; cDNA EST yk303h1.5 comes from this gene; cDN... >gi 3924825_emb_CAB05549.1_ (Z83113) similar to Yeast hypothetical protein YEY6 like; cDNA EST yk206h5.3 comes from this gene; cDNA EST yk206h5.5 comes from this gene; cDNA EST yk303h1.3 comes from this gene; cDNA EST yk303h1.5

comes from this gene; cDN

411972 Seq. No.

uC-osflcyp088g10a1 Seq. ID

Method BLASTX q3036812 NCBI GI 198 BLAST score 3.0e-15E value Match length 40 % identity 88

NCBI Description (AL022373) ATM-like protein [Arabidopsis thaliana]

411973 Seq. No.

uC-osflcyp088g10b1 Seq. ID

Method BLASTX

```
g2708741
NCBI GI
BLAST score
                  743
                  5.0e-79
E value
Match length
                  170
                  78
% identity
                 (AC003952) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                  411974
Seq. No.
Seq. ID
                  uC-osflcyp088g12a1
                  BLASTX
Method
                  q4567246
NCBI GI
                  195
BLAST score
                  7.0e-15
E value
                  55
Match length
                  65
% identity
NCBI Description (AC007070) unknown protein [Arabidopsis thaliana]
                  411975
Seq. No.
Seq. ID
                  uC-osflcyp088g12b1
Method
                  BLASTX
NCBI GI
                  q4567246
                  430
BLAST score
                  3.0e-42
E value
                  147
Match length
                  59
% identity
NCBI Description (AC007070) unknown protein [Arabidopsis thaliana]
                   411976
Seq. No.
Seq. ID
                  uC-osflcyp088h01b1
Method
                  BLASTX
                   q4581164
NCBI GI
BLAST score
                   341
                  7.0e-32
E value
                  168
Match length
% identity
                   42
NCBI Description (AC006220) putative polyprotein [Arabidopsis thaliana]
                   411977
Seq. No.
                   uC-osflcyp088h02b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   q131225
BLAST score
                   652
                   2.0e-68
E value
Match length
                   153
                   84
% identity
                  PHOTOSYSTEM I REACTION CENTRE SUBUNIT XI PRECURSOR (SUBUNIT
NCBI Description
                   V) (PSI-L) >gi 100605_pir__A39759 photosystem I 18K protein
                   precursor - barley >gi_167087 (M61146) photosystem I
                   hydrophobic protein [Hordeum vulgare]
                   411978
Seq. No.
                   uC-osflcyp088h03a1
Seq. ID
Method
                   BLASTN
                   g4426561
NCBI GI
```

53563

327

355

0.0e + 00

BLAST score

E value Match length

NCBI GI

```
98
% identity
                 Oryza sativa mRNA for chitinase IIb, complete cds
NCBI Description
                  411979
Seq. No.
Seq. ID
                  uC-osflcyp088h03b1
                  BLASTX
Method
                  q2055262
NCBI GI
BLAST score
                  800
E value
                  1.0e-85
                  151
Match length
                  99
% identity
                 (AB003194) chitinase IIb [Oryza sativa]
NCBI Description
                  411980
Seq. No.
                  uC-osflcyp088h04b1
Seq. ID
                  BLASTX
Method
NCBI GI
                  g3128177
BLAST score
                  185
E value
                  3.0e-14
                  56
Match length
                  66
% identity
NCBI Description (AC004521) unknown protein [Arabidopsis thaliana]
Seq. No.
                  411981
                  uC-osflcyp088h05a1
Seq. ID
                  BLASTN
Method
                  g3411151
NCBI GI
BLAST score
                  131
E value
                  2.0e-67
                  244
Match length
                  94
% identity
NCBI Description Oryza sativa thymidine kinase (TK) mRNA, complete cds
                  411982
Seq. No.
                  uC-osflcyp088h06a1
Seq. ID
                  BLASTX
Method
                  g5802606
NCBI GI
                  364
BLAST score
                   1.0e-34
E value
Match length
                  78
                   82
% identity
NCBI Description (AF174486) methylenetetrahydrofolate reductase [Zea mays]
                   411983
Seq. No.
                   uC-osflcyp088h06b1
Seq. ID
                   BLASTX
Method
                   g5802606
NCBI GI
BLAST score
                   683
                   5.0e-72
E value
Match length
                   146
                   86
% identity
NCBI Description (AF174486) methylenetetrahydrofolate reductase [Zea mays]
                   411984
Seq. No.
Seq. ID
                   uC-osflcyp088h08b1
Method
                   BLASTX
```

53564

g1778149

BLAST score 160 E value 7.0e-11 Match length 42 % identity 81

NCBI Description (U66404) phosphate/phosphoenolpyruvate translocator

precursor [Zea mays]

Seq. No. 411985

Seq. ID uC-osflcyp088h09a1

Method BLASTX
NCBI GI g547712
BLAST score 204
E value 6.0e-16
Match length 40
% identity 100

NCBI Description EUKARYOTIC INITIATION FACTOR 4A (EIF-4A)

>gi 542153 pir S38358 translation initiation factor eIF-4A

- rice >qi 303844 dbj BAA02152 (D12627) eukaryotic

initiation factor 4A [Oryza sativa]

Seq. No. 411986

Seq. ID uC-osflcyp088h09b1

Method BLASTX
NCBI GI g547712
BLAST score 703
E value 4.0e-75
Match length 148
% identity 95

NCBI Description EUKARYOTIC INITIATION FACTOR 4A (EIF-4A)

>gi 542153 pir S38358 translation initiation factor eIF-4A

- rice >gi 303844 dbj BAA02152 (D12627) eukaryotic

initiation factor 4A [Oryza sativa]

Seq. No. 411987

Seq. ID uC-osflcyp088h10a1

Method BLASTN
NCBI GI g1167556
BLAST score 219
E value 1.0e-120
Match length 247
% identity 97

NCBI Description Oryza sativa glycine-rich cell wall protein (Angrp-1) gene,

complete cds

Seq. No. 411988

Seq. ID uC-osflcyp088h10b1

Method BLASTN
NCBI GI g1167556
BLAST score 236
E value 1.0e-130
Match length 244
% identity 99

NCBI Description Oryza sativa glycine-rich cell wall protein (Angrp-1) gene,

complete cds

Seq. No. 411989

Seq. ID uC-osflcyp088h11b1

Method BLASTX NCBI GI q5103831 281 BLAST score 8.0e-25 E value Match length 97 58 % identity (AC007591) ESTs gb H37032, gb R6425, gb Z34651, gb N37268, NCBI Description gb AA713172 and gb Z34241 come from this gene. [Arabidopsis thaliana] 411990 Seq. No. Seq. ID uC-osflcyp088h12b1 Method BLASTX NCBI GI g4914683 BLAST score 207 E value 4.0e-16 Match length 181 % identity 30 NCBI Description (AF067728) transactivating protein BRIDGE [Rattus norvegicus] Seq. No. 411991 Seq. ID uC-osflcyp089a01b1 Method BLASTX NCBI GI g4510381 BLAST score 213 E value 1.0e-17 Match length 64 % identity 73 NCBI Description (AC007017) unknown protein [Arabidopsis thaliana] Seq. No. 411992 Seq. ID uC-osflcyp089a02a1 Method BLASTN NCBI GI g6013290 BLAST score 108 E value 3.0e-54Match length 108 100 % identity NCBI Description Oryza sativa polyubiquitin (RUBQ2) gene, complete cds 411993 Seq. No. Seq. ID uC-osflcyp089a02b1 Method

Method BLASTX
NCBI GI g3335355
BLAST score 597
E value 7.0e-62
Match length 149
% identity 25

NCBI Description (AC004512) Match to polyubiquitin DNA gb L05401 from A.

thaliana. Contains insertion of mitochondrial NADH

dehydrogenase gb_X82618 and gb_X98301. May be a pseudogene with an expressed insert. EST gb_AA586248 comes from this

region. [Arabi

Seq. No. 411994

Seq. ID uC-osflcyp089a05b1

NCBI GI

```
Method
                  BLASTX
                  g4538911
NCBI GI
BLAST score
                  149
E value
                  2.0e-09
Match length
                  36
                  81
% identity
NCBI Description (AL049482) hypothetical protein [Arabidopsis thaliana]
                  411995
Seq. No.
Seq. ID
                  uC-osflcyp089a07b1
Method
                  BLASTX
NCBI GI
                  q1438883
BLAST score
                  366
                  5.0e - 35
E value
                  113
Match length
% identity
                  62
NCBI Description (U43840) GmCK3p [Glycine max]
                  411996
Seq. No.
                  uC-osflcyp089a09a1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1706328
BLAST score
                  218
E value
                  6.0e-28
Match length
                  66
                  93
% identity
NCBI Description
                  PYRUVATE DECARBOXYLASE ISOZYME 2 (PDC) >gi 1009710 (U27350)
                  pyruvate decarboxylase 2 [Oryza sativa] >gi 1777455
                   (U38199) pyruvate decarboxylase 2 [Oryza sativa]
Seq. No.
                  411997
                  uC-osflcyp089a09b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1706330
BLAST score
                  393
E value
                  2.0e-38
Match length
                  89
                  80
% identity
NCBI Description
                  PYRUVATE DECARBOXYLASE ISOZYME 2 (PDC)
                  >gi_1362116_pir__S57821 pyruvate decarboxylase (EC 4.1.1.1)
                  2 - common tobacco >gi_551263_emb_CAA57448_ (X81855)
                  pyruvate decarboxylase [Nicotiana tabacum]
Seq. No.
                  411998
Seq. ID
                  uC-osflcyp089a10b1
Method
                  BLASTX
NCBI GI
                  g3790441
BLAST score
                  269
E value
                  2.0e-23
Match length
                  57
% identity
NCBI Description (AF030515) chaperonin 60 alpha subunit [Canavalia lineata]
Seq. No.
                  411999
Seq. ID
                  uC-osflcyp089a12b1
Method
                  BLASTX
```

53567

g2286153



BLAST score 749 E value 9.0e-80 Match length 158 % identity 92

NCBI Description (AF007581) cytoplasmic malate dehydrogenase [Zea mays]

Seq. No. 412000

Seq. ID uC-osflcyp089b01b1

Method BLASTX
NCBI GI g2407281
BLAST score 524
E value 1.0e-53
Match length 102
% identity 98

NCBI Description (AF017363) ribulose 1,5-bisphosphate carboxylase small

subunit [Oryza sativa]

Seq. No. 412001

Seq. ID uC-osflcyp089b02b1

Method BLASTX
NCBI GI g4049401
BLAST score 286
E value 1.0e-25
Match length 77
% identity 70

NCBI Description (AJ131580) glutathione transferase AtGST 10 [Arabidopsis

thaliana]

Seq. No. 412002

Seq. ID uC-osflcyp089b03b1

Method BLASTX
NCBI GI g3608152
BLAST score 164
E value 4.0e-11
Match length 45
% identity 62

NCBI Description (AC005314) hypothetical protein [Arabidopsis thaliana]

Seq. No. 412003

Seq. ID uC-osflcyp089b07a1

Method BLASTN
NCBI GI g1154888
BLAST score 130
E value 5.0e-67
Match length 146
% identity 99

NCBI Description O.sativa 3-hydroxy-3-methylglutaryl-CoA reductase gene

Seq. No. 412004

Seq. ID uC-osflcyp089b07b1

Method BLASTN
NCBI GI g4165327
BLAST score 91
E value 7.0e-44
Match length 107
% identity 96

NCBI Description Oryza sativa 3-hydroxy-3-methylglutaryl-CoA reductase gene,

promoter region and complete cds

```
Seq. No.
                   412005
                   uC-osflcyp089b08a1
Seq. ID
Method
                   BLASTN
NCBI GI
                   q1835730
BLAST score
                   90
                   4.0e-43
E value
Match length
                   106
                   97
% identity
                  Oryza sativa photosystem II 10 kDa polypeptide mRNA,
NCBI Description
                   complete cds
                   412006
Seq. No.
Seq. ID
                   uC-osflcyp089b08b1
                   BLASTX
Method
NCBI GI
                   q1835731
BLAST score
                   314
                   3.0e-29
E value
Match length
                   62
                   100
% identity
NCBI Description (U86018) photosystem II 10 kDa polypeptide [Oryza sativa]
Seq. No.
                   412007
                   uC-osflcyp089b09a1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g1305525
BLAST score
                   242
E value
                   2.0e-20
                   47
Match length
                   98
% identity
NCBI Description (U55212) Wilms' tumor-related protein QM [Oryza sativa]
                   412008
Seq. No.
                   uC-osflcyp089b09b1
Seq. ID
                   BLASTX
Method
                   g1172811
NCBI GI
                   295
BLAST score
                   3.0e-27
E value
                   52
Match length
                   98
% identity
NCBI Description 60S RIBOSOMAL PROTEIN L10-1 (PUTATIVE TUMOR SUPRESSOR SC34)
                   >gi 1076751 pir S49575 ribosomal protein L10.e, cytosolic
                   - rice > gi \overline{575355} emb CAA57339 (X81691) putative tumor
                   suppresser [Oryza sativa]
                   412009
Seq. No.
Seq. ID
                   uC-osflcyp089b10a1
                   BLASTN
Method
                   g218209
NCBI GI
BLAST score
                   67
                   3.0e-29
E value
Match length
                   115
% identity
NCBI Description Oryza sativa mRNA for the small subunit of
                   ribulose-1,5-bisphosphate carboxylase, complete cds, clone
```

posss2106

```
412010
Seq. No.
                  uC-osflcyp089b10b1
Seq. ID
Method
                  BLASTX
                  q2407281
NCBI GI
BLAST score
                  487
                  2.0e-49
E value
Match length
                  95
                  99
% identity
                 (AF017363) ribulose 1,5-bisphosphate carboxylase small
NCBI Description
                  subunit [Oryza sativa]
                  412011
Seq. No.
                  uC-osflcyp089b12b1
Seq. ID
                  BLASTX
Method
NCBI GI
                  q4468985
BLAST score
                  164
E value
                  4.0e-11
                  73
Match length
                  47
% identity
NCBI Description (AL035605) hypothetical protein [Arabidopsis thaliana]
                  412012
Seq. No.
                  uC-osflcyp089c01b1
Seq. ID
Method
                  BLASTX
                  g4432841
NCBI GI
BLAST score
                  384
                  5.0e-37
E value
                  146
Match length
                  51
% identity
NCBI Description (AC006283) hypothetical protein [Arabidopsis thaliana]
                  412013
Seq. No.
                  uC-osflcyp089c02b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q5031275
BLAST score
                  523
                  2.0e-53
E value
Match length
                  137
                  73
% identity
NCBI Description (AF139496) unknown [Prunus armeniaca]
                   412014
Seq. No.
                  uC-osflcyp089c03b1
Seq. ID
                  BLASTX
Method
NCBI GI
                  g2129742
BLAST score
                  263
E value
                   1.0e-22
Match length
                  71
                   65
% identity
                  stress-induced protein OZI1 precursor - Arabidopsis
NCBI Description
                   thaliana >gi 790583 (U20347) mRNA corresponding to this
                   gene accumulates in response to ozone stress and pathogen
                   (bacterial) infection; putative pathogenesis-related
                   protein [Arabidopsis thaliana] >gi_2252869 (AF013294) No
                   definition line found [Arabidopsis thaliana]
```

```
412015
Seq. No.
                  uC-osflcyp089c04b1
Seq. ID
                  BLASTX
Method
NCBI GI
                  q3786008
BLAST score
                  229
                  9.0e-19
E value
                  71
Match length
                   61
% identity
                  (AC005499) unknown protein [Arabidopsis thaliana]
NCBI Description
                   412016
Seq. No.
                  uC-osflcyp089c07b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3242789
                   267
BLAST score
                   6.0e-24
E value
                   67
Match length
                   67
% identity
                  (AF055357) respiratory burst oxidase protein D [Arabidopsis
NCBI Description
                   thaliana]
                   412017
Seq. No.
                   uC-osflcyp089c08b1
Seq. ID
                   BLASTX
Method
                   g4321401
NCBI GI
BLAST score
                   335
E value
                   3.0e-31
                   90
Match length
                   36
% identity
NCBI Description (AF047353) LIM domain protein PLIM-2 [Helianthus annuus]
                   412018
Seq. No.
                   uC-osflcyp089d02b1
Seq. ID
Method
                   BLASTX
                   g4680207
NCBI GI
BLAST score
                   193
E value
                   2.0e-14
                   129
Match length
% identity
                   36
                   (AF114171) disease resistance protein RPM1 homolog [Sorghum
NCBI Description
                   bicolor]
                   412019
Seq. No.
                   uC-osflcyp089d03a1
Seq. ID
                   BLASTN
Method
NCBI GI
                   g16086
BLAST score
                   38
E value
                   7.0e-12
Match length
                   50
                   94
% identity
```

NCBI Description A.porrum dnaJ mRNA for DNA J protein (partial)

Seq. No. 412020

uC-osflcyp089d03b1 Seq. ID

Method BLASTX NCBI GI g5802244 BLAST score 139

```
E value
                   7.0e-09
Match length
                   31
 % identity
                   84
NCBI Description (AF169022) seed maturation protein PM37 [Glycine max]
Seq. No.
                   412021
Seq. ID
                   uC-osflcyp089d11b1
Method
                   BLASTX
NCBI GI
                   q4826572
BLAST score
                   454
E value
                   8.0e-49
Match length
                   121
                   77
% identity
NCBI Description (AJ238848) polygalacturonase [Phleum pratense]
Seq. No.
                   412022
Seq. ID
                   uC-osflcyp089d12b1
Method
                   BLASTX
NCBI GI
                   g2983642
BLAST score
                   185
E value
                   9.0e-14
Match length
                   109
% identity
                   37
NCBI Description (AE000728) diaminopimelate decarboxylase [Aquifex aeolicus]
Seq. No.
                   412023
Seq. ID
                   uC-osflcyp089e03b1
Method
                   BLASTX
NCBI GI
                   g5668667
BLAST score
                   757
E value
                   9.0e-81
Match length
                   149
% identity
                   97
NCBI Description (D63136) Beta-tubulin [Zinnia elegans]
Seq. No.
                   412024
Seq. ID
                  uC-osflcyp089e11a1
Method
                  BLASTN
NCBI GI
                  q4158220
BLAST score
                  139
E value
                  5.0e-72
Match length
                  143
% identity
                  99
NCBI Description Oryza sativa mRNA for reversibly glycosylated polypeptide
Seq. No.
                  412025
Seq. ID
                  uC-osflcyp089e11b1
Method
                  BLASTN
NCBI GI
                  q3646372
BLAST score
                  49
E value
                  3.0e-18
Match length
                  61
% identity
                  95
NCBI Description Oryza sativa mRNA for RGP1 protein
Seq. No.
                  412026
Seq. ID
```

53572

uC-osflcyp089e12a1

NCBI GI

```
Method
                   BLASTN
NCBI GI
                   g1293783
BLAST score
                   40
E value
                   1.0e-13
Match length
                   72
% identity
                   90
NCBI Description Oryza sativa QM gene, complete cds
Seq. No.
                   412027
Seq. ID
                   uC-osflcyp089e12b1
Method
                   BLASTX
NCBI GI
                   g2500353
BLAST score
                   270
E value
                   3.0e-24
Match length
                   52
% identity
                   94
NCBI Description
                  60S RIBOSOMAL PROTEIN L10-3 (QM/R22) >gi 1293784 (U55048)
                   similar to human QM protein, a putative tumor supressor,
                   and to maize ubiquinol-cytochrome C reductase complex
                   subunit VI requiring protein SC34 [Oryza sativa]
Seq. No.
                   412028
Seq. ID
                   uC-osflcyp089f04b1
Method
                   BLASTX
NCBI GI
                   q3925265
BLAST score
                   193
E value
                   3.0e-15
Match length
                  55
% identity
                   58
NCBI Description (Z93394) similar to Probable rabGAP domains [Caenorhabditis
                  elegans]
Seq. No.
                   412029
Seq. ID
                  uC-osflcyp089f05b1
Method
                  BLASTN
NCBI GI
                  g1814402
BLAST score
                  50
E value
                  1.0e-19
Match length
                  82
% identity
                  90
NCBI Description
                  Mesembryanthemum crystallinum methionine synthase (MetE)
                  mRNA, complete cds
Seq. No.
                  412030
Seq. ID
                  uC-osflcyp089f08b1
Method
                  BLASTN
NCBI GI
                  g1103627
BLAST score
                  42
E value
                  2.0e-14
Match length
                  62
                  92
% identity
NCBI Description Z.mays Fer1 gene
Seq. No.
                  412031
Seq. ID
                  uC-osflcyp089f10a1
Method
                  BLASTN
```

53573

g5257255

BLAST score 124 E value 2.0e-63 Match length 132 99 % identity

NCBI Description Oryza sativa genomic DNA, chromosome 8, clone:P0026F07

Seq. No. 412032

Seq. ID uC-osflcyp089f10b1

Method BLASTX NCBI GI g5257275 BLAST score 435 E value 3.0e-43 Match length 85 % identity 99

NCBI Description (AP000364) ESTs AU030740(E60171), AU030739(E60171)

correspond to a region of the predicted gene.; Similar to Populus tremuloides caffeoyl-CoA 3-O-methyltransferase.

(U27116) [Oryza sativa]

Seq. No. 412033

Seq. ID uC-osflcyp089f12a1

Method BLASTN NCBI GI g3789949 BLAST score 125 E value 3.0e-64Match length 156 % identity 97

Oryza sativa translation initiation factor (GOS2) mRNA, NCBI Description

complete cds

Seq. No. 412034

Seq. ID uC-osflcyp089f12b1

Method BLASTX NCBI GI g462195 BLAST score 227 E value 5.0e-19 Match length 51 90 % identity

NCBI Description PROTEIN TRANSLATION FACTOR SUI1 HOMOLOG (GOS2 PROTEIN)

>gi 100682_pir__S21636 GOS2 protein - rice

>gi_20238_emb_CAA36190_ (X51910) GOS2 [Oryza sativa]
>gi_3789950 (AF094774) translation initiation factor [Oryza

 $sat\overline{i}va$

Seq. No. 412035

Seq. ID uC-osflcyp089g02b1

Method BLASTN NCBI GI g20321 BLAST score 77 E value 1.0e-35 Match length 129 % identity 90

NCBI Description Oryza sativa RAc1 mRNA for actin

Seq. No. 412036

Seq. ID uC-osflcyp089g05b1

Method BLASTX

NCBI GI

BLAST score

```
NCBI GI
                   g5262191
BLAST score
                   242
E value
                   5.0e-21
Match length
                   59
% identity
                   81
NCBI Description (AL080252) putative protein [Arabidopsis thaliana]
Seq. No.
                   412037
Seq. ID
                   uC-osflcyp089g07a1
Method
                   BLASTN
NCBI GI
                   q20094
BLAST score
                  80
E value
                   2.0e-37
Match length
                   100
% identity
                   95
NCBI Description O.sativa RSs2 gene for sucrose-UDP glucosyltransferase
                   (isozyme 2)
Seq. No.
                   412038
Seq. ID
                  uC-osflcyp089g07b1
Method
                  BLASTX
NCBI GI
                  q401140
BLAST score
                  556
E value
                   2.0e-57
Match length
                  105
% identity
                   99
NCBI Description SUCROSE SYNTHASE 2 (SUCROSE-UDP GLUCOSYLTRANSFERASE 2)
                  >gi_20095_emb_CAA41774_ (X59046) sucrose-UDP
                  glucosyltransferase (isoenzyme 2) [Oryza sativa]
                  >gi_1587662_prf__2207194A sucrose synthase:ISOTYPE=2 [Oryza
                  sativa]
Seq. No.
                  412039
Seq. ID
                  uC-osflcyp089g08a1
Method
                  BLASTN
NCBI GI
                  g1261857
BLAST score
                  142
E value
                  3.0e-74
Match length
                  142
% identity
                  100
NCBI Description Rice CatA gene for catalase, complete cds
Seq. No.
                  412040
Seq. ID
                  uC-osflcyp089g08b1
Method
                  BLASTN
NCBI GI
                  g20191
BLAST score
                  55
E value
                  9.0e-23
Match length
                  59
% identity
                  98
NCBI Description O.sativa mRNA for catalase
Seq. No.
                  412041
Seq. ID
                  uC-osflcyp089g11b1
Method
                  BLASTX
```

53575

g3023816

Match length

% identity

75

71

```
E value
                   1.0e-26
Match length
                   71
% identity
                   85
                  GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC
NCBI Description
                   >gi_968996 (U31676) glyceraldehyde-3-phosphate
                  dehydrogenase [Oryza sativa]
Seq. No.
                   412042
Seq. ID
                  uC-osflcyp089h01b1
Method
                  BLASTX
NCBI GI
                  q4126809
BLAST score
                   383
E value
                   3.0e-37
Match length
                  88
% identity
                   45
NCBI Description (AB017042) glyoxalase I [Oryza sativa]
Seq. No.
                  412043
Seq. ID
                  uC-osflcyp089h02a1
Method
                  BLASTN
NCBI GI
                  q5734616
BLAST score
                  40
E value
                  2.0e-13
Match length
                  60
% identity
                  92
NCBI Description Oryza sativa genomic DNA, chromosome 6, clone:P0538C01
                  412044
Seq. No.
Seq. ID
                  uC-osflcyp089h02b1
Method
                  BLASTX
NCBI GI
                  g1620369
BLAST score
                  153
E value
                  1.0e-10
Match length
                  52
% identity
                  60
NCBI Description (Y08781) peroxidase ATP22a [Arabidopsis thaliana]
Seq. No.
                  412045
Seq. ID
                  uC-osflcyp089h07b1
Method
                  BLASTX
NCBI GI
                  q117953
BLAST score
                  142
E value
                  3.0e-09
Match length
                  68
% identity
                  43
NCBI Description CYTOCHROME C >gi_65508_pir__CCBX cytochrome c - box elder
Seq. No.
                  412046
Seq. ID
                  uC-osflcyp089h09b1
Method
                  BLASTX
NCBI GI
                  q5902363
BLAST score
                  204
E value
                  5.0e-22
```

NCBI Description (AC009322) Putative coatomer protein complex, subunit beta 2 (beta prime) [Arabidopsis thaliana]

```
Seq. No.
                   412047
Seq. ID
                   uC-osflcyp090a12b1
Method
                  BLASTX
NCBI GI
                   q1084455
BLAST score
                   659
E value
                   3.0e-69
Match length
                   136
                   90
% identity
NCBI Description
                  peptidylprolyl isomerase (EC 5.2.1.8) Cyp2 - rice
                  >gi 600767 (L29469) cyclophilin 2 [Oryza sativa]
Seq. No.
                   412048
Seq. ID
                  uC-osflcyp090b12b1
Method
                  BLASTX
NCBI GI
                   g2570505
BLAST score
                   535
E value
                   7.0e-55
Match length
                  108
% identity
                   95
NCBI Description
                 (AF022735) proteasome component [Oryza sativa]
Seq. No.
                   412049
                  uC-osflcyp090c07b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1709563
                   503
BLAST score
E value
                   4.0e-51
Match length
                  104
% identity
                  94
NCBI Description PHENYLALANINE AMMONIA-LYASE >gi_2130081 pir S66313
                  phenylalanine ammonia-lyase (EC 4.3.1.5) - rice
                  >gi_871494_emb_CAA61198_ (X87946) phenylalanine
                  ammonia-lyase [Oryza sativa]
Seq. No.
                  412050
Seq. ID
                  uC-osflcyp090c09b1
Method
                  BLASTN
NCBI GI
                  a871493
BLAST score
                  81
E value
                  1.0e-37
Match length
                  249
% identity
                  84
NCBI Description O.sativa ZB8 gene
Seq. No.
                  412051
Seq. ID
                  uC-osflcyp090d11b1
Method
                  BLASTX
NCBI GI
                  q1353193
BLAST score
                  200
E value
                  7.0e-16
Match length
                  79
% identity
                  46
NCBI Description
                  O-METHYLTRANSFERASE ZRP4 (OMT) >gi 542186 pir JQ2268
                  O-methyltransferase (EC 2.1.1.-) - maize \overline{>}gi\overline{40}4070
```

(L14063) O-methyltransferase [Zea mays]



412052 Seq. No. Seq. ID uC-osflcyp090d12b1 Method BLASTX NCBI GI q4454466 BLAST score 155 E value 8.0e-11 42 Match length 67 % identity NCBI Description (AC006234) unknown protein [Arabidopsis thaliana] 412053 Seq. No. uC-osflcyp090e11b1 Seq. ID Method BLASTX NCBI GI g115772 BLAST score 324 2.0e-30 E value Match length 72 89 % identity NCBI Description CHLOROPHYLL A-B BINDING PROTEIN 1 PRECURSOR (LHCII TYPE I CAB-1) (LHCP) >gi 82460 pir S03705 chlorophyll a/b-binding protein 1R precursor - rice >gi 20178 emb CAA32108 (X13908) chlorophyll a/b-binding preprotein (AA -31 to 235) [Oryza sativa] 412054 Seq. No. uC-osflcyp090e12b1 Seq. ID Method BLASTX NCBI GI g3080420 279 BLAST score E value 7.0e-25 94 Match length % identity 63 (AL022604) putative sugar transporter protein [Arabidopsis NCBI Description thaliana] Seq. No. 412055 Seq. ID uC-osflcyp090f10b1 Method BLASTX NCBI GI q4454484 BLAST score 218 E value 1.0e-17 Match length 97 % identity 48 NCBI Description (AC006234) putative diacylglycerol kinase [Arabidopsis thaliana] Seq. No. 412056 Seq. ID

uC-osflcyp090f11b1

Method BLASTX NCBI GI q4587519 BLAST score 190 E value 9.0e-15 Match length 61 % identity

NCBI Description (AC007060) Strong similarity to F19I3.7 gi 3033380 putative

coatomer epsilon subunit from Arabidopsis thaliana BAC gb_AC004238. ESTs gb_Z17908, gb_AA728673, gb_N96555,

gb_H76335, gb_AA712463, gb_W43247, gb_T45611, g 412057 uC-osflcyp090f12b1

Method BLASTN
NCBI GI g1619603
BLAST score 63
E value 2.0e-27
Match length 83
% identity 94

Seq. No.

Seq. ID

NCBI Description O.sativa mRNA for lipid transfer protein

>gi_1667589_gb_U77295_OSU77295 Oryza sativa lipid transfer

protein (LTP) mRNA, complete cds

Seq. No. 412058

Seq. ID uC-osflcyp090h10b1

Method BLASTX
NCBI GI g2832641
BLAST score 141
E value 3.0e-09
Match length 45
% identity 58

NCBI Description (AL021710) glycolate oxidase - like protein [Arabidopsis

thaliana]

Seq. No. 412059

Seq. ID uC-osflcyp091a04a1

Method BLASTN
NCBI GI g6063530
BLAST score 62
E value 3.0e-26
Match length 158

% identity 85

NCBI Description Oryza sativa genomic DNA, chromosome 3, clone:P0043E01

Seq. No. 412060

Seq. ID uC-osflcyp091a04b1

Method BLASTX
NCBI GI g1705735
BLAST score 635
E value 2.0e-66
Match length 122
% identity 100

NCBI Description CALCIUM-DEPENDENT PROTEIN KINASE, ISOFORM 11 (CDPK 11)

>gi_1362175_pir__S56651 probable calcium-dependent protein
kinase (clone OSCPK11) - rice >gi_587500_emb_CAA57156_
(X81393) calcium-dependent protein kinase [Oryza sativa]

Seq. No. 412061

Seq. ID uC-osflcyp091a05a1

Method BLASTN
NCBI GI g633109
BLAST score 394
E value 0.0e+00
Match length 414
% identity 99

NCBI Description Rice mRNA for plasma membrane H+-ATPase, complete cds

```
Seq. No.
                  412062
Seq. ID
                  uC-osflcyp091a05b1
Method
                  BLASTX
NCBI GI
                  q633110
BLAST score
                  477
E value
                  6.0e-48
Match length
                  118
% identity
NCBI Description (D31843) plasma membrane H+-ATPase [Oryza sativa]
Seq. No.
                  412063
Seq. ID
                  uC-osflcyp091a06a1
Method
                  BLASTX
NCBI GI
                  q82496
BLAST score
                  179
E value
                  5.0e-13
Match length
                 32
% identity
                 100
NCBI Description phenylalanine ammonia-lyase (EC 4.3.1.5) - rice
Seq. No.
                 412064
Seq. ID
                 uC-osflcyp091a06b1
Method
                 BLASTN
NCBI GI
                 q20280
BLAST score
                 91
                  5.0e-44
E value
Match length
                 119
% identity
                 94
NCBI Description Rice gene for phenylalanine ammonia-lyase (EC 4.3.1.5)
Seq. No.
                  412065
Seq. ID
                 uC-osflcyp091a07b1
Method
                 BLASTX
NCBI GI
                 g130709
BLAST score
                 158
E value
                  4.0e-11
Match length
                 37
                 78
% identity
NCBI Description
                 SERINE/THREONINE PROTEIN PHOSPHATASE PP1
                 >gi_322875_pir__S29317 phosphoprotein phosphatase (EC
                 phosphatase 1 [Zea mays]
Seq. No.
                 412066
Seq. ID
                 uC-osflcyp091a08b1
Method
                 BLASTX
NCBI GI
                 g1346057
BLAST score
                 323
                 2.0e-30
E value
                 71
Match length
% identity
                 89
NCBI Description PROTEIN KINASE G11A >gi_100705 pir B30311 protein kinase C
                 (EC 2.7.1.-) homolog - rice (fragment) >gi 169788 (J04556)
```

G11A protein [Oryza sativa]

BLAST score

313

```
Seq. No.
                   412067
Seq. ID
                   uC-osflcyp091a11a1
Method
                   BLASTN
NCBI GI
                   g633109
BLAST score
                   77
E value
                   3.0e - 35
Match length
                   160
% identity
                   88
NCBI Description Rice mRNA for plasma membrane H+-ATPase, complete cds
Seq. No.
                   412068
Seq. ID
                   uC-osflcyp091b01a1
Method
                   BLASTX
NCBI GI
                   g479406
BLAST score
                   387
E value
                   2.0e-37
Match length
                   82
% identity
                   89
NCBI Description chlorophyll a/b-binding protein - garden pea
                   >gi_20671_emb_CAA49149_ (X69215) chlorophyll a/b-binding
                   protein [Pisum sativum]
Seq. No.
                   412069
Seq. ID
                   uC-osflcyp091b01b1
Method
                   BLASTX
NCBI GI
                   g2570511
BLAST score
                   311
E value
                   5.0e-29
Match length
                   69
% identity
                   86
NCBI Description (AF022738) chlorophyll a-b binding protein [Oryza sativa]
Seq. No.
                   412070
Seq. ID
                   uC-osflcyp091b02b1
Method
                   BLASTX
NCBI GI
                   g2827699
BLAST score
                   276
E value
                   3.0e-24
Match length
                   147
% identity
                   46
NCBI Description
                  (AL021684) predicted protein [Arabidopsis thaliana]
Seq. No.
                   412071
Seq. ID
                   uC-osflcyp091b03a1
Method
                  BLASTX
NCBI GI
                   g861170
BLAST score
                   611
E value
                   1.0e-63
Match length
                  127
% identity
                   94
NCBI Description
                 (X03697) heat shock protein 70 [Zea mays]
Seq. No.
                  412072
Seq. ID
                  uC-osflcyp091b03b1
Method
                  BLASTX
NCBI GI
                  g123620
```

BLAST score

E value

174

2.0e-12

```
E value
                   4.0e-29
Match length
                   72
% identity
                   86
NCBI Description
                  HEAT SHOCK COGNATE 70 KD PROTEIN 2 >gi_100224_pir S14950
                   heat shock cognate protein 70 - tomato
                   >gi_19258_emb_CAA37971_ (X54030) heat shock protein cognate
                   70 [Lycopersicon esculentum]
Seq. No.
                   412073
Seq. ID
                   uC-osflcyp091b11a1
Method
                  BLASTX
NCBI GI
                  q3337356
BLAST score
                  176
E value
                   1.0e-12
Match length
                  49
% identity
                   73
NCBI Description (AC004481) putative protein transport protein SEC61 alpha
                  subunit [Arabidopsis thaliana]
Seq. No.
                   412074
Seq. ID
                  uC-osflcyp091c01b1
Method
                  BLASTX
NCBI GI
                  g4895241
BLAST score
                  300
E value
                  1.0e-27
Match length
                  88
% identity
                  57
NCBI Description (AC007659) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  412075
Seq. ID
                  uC-osflcyp091c03b1
Method
                  BLASTX
NCBI GI
                  g3258575
BLAST score
                  205
E value
                  2.0e-16
Match length
                  59
% identity
                  64
NCBI Description (U89959) Hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  412076
Seq. ID
                  uC-osflcyp091c04b1
Method
                  BLASTX
NCBI GI
                  q3850576
BLAST score
                  393
                  5.0e-38
E value
Match length
                  98
% identity
                  76
NCBI Description
                  (AC005278) Strong similarity to gb_U04968 nucleotide
                  excision repair protein (ERCC2) from Cricetulus grisseus.
                  [Arabidopsis thaliana]
Seq. No.
                  412077
Seq. ID
                  uC-osflcyp091c09b1
Method
                  BLASTX
NCBI GI
                  q1076809
```

53582



```
Match length
                   77
% identity
NCBI Description
Seq. No.
Seq. ID
Method
```

H+-transporting ATPase (EC 3.6.1.35) - maize

>gi 758355 emb CAA59800 (X85805) H(+)-transporting ATPase

[Zea mays]

412078

uC-osflcyp091c10a1

BLASTX NCBI GI g3287835 BLAST score 148 2.0e-09 E value Match length 86 % identity 40

NCBI Description (+)-DELTA-CADINENE SYNTHASE ISOZYME A (D-CADINENE SYNTHASE)

>gi_1002523 (U27535) (+)-delta-cadinene synthase isozyme A [Gossypium arboreum] >gi 1217956 emb CAA65289 (X96429)

(+)-delta-cadinene synthase [Gossypium arboreum]

Seq. No. 412079

Seq. ID uC-osflcyp091d01a1

Method BLASTX NCBI GI q1666234 BLAST score 167 E value 1.0e-11 Match length 32 % identity 100

NCBI Description (U76193) actin [Pisum sativum] >gi 1724143 (U81049) actin

[Pisum sativum]

Seq. No. 412080

Seq. ID uC-osflcyp091d11a1

Method BLASTN NCBI GI g5777612 BLAST score 44 E value 2.0e-15 Match length 160 % identity 82

NCBI Description Oryza sativa chromosome 4 BAC q3037-207F1 complete genome

Seq. No. 412081

Seq. ID uC-osflcyp091e01b1

Method BLASTN NCBI GI g1256711 BLAST score 58 E value 3.0e-2498 Match length 90 % identity

NCBI Description Zea mays O-methyltransferase (OMT) gene, complete cds

Seq. No. 412082

Seq. ID uC-osflcyp091e04a1

Method BLASTN NCBI GI g1785855 BLAST score 96 E value 9.0e-47 Match length 128

Match length

59

```
% identity
                  Oryza sativa mRNA for w-3 fatty acid desaturase, partial
NCBI Description
Seq. No.
                   412083
Seq. ID
                   uC-osflcyp091e10b1
Method
                   BLASTX
NCBI GI
                   q1168537
BLAST score
                   431
E value
                   1.0e-42
Match length
                   122
% identity
                   65
NCBI Description ASPARTIC PROTEINASE PRECURSOR >gi_82458_pir__JS0732
                   aspartic proteinase (EC 3.4.23.-) - rice
                   >gi_218143_dbj_BAA02242 (D12777) aspartic proteinase
                   [Oryza sativa]
Seq. No.
                   412084
Seq. ID
                  uC-osflcyp091f01b1
Method
                  BLASTX
NCBI GI
                   q5106926
BLAST score
                   319
E value
                   2.0e-29
Match length
                  116
% identity
                   59
NCBI Description (AF106930) putative translation initiation protein
                   [Medicago truncatula]
Seq. No.
                   412085
Seq. ID
                  uC-osflcyp091f04a1
Method
                  BLASTN
NCBI GI
                  g5478796
BLAST score
                  411
E value
                  0.0e + 00
Match length
                  419
% identity
                  100
NCBI Description Oryza sativa CAO mRNA for chlorophyll b synthase, partial
                  cds
Seq. No.
                  412086
Seq. ID
                  uC-osflcyp091f06a1
Method
                  BLASTN
NCBI GI
                  g169660
BLAST score
                  40
E value
                  5.0e-13
Match length
                  76
% identity
                  88
                  Parsley S-adenosylhomocysteine hydrolase (SHH) mRNA,
NCBI Description
                  complete cds
Seq. No.
                  412087
Seq. ID
                  uC-osflcyp091f07b1
Method
                  BLASTX
NCBI GI
                  g1084455
BLAST score
                  308
                  3.0e-28
E value
```

BLAST score

640

```
% identity
NCBI Description
                   peptidylprolyl isomerase (EC 5.2.1.8) Cyp2 - rice
                   >qi 600767 (L29469) cyclophilin 2 [Oryza sativa]
Seq. No.
                   412088
Seq. ID
                   uC-osflcyp091f09b1
Method
                   BLASTX
NCBI GI
                   g2832681
                   232
BLAST score
E value
                   2.0e-19
Match length
                   44
% identity
                   91
NCBI Description (AL021712) putative protein [Arabidopsis thaliana]
Seq. No.
                   412089
Seq. ID
                   uC-osflcyp091f10b1
Method
                   BLASTX
NCBI GI
                   g4490706
BLAST score
                   238
E value
                   3.0e-20
                   67
Match length
% identity
                   66
NCBI Description (AL035680) putative protein [Arabidopsis thaliana]
Seq. No.
                   412090
Seq. ID
                   uC-osflcyp091f11b1
Method
                   BLASTX
NCBI GI
                   q136632
BLAST score
                   593
E value
                   2.0e-61
Match length
                   145
% identity
NCBI Description UBIQUITIN-ACTIVATING ENZYME E1 1 >gi 100841 pir A38373
                   ubiquitin--protein ligase (EC 6.3.2.19) E1 - wheat >gi_285451_pir__A42873 ubiquitin-activating enzyme E1, UBA1
                   - Wheat >gi 170780 (M55604) ubiquitin-activating enzyme E1
                   [Triticum aestivum]
Seq. No.
                   412091
Seq. ID
                   uC-osflcyp091g07b1
Method
                   BLASTX
NCBI GI
                   g115785
BLAST score
                   227
E value
                   3.0e-19
                   46
Match length
% identity
NCBI Description
                   CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I
                   CAB-2) (LHCP) >gi_82380 pir S04028 chlorophyll a/b-binding
                   protein 2 precursor - barley >gi 18943 emb CAA31232
                   (X12735) LHC precursor protein (AA -34 to 230) [Hordeum
                   vulgare]
Seq. No.
                   412092
Seq. ID
                   uC-osflcyp091g09b1
Method
                   BLASTX
NCBI GI
                   g1087073
```

BLAST score

142

```
6.0e-67
E value
Match length
                  170
                  72
% identity
NCBI Description
                  (S79243) calmodulin-binding heat-shock protein, CaMBP
                   [Nicotiana tabacum=tobacco, Wisconsin-38, Peptide, 449 aa]
                  [Nicotiana tabacum]
                  412093
Seq. No.
Seq. ID
                  uC-osflcyp091g10a1
Method
                  BLASTX
NCBI GI
                  q1730878
BLAST score
                  245
E value
                  9.0e-21
Match length
                  130
                  43
% identity
NCBI Description
                 HYPOTHETICAL 69.1 KD PROTEIN (ORF4)
                  >gi 1200047 emb CAA64951 (X95649) function unknown
                  [Corynebacterium glutamicum]
                  412094
Seq. No.
Seq. ID
                  uC-osflcyp091h02a1
                  BLASTX
Method
                  g505136
NCBI GI
BLAST score
                  276
E value
                  2.0e-24
                  51
Match length
% identity
                  100
NCBI Description (D30794) ferredoxin [Oryza sativa]
                  412095
Seq. No.
Seq. ID
                  uC-osflcyp091h02b1
Method
                  BLASTN
NCBI GI
                  q505135
BLAST score
                  166
E value
                  2.0e-88
Match length
                  202
% identity
                  96
NCBI Description Rice gene for ferredoxin, complete cds
Seq. No.
                   412096
Seq. ID
                  uC-osflcyp091h04b1
Method
                  BLASTX
NCBI GI
                  g1709932
BLAST score
                  288
E value
                  2.0e-26
Match length
                  68
                  79
% identity
NCBI Description
                  PHOSPHORIBOSYLAMIDOIMIDAZOLE-SUCCINOCARBOXAMIDE SYNTHASE
                  PRECURSOR (SAICAR SYNTHETASE) >gi 629655 pir S45524
                   5'-phosphoribosyl-4-(N-succinocarboxamide
                  )-5-aminoimidazole synthetase - moth bean
Seq. No.
                   412097
Seq. ID
                  uC-osflcyp091h06a1
Method
                  BLASTX
NCBI GI
                  g584825
```

E value

4.0e-31

```
E value
                  8.0e-09
Match length
                  32
                  78
% identity
NCBI Description
                  B2 PROTEIN >gi 322726 pir S32124 B2 protein - carrot
                  >gi_297889_emb_CAA51078_ (X72385) B2 protein [Daucus
                  carota]
                  412098
Seq. No.
Seq. ID
                  uC-osflcyp091h07a1
Method
                  BLASTX
NCBI GI
                  q2493650
BLAST score
                  319
E value
                  2.0e-29
Match length
                  65
                  94
% identity
NCBI Description RUBISCO SUBUNIT BINDING-PROTEIN BETA SUBUNIT (60 KD
                  CHAPERONIN BETA SUBUNIT) (CPN-60 BETA)
                  >gi 1167858 emb CAA93139 (Z68903) chaperonin [Secale
                  cereale]
Seq. No.
                  412099
                  uC-osflcyp092a02b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1350548
BLAST score
                  187
E value
                  4.0e-14
                  84
Match length
% identity
                  50
NCBI Description (L47609) heat shock-like protein [Picea glauca]
Seq. No.
                  412100
Seq. ID
                  uC-osflcyp092a04b1
Method
                  BLASTX
NCBI GI
                  g1449179
BLAST score
                  344
E value
                  1.0e-32
Match length
                  94
                  71
% identity
NCBI Description (D86506) N-ethylmaleimide sensitive fusion protein
                   [Nicotiana tabacum]
Seq. No.
                   412101
Seq. ID
                  uC-osflcyp092a10b1
Method
                  BLASTX
NCBI GI
                  g312290
BLAST score
                  154
E value
                  3.0e-10
                  38
Match length
% identity
                  79
NCBI Description (X64775) ORF [Oryza sativa]
Seq. No.
                  412102
Seq. ID
                  uC-osflcyp092a12b1
Method
                  BLASTN
NCBI GI
                  g3819198
BLAST score
                  70
```

Match length 253 % identity 87 NCBI Description Hordeum vulgare partial mRNA; clone cMWG0676.rev 412103 Seq. No. Seq. ID uC-osflcyp092b02b1 Method BLASTN NCBI GI g20181 BLAST score 100 E value 2.0e-49Match length 108 98 % identity NCBI Description Rice cab2R gene for light harvesting chlorophyll a/b-binding protein 412104 Seq. No. Seq. ID uC-osflcyp092b11b1 Method BLASTX NCBI GI g132105 BLAST score 322 E value 4.0e-30 Match length 87 % identity 76 NCBI Description (RUBISCO SMALL SUBUNIT C) >gi_68094_pir__RKRZS9

RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR

ribulose-bisphosphate carboxy \overline{l} ase ($\overline{E}C$ 4 $\overline{.1}$.1.39) small chain

precursor (clone pOSSS1139) - rice >gi 218208 dbj BAA00538 (D00643) small subunit of ribulose-1,5-bisphosphate carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa] >gi 226375 prf 1508256A ribulose bisphosphate

carboxylase S [Oryza sativa]

Seq. No. 412105

Seq. ID uC-osflcyp092c01b1

Method BLASTX NCBI GI g267056 BLAST score 260 E value 2.0e-22 53 Match length 92 % identity

NCBI Description SUCROSE SYNTHASE 1 (SUCROSE-UDP GLUCOSYLTRANSFERASE 1)

>gi_100710_pir__S25526 sucrose synthase (EC 2.4.1.13) rice >gi_20374_emb_CAA78747_ (Z15028) sucrose synthase

[Oryza sativa]

Seq. No. 412106

Seq. ID uC-osflcyp092c02b1

Method BLASTX NCBI GI q2454182 BLAST score 350 E value 3.0e-33 Match length 88 % identity 77

NCBI Description (U80185) pyruvate dehydrogenase E1 alpha subunit

[Arabidopsis thaliana]

```
Seq. No.
                  412107
Seq. ID
                  uC-osflcyp092c11b1
Method
                  BLASTX
NCBI GI
                  q3582335
BLAST score
                  242
                  2.0e-20
E value
                  58
Match length
                  76
% identity
NCBI Description
                  (AC005496) unknown protein [Arabidopsis thaliana]
                  412108
Seq. No.
Seq. ID
                  uC-osflcyp092d02b1
Method
                  BLASTX
                  g3249095
NCBI GI
BLAST score
                  192
E value
                  1.0e-14
Match length
                  104
                  42
% identity
                  (AC003114) Contains similarity to dihydrofolate reductase
NCBI Description
                   (dfr1) gb_L13703 from Schizosaccharomyces pombe. ESTs
                  gb_N37567 and gb_T43002 come from this gene. [Arabidopsis
                  thaliana]
Seq. No.
                  412109
                  uC-osflcyp092e01b1
Seq. ID
Method
                  BLASTN
NCBI GI
                  q2407274
BLAST score
                  158
                  2.0e-83
E value
Match length
                  162
% identity
                  99
                  Oryza sativa lipid transfer protein LPT III mRNA, complete
NCBI Description
Seq. No.
                  412110
Seq. ID
                  uC-osflcyp092e02b1
Method
                  BLASTN
NCBI GI
                  q4097337
BLAST score
                  140
                  4.0e-73
E value
Match length
                  144
% identity
                  99
NCBI Description Oryza sativa metallothionein-like protein mRNA, complete
                  cds
Seq. No.
                  412111
Seq. ID
                  uC-osflcyp092e11b1
Method
                  BLASTX
NCBI GI
                  g1658503
BLAST score
                  156
E value
                  3.0e-10
Match length
                  89
% identity
                  40
NCBI Description (U75467) Atu [Drosophila melanogaster]
Seq. No.
                  412112
Seq. ID
                  uC-osflcyp092e12b1
```

Method

BLASTX

```
Method
                   BLASTX
NCBI GI
                    q3885334
BLAST score
                   174
E value
                   8.0e-19
Match length
                   95
% identity
                   50
NCBI Description
                   (AC005623) putative argonaute protein [Arabidopsis
Seq. No.
                   412113
Seq. ID
                   uC-osflcyp092f01b1
Method
                   BLASTX
NCBI GI
                   q3337356
BLAST score
                   528
E value
                   8.0e-54
Match length
                   114
% identity
                   91
NCBI Description
                   (AC004481) putative protein transport protein SEC61 alpha
                   subunit [Arabidopsis thaliana]
Seq. No.
                   412114
Seq. ID
                   uC-osflcyp092f10b1
Method
                   BLASTX
NCBI GI
                   q2130073
BLAST score
                   395
E value
                    1.0e-38
Match length
                   78
% identity
                   100
                   fructose-bisphosphate aldolase (EC 4.1.2.13) isoenzyme C-1, cytosolic - rice >gi_786178_dbj_BAA08845_ (D50307) aldolase
NCBI Description
                    C-1 [Oryza sativa] >gi_790970_dbj_BAA08830_ (D50301)
                   aldolase C-1 [Oryza sativa]
Seq. No.
                   412115
Seq. ID
                   uC-osflcyp092f11b1
Method
                   BLASTX
NCBI GI
                   q445613
BLAST score
                   336
E value
                   1.0e-31
                   90
Match length
                   70
% identity
NCBI Description ribosomal protein L7 [Solanum tuberosum]
                   412116
Seq. No.
Seq. ID
                   uC-osflcyp092g01b1
Method
                   BLASTX
NCBI GI
                   g2914710
BLAST score
                   193
E value
                   3.0e-15
Match length
                   65
% identity
NCBI Description
                   (AC003974) putative beta-D-galactosidase [Arabidopsis
                   thaliana]
Seq. No.
                   412117
Seq. ID
                   uC-osflcyp092g03b1
```

Method

BLASTX

```
NCBI GI
                    q1705677
 BLAST score
                    190
 E value
                    2.0e-14
                    38
 Match length
                    97
 % identity
                    CELL DIVISION CYCLE PROTEIN 48 HOMOLOG
 NCBI Description
                    >gi 2118115 pir S60112 cell division control protein CDC48
                    homolog - Arabidopsis thaliana >gi 1019904 (U37587) cell
                    division cycle protein [Arabidopsis thaliana]
                    412118
 Seq. No.
 Seq. ID
                    uC-osflcyp092g05b1
 Method
                    BLASTX
 NCBI GI
                    q4586025
 BLAST score
                    356
 E value
                    4.0e-34
 Match length
                    84
 % identity
                    83
 NCBI Description (AC007109) putative succinyl-CoA-ligase beta subunit; 5'
                    partial [Arabidopsis thaliana]
 Seq. No.
                    412119
 Seq. ID
                    uC-osflcyp092g12b1
Method
                    BLASTX
 NCBI GI
                    q2642448
 BLAST score
                    189
                    8.0e-15
 E value
 Match length
                    70
                    57
 % identity
 NCBI Description
                   (AC002391) hypothetical protein [Arabidopsis thaliana]
                    >gi_3169187_gb_AAC17830.1_ (AC004401) hypothetical protein
                    [Arabidopsis thaliana]
                    412120
 Seq. No.
 Seq. ID
                    uC-osflcyp092h01b1
                    BLASTN
 Method
 NCBI GI
                    g434786
 BLAST score
                    43
                    9.0e-15
 E value
                    67
 Match length
                    91
 % identity
 NCBI Description Crayfish mRNA for ribosomal protein, complete cds
 Seq. No.
                    412121
 Seq. ID
                    uC-osflcyp092h04b1
 Method
                    BLASTX
 NCBI GI
                    g1495768
 BLAST score
                    347
 E value
                    7.0e-33
 Match length
                    108
 % identity
                    60
 NCBI Description
                   (Z68506) chloroplast inner envelope protein, 110 kD
                    (IEP110) [Pisum sativum]
 Seq. No.
                    412122
 Seq. ID
                    uC-osflcyp092h08b1
```

```
NCBI GI
                   q462195
BLAST score
                   147
E value
                   2.0e-09
Match length
                   45
                   67
% identity
NCBI Description
                   PROTEIN TRANSLATION FACTOR SUI1 HOMOLOG (GOS2 PROTEIN)
                   >gi_100682_pir__S21636 GOS2 protein - rice
                   >gi_20238 emb_CAA36190_ (X51910) GOS2 [Oryza sativa] >gi_3789950 (AF094774) translation initiation factor [Oryza
                   satīva]
                   412123
Seq. No.
Seq. ID
                   uC-osflcyp092h10b1
Method
                   BLASTN
NCBI GI
                   q606418
BLAST score
                   88
                   4.0e-42
E value
Match length
                   92
                   99
% identity
NCBI Description Oryza Sativa (clone RGAE8) G protein alpha subunit (RGA1)
                   gene, complete cds
Seq. No.
                   412124
Seq. ID
                   uC-osflcyp093a04b1
Method
                   BLASTX
NCBI GI
                   q3023713
BLAST score
                   218
                   3.0e-18
E value
Match length
                   48
                   88
% identity
NCBI Description
                   ENOLASE (2-PHOSPHOGLYCERATE DEHYDRATASE)
                   (2-PHOSPHO-D-GLYCERATE HYDRO-LYASE) (OSE1) >gi 780372
                   (U09450) enolase [Oryza sativa]
Seq. No.
                   412125
Seq. ID
                   uC-osflcyp093a08b1
Method
                   BLASTX
NCBI GI
                   q2773154
BLAST score
                   272
E value
                   8.0e-25
Match length
                   119
% identity
                   57
                   (AF039573) abscisic acid- and stress-inducible protein
NCBI Description
                   [Oryza sativa]
Seq. No.
                   412126
Seq. ID
                   uC-osflcyp093a09b1
Method
                   BLASTX
NCBI GI
                   q129916
BLAST score
                   312
E value
                   4.0e-29
Match length
                   66
% identity
                   92
NCBI Description
                   PHOSPHOGLYCERATE KINASE, CYTOSOLIC >gi_66911_pir__TVWTGY
                   phosphoglycerate kinase (EC 2.7.2.3), cytosolic - wheat
                   >gi_21835_emb_CAA33302_ (X15232) phosphoglycerate kinase
```

(AA 1 - 401) [Triticum aestivum]

```
Seq. No.
                  412127
Seq. ID
                  uC-osflcyp093a10b1
Method
                  BLASTX
NCBI GI
                  g1170937
BLAST score
                  176
E value
                  2.0e-21
Match length
                  92
% identity
                  69
NCBI Description S-ADENOSYLMETHIONINE SYNTHETASE 1 (METHIONINE
                  ADENOSYLTRANSFERASE 1) (ADOMET SYNTHETASE 1)
                  >gi_450549_emb_CAA81481_ (Z26867) S-adenosyl methionine
                  synthetase [Oryza sativa]
Seq. No.
                  412128
Seq. ID
                  uC-osflcyp093a11b1
Method
                  BLASTX
NCBI GI
                  g1353193
BLAST score
                  204
E value
                  1.0e-16
Match length
                  56
                  73
% identity
NCBI Description O-METHYLTRANSFERASE ZRP4 (OMT) >gi_542186_pir__JQ2268
                  O-methyltransferase (EC 2.1.1.-) - maize >gi_404070
                  (L14063) O-methyltransferase [Zea mays]
Seq. No.
                  412129
Seq. ID
                  uC-osflcyp093b01b1
Method
                  BLASTX
NCBI GI
                  g2613143
BLAST score
                  313
E value
                  3.0e-30
Match length
                  79
% identity
                  87
NCBI Description (AF030548) tubulin [Oryza sativa]
Seq. No.
                  412130
Seq. ID
                  uC-osflcyp093b03b1
Method
                  BLASTX
NCBI GI
                  g3126854
BLAST score
                  234
E value
                  4.0e-20
Match length
                  49
% identity
NCBI Description (AF061577) chlorophyll a/b binding protein [Oryza sativa]
Seq. No.
                  412131
Seq. ID
                  uC-osflcyp093b05b1
Method
                  BLASTX
NCBI GI
                  g132096
BLAST score
                  165
                  3.0e-11
E value
Match length
                  41
                  85
% identity
NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN A PRECURSOR
                  (RUBISCO SMALL SUBUNIT A) >gi_68095_pir RKRZS6
```

ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain

```
precursor (clone pOSSS2106) - rice >gi_218210_dbj_BAA00539_
  (D00644) small subunit of ribulose-1,5-bisphosphate
  carboxylase (RuBPC) [Oryza sativa]
412132
uC-osflcyp093b07b1
```

Seq. ID uC-osflcy
Method BLASTX
NCBI GI g2827711
BLAST score 308
E value 3.0e-28
Match length 111
% identity 52

Seq. No.

NCBI Description (AL021684) oxoglutarate dehydrogenase - like protein

[Arabidopsis thaliana]

Seq. No. 412133

Seq. ID uC-osflcyp093b08b1

Method BLASTX
NCBI GI g1743277
BLAST score 324
E value 1.0e-30
Match length 66
% identity 94

NCBI Description (Y09741) beta-tubulin 1 [Hordeum vulgare]

Seq. No. 412134

Seq. ID uC-osflcyp093c02b1

Method BLASTX
NCBI GI g4580389
BLAST score 187
E value 4.0e-14
Match length 75
% identity 51

NCBI Description (AC007171) unknown protein [Arabidopsis thaliana]

Seq. No. 412135

Seq. ID uC-osflcyp093c08b1

Method BLASTX
NCBI GI g322854
BLAST score 355
E value 6.0e-34
Match length 74
% identity 95

NCBI Description pollen-specific protein - rice >gi_20310_emb_CAA78897_

(Z16402) pollen specific gene [Oryza sativa]

Seq. No. 412136

Seq. ID uC-osflcyp093c10b1

Method BLASTX
NCBI GI g2662343
BLAST score 208
E value 9.0e-17
Match length 42
% identity 98

NCBI Description (D63581) EF-1 alpha [Oryza sativa]

Seq. No. 412137

```
uC-osflcyp093c11b1
Seq. ID
Method
                  BLASTN
                  a6013288
NCBI GI
BLAST score
                  57
                  8.0e-24
E value
                  93
Match length
                  39
% identity
NCBI Description Oryza sativa polyubiquitin (RUBQ1) gene, complete cds
                  412138
Seq. No.
                  uC-osflcyp093d06b1
Seq. ID
Method
                  BLASTN
                  g1136123
NCBI GI
                  45
BLAST score
                  7.0e-16
E value
Match length
                  65
                  92
% identity
NCBI Description O.sativa mRNA for alpha-tubulin (clone OSTA-274)
                  412139
Seq. No.
                  uC-osflcyp093d10b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3776001
BLAST score
                  177
                   6.0e-13
E value
Match length
                  44
                   80
% identity
NCBI Description (AJ010464) RNA helicase [Arabidopsis thaliana]
                   412140
Seq. No.
Seq. ID
                   uC-osflcyp093e03b1
Method
                  BLASTX
NCBI GI
                   q1052960
BLAST score
                   705
E value
                   1.0e-74
Match length
                   141
% identity
                   91
NCBI Description (U37437) PNIL34 [Ipomoea nil]
Seq. No.
                   412141
Seq. ID
                   uC-osflcyp093e06b1
Method
                   BLASTX
NCBI GI
                   g1167836
BLAST score
                   465
                   2.0e-46
E value
Match length
                   128
% identity
                   62
                  (Z68893) protein with incomplete signal sequence [Holcus
NCBI Description
                   lanatus]
Seq. No.
                   412142
Seq. ID
                   uC-osflcyp093e10b1
                   BLASTN
Method
NCBI GI
                   g20280
BLAST score
                   113
E value
                   4.0e-57
Match length
                   121
```

```
% identity
NCBI Description Rice gene for phenylalanine ammonia-lyase (EC 4.3.1.5)
                  412143
Seq. No.
Seq. ID
                  uC-osflcyp093f01b1
                  BLASTN
Method
                  q20181
NCBI GI
BLAST score
                  94
E value
                  8.0e-46
                  106
Match length
                  97
% identity
NCBI Description
                  Rice cab2R gene for light harvesting chlorophyll
                  a/b-binding protein
Seq. No.
                  412144
                  uC-osflcyp093f05b1
Seq. ID
Method
                  BLASTX
                  g5802606
NCBI GI
                  569
BLAST score
E value
                  8.0e-59
Match length
                  122
                  84
% identity
NCBI Description
                  (AF174486) methylenetetrahydrofolate reductase [Zea mays]
Seq. No.
                  412145
                  uC-osflcyp093f06b1
Seq. ID
Method
                  BLASTN
NCBI GI
                  q6041757
                  251
BLAST score
                  1.0e-139
E value
Match length
                  295
                   96
% identity
                  Genomic Sequence For Oryza sativa Clone 10P20, Lemont
NCBI Description
                  Strain, Complete Sequence, complete sequence
Seq. No.
                   412146
Seq. ID
                  uC-osflcyp093f10b1
Method
                  BLASTN
NCBI GI
                   g5091597
BLAST score
                   38
E value
                   5.0e-12
                  38
Match length
% identity
                   100
NCBI Description Oryza sativa chromosome 1 BAC 10A19I, complete sequence
Seq. No.
                   412147
Seq. ID
                  uC-osflcyp093f11b1
Method
                  BLASTX
NCBI GI
                  q2407617
BLAST score
                  293
E value
                   4.0e-31
                  137
Match length
                   55
% identity
                  (AF017984) glutathione synthetase [Lycopersicon esculentum]
NCBI Description
Seq. No.
                   412148
Seq. ID
                  uC-osflcyp093g01b1
```

```
Method
                  BLASTN
NCBI GI
                  g218171
BLAST score
                  123
E value
                  6.0e-63
Match length
                  179
                  93
% identity
                  Oryza sativa mRNA for type I light-harvesting chlorophyll
NCBI Description
                  a/b binding protein of photosystem II (LHCPII), complete
Seq. No.
                  412149
Seq. ID
                  uC-osflcyp093g07b1
Method
                  BLASTX
NCBI GI
                  q322854
BLAST score
                  426
                  4.0e-42
E value
Match length
                  88
                  94
% identity
                  pollen-specific protein - rice >gi_20310_emb CAA78897_
NCBI Description
                  (Z16402) pollen specific gene [Oryza sativa]
                  412150
Seq. No.
Seq. ID
                  uC-osflcyp093g10b1
Method
                  BLASTN
NCBI GI
                  q3885887
BLAST score
                  45
E value
                  8.0e-17
Match length
                  69
% identity
                  91
NCBI Description Oryza sativa high mobility group protein (HMG) mRNA,
                  complete cds
Seq. No.
                   412151
Seq. ID
                  uC-osflcyp093g12b1
Method
                  BLASTN
NCBI GI
                  g4426561
BLAST score
                  55
E value
                  1.0e-22
                  83
Match length
                  92
% identity
NCBI Description Oryza sativa mRNA for chitinase IIb, complete cds
                   412152
Seq. No.
Seq. ID
                  uC-osflcyp093h01b1
Method
                  BLASTX
NCBI GI
                  g5103831
                  159
BLAST score
                   7.0e-11
E value
                  59
Match length
% identity
                  (AC007591) ESTs gb_H37032, gb_R6425, gb_Z34651, gb_N37268,
NCBI Description
                   gb_AA713172 and gb_Z34241 come from this gene. [Arabidopsis
                   thaliana]
                   412153
Seq. No.
Seq. ID
                   uC-osflcyp093h03b1
```

BLASTN

Method

q2293565 NCBI GI BLAST score 50 E value 1.0e-19 Match length 50 100 % identity Oryza sativa ADP-ribosylation factor 1 (Os-ARF1) mRNA, NCBI Description complete cds Seq. No. 412154 Seq. ID uC-osflcyp093h04b1 Method BLASTX NCBI GI q2286153 BLAST score 355 7.0e - 34E value Match length 75 93 % identity (AF007581) cytoplasmic malate dehydrogenase [Zea mays] NCBI Description 412155 Seq. No. Seq. ID uC-osflcyp095a01a1 Method BLASTN NCBI GI g1107460 BLAST score 130 E value 4.0e-67 Match length 138 % identity 99 NCBI Description Rice mRNA for aspartate kinase-homoserine dehydrogenase, complete cds Seq. No. 412156 Seq. ID uC-osflcyp095a01b1 Method BLASTN NCBI GI g1107460 BLAST score 49 E value 9.0e-19 69 Match length 93 % identity NCBI Description Rice mRNA for aspartate kinase-homoserine dehydrogenase, complete cds 412157 Seq. No. Seq. ID uC-osflcyp095a02a1 Method BLASTN NCBI GI g287398 BLAST score 128 E value 2.0e-65 232 Match length 88 % identity NCBI Description Oryza sativa mRNA for chilling tolerance related protein, complete cds, clone:pBC591

Seq. No. 412158

Seq. ID uC-osflcyp095a02b1

Method BLASTX
NCBI GI g729206
BLAST score 324
E value 3.0e-30

Match length 64 100 % identity NCBI Description PROBABLE GLUTATHIONE S-TRANSFERASE (28 KD COLD-INDUCED PROTEIN) >gi_287399_dbj_BAA01632_ (D10861) chilling tolerance related protein [Oryza sativa] >gi 445133 prf 1908434C chilling tolerance-related protein:ISOTYPE=pBC591 [Oryza sativa] Seq. No. 412159 Seq. ID uC-osflcyp095a03a1 Method BLASTN NCBI GI q5734616 BLAST score 55 5.0e-22 E value Match length 83 92 % identity NCBI Description Oryza sativa genomic DNA, chromosome 6, clone:P0538C01 412160 Seq. No. Seq. ID uC-osflcyp095a04a1 Method BLASTN q3885887 NCBI GI BLAST score 275 E value 1.0e-153 Match length 294 % identity 99 NCBI Description Oryza sativa high mobility group protein (HMG) mRNA, complete cds 412161 Seq. No. Seq. ID uC-osflcyp095a04b1 Method BLASTX NCBI GI g3885888 BLAST score 303 E value 2.0e-27 Match length 106 % identity 63 NCBI Description (AF093632) high mobility group protein [Oryza sativa] Seq. No. 412162 Seq. ID uC-osflcyp095a07a1 Method BLASTX NCBI GI g1170937 BLAST score 162 E value 1.0e-14 Match length 44 95 % identity S-ADENOSYLMETHIONINE SYNTHETASE 1 (METHIONINE NCBI Description

ADENOSYLTRANSFERASE 1) (ADOMET SYNTHETASE 1)

>gi 450549 emb CAA81481 (Z26867) S-adenosyl methionine

synthetase [Oryza sativa]

412163 Seq. No.

Seq. ID uC-osflcyp095a07b1

Method BLASTX NCBI GI g1170937 BLAST score 604

7.0e-63

E value 7.0e-63 Match length 116 % identity 100

NCBI Description S-ADENOSYLMETHIONINE SYNTHETASE 1 (METHIONINE ADENOSYLTRANSFERASE 1) (ADOMET SYNTHETASE 1)

>gi_450549_emb_CAA81481_ (Z26867) S-adenosyl methionine

synthetase [Oryza sativa]

Seq. No. 412164

Seq. ID uC-osflcyp095a08b1

Method BLASTN
NCBI GI g5852170
BLAST score 41
E value 1.0e-13
Match length 49
% identity 96

NCBI Description Oryza sativa indica(GLA4) genomic DNA, chromosome 4, BAC

clone:t17804

Seq. No. 412165

Seq. ID uC-osflcyp095a10b1

Method BLASTX
NCBI GI g3335341
BLAST score 324
E value 5.0e-30
Match length 138
% identity 54

NCBI Description (AC004512) T8F5.10 [Arabidopsis thaliana]

Seq. No. 412166

Seq. ID uC-osflcyp095a12b1

Method BLASTX
NCBI GI g3790188
BLAST score 207
E value 1.0e-16
Match length 67
% identity 63

NCBI Description (Y14431) NAD-dependent isocitrate dehydrogenase [Nicotiana

tabacum]

Seq. No. 412167

Seq. ID uC-osflcyp095b02a1

Method BLASTN
NCBI GI g20163
BLAST score 81
E value 2.0e-37
Match length 292
% identity 84

NCBI Description O.sativa Rrl5 mRNA for 5S ribosomal RNA

Seq. No. 412168

Seq. ID uC-osflcyp095b02b1

Method BLASTX
NCBI GI g542157
BLAST score 610
E value 1.0e-63
Match length 129



% identity 90

ribosomal 5S RNA-binding protein - Rice NCBI Description

412169 Seq. No.

uC-osflcyp095b03b1 Seq. ID

BLASTX Method q3757514 NCBI GI 413 BLAST score 2.0e-40 E value 102 Match length 79 % identity

(AC005167) putative plasma membrane intrinsic protein NCBI Description

[Arabidopsis thaliana]

>gi_4581129_gb_AAD24619.1_AC005825_26 (AC005825) putative plasma membrane intrinsic protein [Arabidopsis thaliana]

412170 Seq. No.

uC-osflcyp095b11b1 Seq. ID

Method BLASTX q2317901 NCBI GI 148 BLAST score 6.0e-10 E value Match length 38 68 % identity

(U89959) Similar to vesicle transport protein, PIR NCBI Description

Accession Number A55931 [Arabidopsis thaliana]

Seq. No. 412171

uC-osflcyp095b12a1 Seq. ID

BLASTX Method g5921187 NCBI GI 209 BLAST score 2.0e-16 E value 65 Match length 57 % identity

CYTOCHROME P450 71C2 >gi_550438_emb_CAA57423_ (X81829) cytochrome P450 [Zea mays] >gi_1870201_emb_CAA72208_ NCBI Description

(Y11404) cytochrome p450 [Zea mays]

412172 Seq. No.

uC-osflcyp095b12b1 Seq. ID

BLASTX Method NCBI GI q5921189 167 BLAST score 1.0e-11 E value 101 Match length % identity

CYTOCHROME P450 71C4 >gi_550542_emb_CAA57425_ (X81831) NCBI Description

cytochrome P450 [Zea mays] >gi_1850903_emb_CAA72196

(Y11368) cytochrome p450 [Zea mays]

412173 Seq. No.

uC-osflcyp095c02b1 Seq. ID

BLASTX Method g2459420 NCBI GI 483 BLAST score 2.0e-53 E value

```
Match length
                  122
                  89
% identity
                  (AC002332) putative ribosomal protein L17 [Arabidopsis
NCBI Description
                  thaliana]
                  412174
Seq. No.
                  uC-osflcyp095c11b1
Seq. ID
                  BLASTX
Method
NCBI GI
                  q4836901
                  239
BLAST score
E value
                  2.0e-20
Match length
                  66
% identity
                  71
                  (AC007369) Unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  412175
                  uC-osflcyp095c12a1
Seq. ID
                  BLASTN
Method
                  q5051932
NCBI GI
BLAST score
                  189
                  1.0e-102
E value
                  255
Match length
                  99
% identity
NCBI Description Oryza sativa MADS-box protein FDRMADS8 mRNA, complete cds
Seq. No.
                  412176
                  uC-osflcyp095d12b1
Seq. ID
                  BLASTX
Method
NCBI GI
                  g2827709
BLAST score
                  444
E value
                  3.0e-44
Match length
                  111
% identity
                  79
NCBI Description (AL021684) predicted protein [Arabidopsis thaliana]
Seq. No.
                  412177
Seq. ID
                  uC-osflcyp095e01a1
Method
                  BLASTX
NCBI GI
                  q3386621
BLAST score
                  157
                   2.0e-10
E value
Match length
                  36
                   81
% identity
NCBI Description (AC004665) unknown protein [Arabidopsis thaliana]
Seq. No.
                   412178
                  uC-osflcyp095e01b1
Seq. ID
                  BLASTX
Method
                  g3386621
NCBI GI
BLAST score
                  621
                  1.0e-64
E value
                  158
Match length
% identity
NCBI Description (AC004665) unknown protein [Arabidopsis thaliana]
Seq. No.
                   412179
Seq. ID
                   uC-osflcyp095f11a1
```

Match length

177

BLASTX Method NCBI GI q5081779 153 BLAST score 7.0e-20 E value Match length 72 74 % identity NCBI Description (AF150630) cellulose synthase [Gossypium hirsutum] 412180 Seq. No. uC-osflcyp095f11b1 Seq. ID BLASTX Method g4886756 NCBI GI BLAST score 165 5.0e-12E value 40 Match length % identity 80 (AF088917) cellulose synthase catalytic subunit NCBI Description [Arabidopsis thaliana] 412181 Seq. No. uC-osflcyp095f12b1 Seq. ID Method BLASTN g2293479 NCBI GI 65 BLAST score .1.0e-28 E value 101 Match length % identity NCBI Description Oryza sativa glycine-rich protein mRNA, complete cds 412182 Seq. No. Seq. ID uC-osflcyp095g01b1 BLASTX Method NCBI GI g2407281 BLAST score 637 E value 1.0e-66 Match length 132 % identity 93 NCBI Description (AF017363) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa] Seq. No. 412183 uC-osflcyp095h01b1 Seq. ID Method BLASTX NCBI GI g3298540 BLAST score 142 E value 3.0e-09 30 Match length 83 % identity NCBI Description (AC004681) unknown protein [Arabidopsis thaliana] 412184 Seq. No. uC-osflcyp095h02a1 Seq. ID BLASTN Method NCBI GI g1574943 BLAST score 77 E value 2.0e-35



% identity 87

NCBI Description Oryza sativa polyubiquitin (Rubq1) mRNA, complete cds

Seq. No. 412185

Seq. ID uC-osflcyp095h03b1

Method BLASTX
NCBI GI g133867
BLAST score 427
E value 4.0e-42
Match length 103
% identity 82

NCBI Description 40S RIBOSOMAL PROTEIN S11 >gi_82722_pir__S16577 ribosomal

protein S11 - maize >gi_22470_emb_CAA39438_ (X55967)

ribosomal protein S11 [Zea mays]

Seq. No. 412186

Seq. ID uC-osflcyp095h04b1

Method BLASTX
NCBI GI 94455232
BLAST score 158
E value 6.0e-11
Match length 37
% identity 76

NCBI Description (AL035523) putative protein [Arabidopsis thaliana]

Seq. No. 412187

Seq. ID uC-osflcyp095h05b1

Method BLASTX
NCBI GI g2865175
BLAST score 334
E value 1.0e-31
Match length 112
% identity 63

NCBI Description (AB010945) AtRer1A [Arabidopsis thaliana]

>gi 4914434 emb CAB43637.1 (AL050351) AtRer1A [Arabidopsis

thaliana]

Seq. No. 412188

Seq. ID uC-osflcyp096a02b1

Method BLASTX
NCBI GI 94895182
BLAST score 170
E value 2.0e-12
Match length 62
% identity 56

NCBI Description (AC007661) unknown protein [Arabidopsis thaliana]

Seq. No. 412189

Seq. ID uC-osflcyp096b01a1

Method BLASTN
NCBI GI g2613142
BLAST score 105
E value 3.0e-52
Match length 137
% identity 96

NCBI Description Oryza sativa tubulin (RiP3) mRNA, complete cds

BLAST score

379

```
Seq. No.
                  412190
Seq. ID
                  uC-osflcyp096b01b1
Method
                  BLASTX
NCBI GI
                  g1136120
BLAST score
                  203
                  2.0e-16
E value
Match length
                  41
                  93
% identity
NCBI Description (X91806) alpha-tubulin [Oryza sativa]
Seq. No.
                  412191
Seq. ID
                  uC-osflcyp096b03b1
Method
                  BLASTX
NCBI GI
                  q3913427
BLAST score
                  328
                  1.0e-30
E value
Match length
                  74
                  82
% identity
                  S-ADENOSYLMETHIONINE DECARBOXYLASE PROENZYME (ADOMETDC)
NCBI Description
                  (SAMDC) >gi_1532073_emb_CAA69075_ (Y07767)
                  S-adenosylmethionine decarboxylase [Zea mays]
Seq. No.
                  412192
Seq. ID
                  uC-osflcyp096b11b1
Method
                  BLASTN
                  g5257255
NCBI GI
BLAST score
                  53
                  3.0e-21
E value
Match length
                  85
                  91
% identity
NCBI Description Oryza sativa genomic DNA, chromosome 8, clone:P0026F07
Seq. No.
                  412193
Seq. ID
                  uC-osflcyp096b12b1
Method
                  BLASTX
NCBI GI
                  g4063821
BLAST score
                  546
E value
                  5.0e-56
Match length
                  111
% identity
                  94
NCBI Description (AB015204) plastidic ATP sulfurylase [Oryza sativa]
Seq. No.
                  412194
Seq. ID
                  uC-osflcyp096c01b1
Method
                  BLASTX
NCBI GI
                  g3168840
BLAST score
                  154
                  4.0e-10
E value
Match length
                  66
% identity
NCBI Description (U88711) copper homeostasis factor [Arabidopsis thaliana]
                  412195
Seq. No.
Seq. ID
                  uC-osflcyp096c11b1
Method
                  BLASTX
NCBI GI
                  g4914414
```



E value 2.0e-36 Match length 115 % identity 67

NCBI Description (AL050352) Ca2+-transporting ATPase-like protein

[Arabidopsis thaliana]

Seq. No. 412196

Seq. ID uC-osflcyp096d10b1

Method BLASTX
NCBI GI g1174592
BLAST score 226
E value 4.0e-19
Match length 43
% identity 93

NCBI Description TUBULIN ALPHA-1 CHAIN >gi 2119270 pir S60233 alpha-tubulin

- garden pea >gi 525332 (U12589) alpha-tubulin [Pisum

sativum]

Seq. No. 412197

Seq. ID uC-osflcyp096d11b1

Method BLASTX
NCBI GI g1352461
BLAST score 190
E value 9.0e-15
Match length 80
% identity 57

NCBI Description IN2-2 PROTEIN

Seq. No. 412198

Seq. ID uC-osflcyp096d12b1

Method BLASTX
NCBI GI g4467119
BLAST score 558
E value 2.0e-57
Match length 115
% identity 89

NCBI Description (AL035538) Histone deacetylase [Arabidopsis thaliana]

Seq. No. 412199

Seq. ID uC-osflcyp096e01a1

Method BLASTN
NCBI GI g4091009
BLAST score 81

E value 5.0e-38 Match length 101 95

NCBI Description Oryza sativa anther-specific protein gene, complete cds

Seq. No. 412200

Seq. ID uC-osflcyp096e01b1

Method BLASTN
NCBI GI 94091009
BLAST score 181
E value 3.0e-97
Match length 189
% identity 99

NCBI Description Oryza sativa anther-specific protein gene, complete cds

Method

NCBI GI BLAST score

E value

BLASTX q1170937

3.0e-64

616

412201 Seq. No. Seq. ID uC-osflcyp096e02a1 Method BLASTN NCBI GI g607894 BLAST score 125 E value 4.0e-64 Match length 133 % identity 99 NCBI Description Oryza sativa IR54 anther specific (RTS2) gene, complete cds Seq. No. 412202 Seq. ID uC-osflcyp096e02b1 Method BLASTN NCBI GI q607894 BLAST score 92 E value 3.0e-44Match length 179 % identity 97 NCBI Description Oryza sativa IR54 anther specific (RTS2) gene, complete cds Seq. No. 412203 Seq. ID uC-osflcyp096e10b1 Method BLASTN NCBI GI g5821066 BLAST score 96 E value 2.0e-46 Match length 320 % identity 86 NCBI Description Oryza sativa gene for WHO4, complete cds Seq. No. 412204 Seq. ID uC-osflcyp096e11b1 Method BLASTX NCBI GI g3757521 BLAST score 213 E value 4.0e-17 Match length 107 % identity 42 NCBI Description (AC005167) unknown protein [Arabidopsis thaliana] Seq. No. 412205 Seq. ID uC-osflcyp096e12b1 Method BLASTX NCBI GI g2253411 BLAST score 230 E value 5.0e-19 Match length 81 % identity NCBI Description (AF007219) PP2A inhibitor [Tetraodon fluviatilis] Seq. No. 412206 Seq. ID uC-osflcyp096f02b1

BLAST score

E value

160

2.0e-11

```
Match length
                  125
% identity
                  95
NCBI Description
                  S-ADENOSYLMETHIONINE SYNTHETASE 1 (METHIONINE
                  ADENOSYLTRANSFERASE 1) (ADOMET SYNTHETASE 1)
                  >gi_450549_emb_CAA81481 (Z26867) S-adenosyl methionine
                  synthetase [Oryza sativa]
Seq. No.
                  412207
Seq. ID
                  uC-osflcyp096f11a1
Method
                  BLASTX
NCBI GI
                  q1747296
BLAST score
                  196
E value
                  5.0e-15
Match length
                  38
% identity
                  100
NCBI Description
                  (D45384) vacuolar H+-pyrophosphatase [Oryza sativa]
                  >gi 3298476 dbj BAA31524 (AB012766) ovp2 [Oryza sativa]
Seq. No.
                  412208
Seq. ID
                  uC-osflcyp096f11b1
Method
                  BLASTX
NCBI GI
                  q1747296
BLAST score
                  528
E value
                  4.0e-58
Match length
                  125
% identity
                  98
NCBI Description
                  (D45384) vacuolar H+-pyrophosphatase [Oryza sativa]
                  >gi_3298476_dbj_BAA31524 (AB012766) ovp2 [Oryza sativa]
Seq. No.
                  412209
Seq. ID
                  uC-osflcyp096g12b1
Method
                  BLASTX
NCBI GI
                  g2454182
BLAST score
                  153
                  2.0e-10
E value
Match length
                  32
% identity
                  91
NCBI Description
                 (U80185) pyruvate dehydrogenase E1 alpha subunit
                  [Arabidopsis thaliana]
Seq. No.
                  412210
Seq. ID
                  uC-osflcyp096h01b1
Method
                  BLASTX
NCBI GI
                  g5139697
BLAST score
                  407
E value
                  1.0e-39
Match length
                  104
                  82
% identity
NCBI Description
                  (AB029148) expressed in cucumber hypocotyls [Cucumis
                  sativus]
Seq. No.
                  412211
Seq. ID
                  uC-osflcyp096h04b1
Method
                  BLASTX
NCBI GI
                  g2130069
```

```
Match length
                  60
                  58
% identity
NCBI Description
                  catalase (EC 1.11.1.6) catA - rice
                  >gi 1261858 dbj BAA06232 (D29966) catalase [Oryza sativa]
Seq. No.
Seq. ID
                  uC-osflcyp096h07a1
Method
                  BLASTN
NCBI GI
                  g1136121
BLAST score
                  234
E value
                  1.0e-129
Match length
                  294
% identity
                  95
NCBI Description O.sativa mRNA for alpha-tubulin (clone OSTA-136)
Seq. No.
                  412213
Seq. ID
                  uC-osflcyp096h07b1
Method
                  BLASTX
NCBI GI
                  g1136122
BLAST score
                  555
E value
                  8.0e-63
Match length
                  123
% identity
                  97
NCBI Description (X91807) alfa-tubulin [Oryza sativa]
Seq. No.
                  412214
Seq. ID
                  uC-osflcyp096h08b1
Method
                  BLASTX
NCBI GI
                  g544242
BLAST score
                  387
E value
                  2.0e-37
Match length
                  85
                  87
% identity
NCBI Description
                  ENDOPLASMIN HOMOLOG PRECURSOR (GRP94 HOMOLOG)
                  >gi_485498_pir_ S33533 heat shock protein 90 homolog
                  precursor - barley >gi_22652_emb_CAA48143_ (X67960) GRP94
                  homologue [Hordeum vulgare]
Seq. No.
                  412215
Seq. ID
                  uC-osflcyp096h11a1
Method
                  BLASTN
NCBI GI
                  g2239152
BLAST score
                  241
E value
                  1.0e-133
                  365
Match length
% identity
                  92
NCBI Description O.sativa mRNA for putative T3/T7-like RNA polymerase,
                  partial
Seq. No.
                  412216
Seq. ID
                  uC-osflcyp096h12a1
                  BLASTN
Method
NCBI GI
                  g2239152
BLAST score
                  143
E value
                  2.0e-74
Match length
                  206
% identity
                  95
```

```
NCBI Description O.sativa mRNA for putative T3/T7-like RNA polymerase,
                   partial
                   412217
Seq. No.
Seq. ID
                   uC-osflcyp096h12b1
Method
                   BLASTN
NCBI GI
                   g2239152
BLAST score
                   119
E value
                   1.0e-60
Match length
                   127
% identity
                   98
NCBI Description O.sativa mRNA for putative T3/T7-like RNA polymerase,
                   partial
Seq. No.
                   412218
                   uC-osflcyp097a01b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   q3790441
BLAST score
                   519
E value
                   8.0e-53
Match length
                   140
% identity
NCBI Description (AF030515) chaperonin 60 alpha subunit [Canavalia lineata]
Seq. No.
                   412219
Seq. ID
                   uC-osflcyp097a04b1
Method
                   BLASTX
NCBI GI
                   q543711
BLAST score
                   492
E value
                   1.0e-49
Match length
                   101
% identity
                   100
                  14-3-3-LIKE PROTEIN S94 >gi_419796_pir__S30927 14-3-3 protein homolog - rice >gi_303859_dbj_BAA03711_ (D16140)
NCBI Description
                   brain specific protein [Oryza sativa]
Seq. No.
                   412220
Seq. ID
                   uC-osflcyp097a06b1
Method
                   BLASTX
NCBI GI
                   g2072555
BLAST score
                   320
E value
                   2.0e-29
Match length
                   62
% identity
                   92
NCBI Description
                   (AF001396) metallothionein-like protein [Oryza sativa]
                   >gi 6103441 gb AAF03603.1 (AF147786) metallothionein-like
                   protein [Oryza sativa]
Seq. No.
                   412221
Seq. ID
                   uC-osflcyp097a07b1
Method
                   BLASTX
NCBI GI
                   g3184283
BLAST score
                   463
E value
                   3.0e-46
Match length
                   125
% identity
```

NCBI Description (AC004136) putative TBP-binding protein [Arabidopsis

thaliana]

```
Seq. No.
                  412222
Seq. ID
                  uC-osflcyp097a08b1
Method
                  BLASTX
NCBI GI
                  g82734
BLAST score
                  694
E value
                  2.0e-73
Match length
                  139
% identity
                  30
NCBI Description ubiquitin precursor - maize (fragment)
                  >gi 226763 prf 1604470A poly-ubiquitin [Zea mays]
                  412223
Seq. No.
Seq. ID
                  uC-osflcyp097b02b1
Method
                  BLASTX
NCBI GI
                  g4680212
BLAST score
                  157
E value
                  2.0e-10
Match length
                  40
% identity
                  78
NCBI Description (AF114171) hypothetical protein [Sorghum bicolor]
Seq. No.
                  412224
Seq. ID
                  uC-osflcyp097b03b1
Method
                  BLASTX
NCBI GI
                  g5732069
BLAST score
                  304
E value
                  1.0e-27
Match length
                  156
                  50
% identity
NCBI Description
                 (AF147263) contains similarity to Pfam family PF00036 - EF
                  hand; score=11.7, E=0.66, N=1 [Arabidopsis thaliana]
Seq. No.
                  412225
Seq. ID
                  uC-osflcyp097b05b1
Method
                  BLASTX
NCBI GI
                  g140503
BLAST score
                  403
E value
                  3.0e - 39
Match length
                  96
% identity
NCBI Description
                 HYPOTHETICAL 14 KD PROTEIN IN TRNI INTRON (ORF 133)
                  >gi_82518_pir__JQ0279 hypothetical 14.5K protein (trnI
                  intron) - rice chloroplast >gi_12041_emb_CAA33945_ (X15901)
                  ORF133; ORF within trnI intron [Oryza sativa]
                  >gi_12061_emb_CAA33915 (X15901) ORF133; ORF within trnI
                  intron [Oryza sativa] >gi 226660 prf 1603356CL trnI intron
                  ORF 133 [Oryza sativa]
Seq. No.
                  412226
Seq. ID
                  uC-osflcyp097b07b1
Method
                  BLASTX
NCBI GI
                  q461753
BLAST score
                  181
E value
                  2.0e-13
Match length
                  56
```



% identity 66

NCBI Description ATP-DEPENDENT CLP PROTEASE ATP-BINDING SUBUNIT CLPA HOMOLOG

PRECURSOR >gi 419773 pir S31164 ATP-dependent ClpB

proteinase regulatory chain homolog precursor, chloroplast
- garden pea >gi_169128 (L09547) nuclear encoded precursor

to chloroplast protein [Pisum sativum]

Seq. No. 412227

Seq. ID uC-osflcyp097b08b1

Method BLASTX
NCBI GI g461753
BLAST score 211
E value 2.0e-17
Match length 68
% identity 69

NCBI Description ATP-DEPENDENT CLP PROTEASE ATP-BINDING SUBUNIT CLPA HOMOLOG

PRECURSOR >gi_419773_pir__S31164 ATP-dependent ClpB

proteinase regulatory chain homolog precursor, chloroplast - garden pea >gi_169128 (L09547) nuclear encoded precursor

to chloroplast protein [Pisum sativum]

Seq. No. 412228

Seq. ID uC-osflcyp097b10b1

Method BLASTX
NCBI GI g121349
BLAST score 699
E value 6.0e-77
Match length 145
% identity 91

NCBI Description GLUTAMINE SYNTHETASE SHOOT ISOZYME (GLUTAMATE--AMMONIA

LIGASE) (CLONE LAMBDA-GS28) >gi 20368 emb CAA32461

(X14245) cytosolic glutamine synthetase (AA 1-356) [Oryza

sativa]

Seq. No. 412229

Seq. ID uC-osflcyp097b11b1

Method BLASTX
NCBI GI g6017117
BLAST score 214
E value 3.0e-17
Match length 99
% identity 42

NCBI Description (AC009895) unknown protein [Arabidopsis thaliana]

>gi 6091765 gb AAF03475.1 AC009327 14 (AC009327) unknown

protein [Arabidopsis thaliana]

Seq. No. 412230

Seq. ID uC-osflcyp097b12b1

Method BLASTX
NCBI GI g3004565
BLAST score 331
E value 2.0e-31
Match length 72
% identity 43

NCBI Description (AC003673) putative protein kinase [Arabidopsis thaliana]

Seq. No. 412231

```
uC-osflcyp097c01b1
Seq. ID
                  BLASTX
Method
NCBI GI
                  q1498390
BLAST score
                  818
                  7.0e-88
E value
Match length
                  159
                  98
% identity
                  (U60511) actin [Zea mays]
NCBI Description
                  412232
Seq. No.
                  uC-osflcyp097c02b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2130080
                  197
BLAST score
E value
                  9.0e-16
Match length
                  61
                  56
% identity
                  Nramp1 protein - rice >gi 1470320 bbs 177441 (S81897)
NCBI Description
                   OsNramp1=Nramp1 homolog/Bcg product homolog [Oryza sativa,
                  indica, cv. IR 36, etiolated shoots, Peptide, 517 aa]
                   [Oryza sativa] >gi_2231132 (L41217) integral membrane
                  protein [Oryza sativa]
                  412233
Seq. No.
                  uC-osflcyp097c03b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1616659
BLAST score
                   462
                   3.0e-46
E value
                  116
Match length
% identity
                   77
NCBI Description (U49387) adenylosuccinate synthetase [Triticum aestivum]
                   412234
Seq. No.
                  uC-osflcyp097d12b1
Seq. ID
Method
                  BLASTN
NCBI GI
                   g2462784
BLAST score
                   39
E value
                   2.0e-12
Match length
                   155
% identity
                   74
                  Streptococcus equi M-like protein (szPSe) gene, complete
NCBI Description
                   412235
Seq. No.
Seq. ID
                   uC-osflcyp097e10b1
Method
                   BLASTN
NCBI GI
                   q168500
BLAST score
                   60
                   3.0e-25
E value
                   124
Match length
                   87
% identity
NCBI Description Maize (Zea mays) histone H4 gene (H4Cl4), complete cds
```

412236

BLASTX

uC-osflcyp097e12b1

Seq. No. Seq. ID

Method

BLAST score

187

```
q417488
NCBI GI
BLAST score
                  470
                  4.0e-47
E value
Match length
                  147
                  59
% identity
                  ALPHA-GLUCAN PHOSPHORYLASE, H ISOZYME (STARCH PHOSPHORYLASE
NCBI Description
                  H) >gi_100452_pir__A40995 starch phosphorylase (EC 2.4.1.1)
                  H - potato >gi_169473 (M69038) alpha-glucan phosphorylase
                  type H isozyme [Solanum tuberosum]
                  412237
Seq. No.
Seq. ID
                  uC-osflcyp097f02b1
                  BLASTX
Method
                  q4090257
NCBI GI
BLAST score
                  465
                  1.0e-46
E value
                  91
Match length
                  97
% identity
                 (AJ131732) ribosomal protein L37A [Pseudotsuga menziesii]
NCBI Description
                  412238
Seq. No.
                  uC-osflcyp097f10b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q5912299
                  239
BLAST score
E value
                  2.0e-20
                  51
Match length
                  86
% identity
NCBI Description (AJ133787) gigantea homologue [Oryza sativa]
Seq. No.
                  412239
                  uC-osflcyp097f11b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1082340
BLAST score
                  327
E value
                   2.0e-30
Match length
                  114
                   61
% identity
                  DNA-binding protein R kappa B - human
NCBI Description
                   >gi_695579_emb_CAA56846_ (X80878) R kappa B [Homo sapiens]
                   412240
Seq. No.
                  uC-osflcyp097g01b1
Seq. ID
                  BLASTX
Method
                   q3021271
NCBI GI
BLAST score
                   236
E value
                   1.0e-34
                  155
Match length
                   50
% identity
                  (AL022347) serine/threonine kinase-like protein
NCBI Description
                   [Arabidopsis thaliana]
                   412241
Seq. No.
Seq. ID
                   uC-osflcyp097g02b1
                   BLASTX
Method
NCBI GI
                   g1084455
```

```
1.0e-14
E value
                   38
Match length
                   95
% identity
                   peptidylprolyl isomerase (EC 5.2.1.8) Cyp2 - rice
NCBI Description
                   >gi_600767 (L29469) cyclophilin 2 [Oryza sativa]
                   412242
Seq. No.
                   uC-osflcyp097g11b1
Seq. ID
                   BLASTX
Method
NCBI GI
                   g462195
                   312
BLAST score
                   1.0e-28
E value
                   64
Match length
                   95
% identity
                   PROTEIN TRANSLATION FACTOR SUI1 HOMOLOG (GOS2 PROTEIN)
NCBI Description
                   >gi_100682_pir__S21636 GOS2 protein - rice
                   >gi_20238_emb_CAA36190_ (X51910) GOS2 [Oryza sativa]
                   >gi_3789950 (AF094774) translation initiation factor [Oryza
                   sativa]
                   412243
Seq. No.
                   uC-osflcyp097h01b1
Seq. ID
Method
                   BLASTX
                   g132790
NCBI GI
BLAST score
                   381
                   1.0e-36
E value
Match length
                   75
                   100
% identity
                   CHLOROPLAST 50S RIBOSOMAL PROTEIN L22 >gi_71290_pir__R5RZ22
NCBI Description
                   ribosomal protein L22 - rice chloroplast >gi_12026_emb_CAA33935_ (X15901) ribosomal protein L22
                    [Oryza sativa] >gi_226647_prf__1603356BX ribosomal protein
                   L22 [Oryza sativa]
                    412244
Seq. No.
Seq. ID
                   uC-osflcyp097h02b1
Method
                   BLASTX
NCBI GI
                    g5734713
                    392
BLAST score
E value
                    7.0e-38
Match length
                    91
% identity
                    (AC008075) Is a member of PF_01169 Uncharacterized
NCBI Description
                    (transmembrane domain) protein family. [Arabidopsis
                    thaliana]
Seq. No.
                    412245
                    uC-osflcyp097h03b1
Seq. ID
Method
                    BLASTX
NCBI GI
                    q3746581
BLAST score
                    147
E value
                    3.0e-11
                    44
Match length
                    70
% identity
                   (AF062403) glutathione S-transferase II [Oryza sativa]
NCBI Description
                    412246
Seq. No.
```

uC-osflcyp097h04b1 Seq. ID BLASTX Method q3183445 NCBI GI BLAST score 266 3.0e-23E value 106 Match length 49 % identity HYPOTHETICAL 30.8 KD PROTEIN IN PPHB-RPOS INTERGENIC REGION NCBI Description >qi 882629 (U29579) ORF o302 [Escherichia coli] >gi_1789092 (AE000357) putative dehydrogenase [Escherichia coli] 412247 Seq. No. Seq. ID uC-osflcyp097h05b1 BLASTX Method NCBI GI g2827524 251 BLAST score 1.0e-21 E value 94 Match length 56 % identity NCBI Description (AL021633) predicted protein [Arabidopsis thaliana] 412248 Seq. No. Seq. ID uC-osflcyp097h06b1 Method BLASTX q2497746 NCBI GI BLAST score 158 8.0e-11 E value Match length 31 97 % identity NONSPECIFIC LIPID-TRANSFER PROTEIN 2 PRECURSOR (LTP 2) NCBI Description >gi_951334 (U31766) lipid transfer protein precursor [Oryza sativa] Seq. No. 412249 Seq. ID uC-osflcyp097h08b1 Method BLASTX q730526 NCBI GI

276 BLAST score

2.0e-24 E value 84 Match length % identity 62

60S RIBOSOMAL PROTEIN L13 (BBC1 PROTEIN HOMOLOG) NCBI Description

>gi 480787 pir S37271 ribosomal protein L13 - Arabidopsis thaliana >gi 404166 emb CAA53005 (X75162) BBC1 protein

[Arabidopsis thaliana]

412250 Seq. No.

Seq. ID uC-osflcyp097h10b1

BLASTN Method NCBI GI g2463334 BLAST score 43 6.0e-15 E value 75 Match length 89 % identity

NCBI Description Oryza sativa mRNA for ribosomal protein S4

Seq. No. 412251



uC-osflcyp097h12b1 Seq. ID BLASTX Method NCBI GI q1169382 BLAST score 224 7.0e-19 E value Match length 49 84 % identity DNAJ PROTEIN HOMOLOG 2 >gi 542196 pir S42031 LDJ2 protein NCBI Description - leek >gi 454303 emb CAA54720 (X77632) LDJ2 [Allium porrum] Seq. No. 412252 uC-osflcyp098a03a1 Seq. ID Method BLASTN NCBI GI q2662344 BLAST score 147 7.0e-77 E value Match length 392 90 % identity NCBI Description Oryza sativa mRNA for EF-1 alpha, complete cds 412253 Seq. No. Seq. ID uC-osflcyp098a05b1 Method BLASTX NCBI GI q4417304 BLAST score 205

3.0e-16 E value

Match length 96 % identity 51

NCBI Description (AC006446) putative beta-1,4-mannosyl-glycoprotein beta-1,4-N-acetylglucosaminyltransferase [Arabidopsis

thaliana]

412254 Seq. No.

Seq. ID uC-osflcyp098a12b1

Method BLASTX NCBI GI q2695931 BLAST score 246 2.0e-21 E value Match length 78 72 % identity

NCBI Description (AJ222779) hypothetical protein [Hordeum vulgare]

412255 Seq. No.

Seq. ID uC-osflcyp098b02b1

BLASTX Method NCBI GI q3859659 BLAST score 242 E value 9.0e-21 84 Match length 56 % identity

NCBI Description (AL031394) putative potassium transporter AtKT5p (AtKT5)

[Arabidopsis thaliana]

Seq. No. 412256

Seq. ID uC-osflcyp098c01a1

Method BLASTN

```
q3850817
NCBI GI
                  123
BLAST score
                  1.0e-62
E value
Match length
                  131
                  99
% identity
                  Oryza sativa mRNA for U2 snRNP auxiliary factor, small
NCBI Description
                  subunit 35a
                  412257
Seq. No.
                  uC-osflcyp098c01b1
Seq. ID
                  BLASTX
Method
NCBI GI
                  q3850819
BLAST score
                  418
                  3.0e-41
E value
                  97
Match length
                  85
% identity
                  (Y18349) U2 snRNP auxiliary factor, small subunit [Oryza
NCBI Description
                  sativa]
                   412258
Seq. No.
                  uC-osflcyp098c03b1
Seq. ID
                  BLASTX
Method
                  g4126809
NCBI GI
                   410
BLAST score
E value
                   3.0e-40
                  77
Match length
                   62
% identity
                  (AB017042) glyoxalase I [Oryza sativa]
NCBI Description
                   412259
Seq. No.
Seq. ID
                   uC-osflcyp098c11a1
                   BLASTN
Method
                   g1136123
NCBI GI
BLAST score
                   142
                   7.0e-74
E value
Match length
                   354
% identity
                   96
NCBI Description O.sativa mRNA for alpha-tubulin (clone OSTA-274)
                   412260
Seq. No.
Seq. ID
                   uC-osflcyp098c12a1
Method
                   BLASTN
NCBI GI
                   g2306980
BLAST score
                   69
E value
                   1.0e-30
Match length
                   86
% identity
                   95
                   Oryza sativa photosystem I antenna protein (Lhca) mRNA,
NCBI Description
                   complete cds
                   412261
Seq. No.
                   uC-osflcyp098d02b1
Seq. ID
                   BLASTX
Method
                   g2129742
NCBI GI
```

142

9.0e-18 74

BLAST score E value

Match length

57 % identity stress-induced protein OZI1 precursor - Arabidopsis NCBI Description thaliana >gi 790583 (U20347) mRNA corresponding to this gene accumulates in response to ozone stress and pathogen (bacterial) infection; putative pathogenesis-related protein [Arabidopsis thaliana] >gi 2252869 (AF013294) No definition line found [Arabidopsis thaliana] Seq. No. 412262 uC-osflcyp098e02b1 Seq. ID Method BLASTX g2708741 NCBI GI BLAST score 173 7.0e-13 E value 46 Match length 70 % identity NCBI Description (AC003952) hypothetical protein [Arabidopsis thaliana] 412263 Seq. No. uC-osflcyp098e06a1 Seq. ID BLASTN Method NCBI GI g1261857 47 BLAST score 5.0e-18 E value Match length 75 92 % identity NCBI Description Rice CatA gene for catalase, complete cds 412264 Seq. No. uC-osflcyp098e09b1 Seq. ID Method BLASTN NCBI GI q6013290 BLAST score 36 3.0e-11E value Match length 115 % identity 90 NCBI Description Oryza sativa polyubiquitin (RUBQ2) gene, complete cds 412265 Seq. No. uC-osflcyp098e10b1 Seq. ID Method BLASTX NCBI GI g1652084 BLAST score 141 E value 3.0e-09 71 Match length % identity NCBI Description (D90902) hypothetical protein [Synechocystis sp.] Seq. No. 412266 uC-osflcyp098e11a1 Seq. ID

Method BLASTN
NCBI GI g1261857
BLAST score 116
E value 2.0e-58
Match length 140
% identity 98

NCBI Description Rice CatA gene for catalase, complete cds

```
412267
Seq. No.
Seq. ID
                   uC-osflcyp098e11b1
Method
                   BLASTX
NCBI GI
                   g2130069
BLAST score
                   273
E value
                   8.0e-27
Match length
                   69
% identity
                   91
                   catalase (EC 1.11.1.6) catA - rice
NCBI Description
                   >gi_1261858_dbj_BAA06232_ (D29966) catalase [Oryza sativa]
                   412268
Seq. No.
                   uC-osflcyp098f02b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g1709000
BLAST score
                   347
                   7.0e-33
E value
                   71
Match length
                   96
% identity
                   S-ADENOSYLMETHIONINE SYNTHETASE 1 (METHIONINE
NCBI Description
                   ADENOSYLTRANSFERASE 1) (ADOMET SYNTHETASE 1)
                   >gi_960357_dbj_BAA09895_ (D63835) S-adenosylmethionine
                   synthetase [Hordeum vulgare]
Seq. No.
                   412269
                   uC-osflcyp098f05a1
Seq. ID
Method
                   BLASTN
NCBI GI
                   g287398
BLAST score
                   48
E value
                   2.0e-18
Match length
                   56
                   98
% identity
NCBI Description Oryza sativa mRNA for chilling tolerance related protein,
                   complete cds, clone:pBC591
                   412270
Seq. No.
                   uC-osflcyp098f09b1
Seq. ID
Method
                   BLASTN
NCBI GI
                   g20181
BLAST score
                   84
                   1.0e-39
E value
Match length
                   132
                   91
% identity
                  Rice cab2R gene for light harvesting chlorophyll
NCBI Description
                   a/b-binding protein
                   412271
Seq. No.
Seq. ID
                   uC-osflcyp098f10b1
                   BLASTX
Method
NCBI GI
                   g4582436
BLAST score
                   231
                   9.0e-25
E value
                   80
. Match length
 % identity
NCBI Description (AC007196) unknown protein [Arabidopsis thaliana]
```

NCBI Description

Seq. No. 412272 Seq. ID uC-osflcyp098f11a1 Method BLASTN NCBI GI g287398 BLAST score 110 E value 8.0e-55 Match length 288 % identity 90 NCBI Description Oryza sativa mRNA for chilling tolerance related protein, complete cds, clone:pBC591 412273 Seq. No. Seq. ID uC-osflcyp098f11b1 Method BLASTX NCBI GI g729206 BLAST score 326 E value 1.0e-30 Match length 73 % identity 92 NCBI Description PROBABLE GLUTATHIONE S-TRANSFERASE (28 KD COLD-INDUCED PROTEIN) >gi_287399_dbj_BAA01632_ (D10861) chilling tolerance related protein [Oryza sativa] >gi 445133_prf__1908434C chilling tolerance-related protein:ISOTYPE=pBC591 [Oryza sativa] 412274 Seq. No. Seq. ID uC-osflcyp098f12a1 Method BLASTN NCBI GI g5815409 BLAST score 110 E value 8.0e-55 135 Match length % identity 94 NCBI Description Oryza sativa blast and wounding induced mitogen-activated protein kinase (BWMK1) mRNA, complete cds 412275 Seq. No. Seq. ID uC-osflcyp098g02a1 Method BLASTN NCBI GI g5734616 137 BLAST score E value 5.0e-71 Match length 157 % identity 98 NCBI Description Oryza sativa genomic DNA, chromosome 6, clone:P0538C01 Seq. No. 412276 uC-osflcyp098g02b1 Seq. ID Method BLASTX q5734633 NCBI GI BLAST score 199 6.0e-16 E value Match length 44 % identity

4, BAC clone F7H19 (AL031018) [Oryza sativa]

(AP000391) Similar to Arabidopsis thaliana DNA chromosome

```
Seq. ID
                   uC-osflcyp098g11b1
Method
                   BLASTN
NCBI GI
                   g416251
BLAST score
                   53
                   9.0e-22
E value
Match length
                   53
                   100
% identity
                   Rice mRNA for acetohydroxy acid reductoisomerase, partial
NCBI Description
                   sequence
                   412278
Seq. No.
                   uC-osflcyp098h01b1
Seq. ID
                   BLASTN
Method
NCBI GI
                   q3859567
                   208
BLAST score
                   1.0e-113
E value
                   267
Match length
                   94
% identity
NCBI Description Oryza sativa clone FIL1 unknown mRNA
                   412279
Seq. No.
Seq. ID
                   uC-osflcyp098h08b1
Method
                   BLASTX
                   q115587
NCBI GI
BLAST score
                   216
                   6.0e-18
E value
Match length
                   45
                   96
% identity
                   PHOSPHOENOLPYRUVATE CARBOXYLASE 1 (PEPCASE) (CP21)
NCBI Description
                   >gi_418801_pir__S31159 phosphoenolpyruvate carboxylase (EC 4.1.1.31) CP21 - sorghum >gi_21630_emb_CAA39197_ (X55664)
                   phosphoenolpyruvate carboxylase [Sorghum bicolor]
                   >gi 22615 emb CAA46267 (X65137) phosphoenolpyruvate
                   carboxylase [Sorghum bicolor]
                    412280
Seq. No.
Seq. ID
                   uC-osflcyp099a03b1
Method
                   BLASTX
NCBI GI
                   g5802606
BLAST score
                    416
                    5.0e-41
E value
                   90
Match length
                    84
% identity
NCBI Description (AF174486) methylenetetrahydrofolate reductase [Zea mays]
                    412281
Seq. No.
Seq. ID
                    uC-osflcyp099a06a1
                   BLASTX
Method
NCBI GI
                    g84169
BLAST score
                    163
E value
                    3.0e-11
                    35
Match length
% identity
NCBI Description tubulin alpha chain - slime mold (Physarum polycephalum)
                    412282
Seq. No.
```

Seq. No.

```
uC-osflcyp099a06b1
Seq. ID
                  BLASTX
Method
NCBI GI
                  q4098272
BLAST score
                  209
                  4.0e-17
E value
                  40
Match length
                  93
% identity
NCBI Description (U76558) alpha-tubulin [Triticum aestivum]
                  412283
Seq. No.
                  uC-osflcyp099a11a1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1136122
                  213
BLAST score
                  5.0e-17
E value
                  44
Match length
                  93
% identity
NCBI Description (X91807) alfa-tubulin [Oryza sativa]
Seq. No.
                  412284
                  uC-osflcyp099a11b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4098272
BLAST score
                  430
                  8.0e-43
E value
Match length
                  87
% identity
                   98
NCBI Description (U76558) alpha-tubulin [Triticum aestivum]
                   412285
Seq. No.
Seq. ID
                  uC-osflcyp099a12a1
Method
                  BLASTN
NCBI GI
                   g2331130
BLAST score
                   106
E value
                   1.0e-52
Match length
                   250
% identity
                   90
                  Oryza sativa glycine-rich protein (OSGRP1) mRNA, complete
NCBI Description
Seq. No.
                   412286
                   uC-osflcyp099b01b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g4406775
BLAST score
                   145
E value
                   9.0e-12
                   145
Match length
% identity
                   35
NCBI Description (AC006836) unknown protein [Arabidopsis thaliana]
                   412287
Seq. No.
                   uC-osflcyp099b02b1
Seq. ID
                   BLASTX
Method
                   g2827715
NCBI GI
BLAST score
                   181
E value
                   2.0e-14
```

80

Match length

% identity 62

NCBI Description (AL021684) receptor protein kinase - like protein

[Arabidopsis thaliana]

Seq. No. 412288

Seq. ID uC-osflcyp099b03b1

Method BLASTX
NCBI GI g2511594
BLAST score 278
E value 5.0e-25
Match length 60
% identity 85

NCBI Description (Y13694) multicatalytic endopeptidase complex, proteasome

precursor, beta subunit [Arabidopsis thaliana]

>gi_2827525_emb_CAA16533.1_ (AL021633) multicatalytic
endopeptidase complex, proteasome precursor, beta subunit
[Arabidopsis thaliana] >gi_3421099 (AF043529) 20S

[Arabidopsis thaliana] >gi_3421099 (AF043529) 20S proteasome subunit PBA1 [Arabidopsis thaliana]

Seq. No. 412289

Seq. ID uC-osflcyp099b05a1

Method BLASTX
NCBI GI 94826399
BLAST score 186
E value 8.0e-14
Match length 139
% identity 33

NCBI Description (AJ012423) wall-associated kinase 2 [Arabidopsis thaliana]

Seq. No. 412290

Seq. ID uC-osflcyp099b10b1

Method BLASTX
NCBI GI g2618699
BLAST score 174
E value 2.0e-12
Match length 96
% identity 40

NCBI Description (AC002510) unknown protein [Arabidopsis thaliana]

Seq. No. 412291

Seq. ID uC-osflcyp099b11a1

Method BLASTX
NCBI GI g115773
BLAST score 238
E value 5.0e-20
Match length 61
% identity 79

NCBI Description CHLOROPHYLL A-B BINDING PROTEIN AB96 (LHCII TYPE I

CAB-AB96) (LHCP) (MAJOR 15) >gi_72744_pir__CDPM96 chlorophyll a/b-binding protein AB96 - garden pea

(fragment) >qi 169051 (J01253) polypeptide 15 precursor

[Pisum sativum]

Seq. No. 412292

Seq. ID uC-osflcyp099b11b1

Method BLASTN NCBI GI g218171



BLAST score 58
E value 2.0e-24
Match length 70
% identity 96

NCBI Description Oryza sativa mRNA for type I light-harvesting chlorophyll a/b binding protein of photosystem II (LHCPII), complete

cds

Seq. No. 412293

Seq. ID uC-osflcyp099b12b1

Method BLASTX
NCBI GI g4138583
BLAST score 351
E value 5.0e-33
Match length 105
% identity 70

NCBI Description (Y10821) plastidic ATP/ADP-transporter [Solanum tuberosum]

Seq. No. 412294

Seq. ID uC-osflcyp099c03a1

Method BLASTN
NCBI GI g4107002
BLAST score 351
E value 0.0e+00
Match length 428
% identity 98

NCBI Description Oryza sativa mRNA for OSK5, complete cds

Seq. No. 412295

Seq. ID uC-osflcyp099c03b1

Method BLASTX
NCBI GI g4107001
BLAST score 642
E value 2.0e-67
Match length 124
% identity 100

NCBI Description (D82035) OSK4 [Oryza sativa]

Seq. No. 412296

Seq. ID uC-osflcyp099c06a1

Method BLASTN
NCBI GI g1574943
BLAST score 225
E value 1.0e-123
Match length 434
% identity 78

NCBI Description Oryza sativa polyubiquitin (Rubq1) mRNA, complete cds

Seq. No. 412297

Seq. ID uC-osflcyp099c06b1

Method BLASTX
NCBI GI g1076678
BLAST score 147
E value 7.0e-10
Match length 51
% identity 73

NCBI Description ubiquitin / ribosomal protein S27a - potato (fragment)

% identity

94

Seq. No. 412298 Seq. ID uC-osflcyp099c11a1 Method BLASTX NCBI GI q3660467 BLAST score 165 2.0e-11 E value Match length 46 % identity 72 NCBI Description (AJ001807) succinyl-CoA-ligase alpha subunit [Arabidopsis thaliana] 412299 Seq. No. uC-osflcyp099c11b1 Seq. ID Method BLASTX NCBI GI g1711572 BLAST score 224 2.0e-18 E value 47 Match length 89 % identity SUCCINYL-COA LIGASE (GDP-FORMING), ALPHA-CHAIN PRECURSOR NCBI Description (SUCCINYL-COA SYNTHETASE, ALPHA CHAIN) (SCS-ALPHA) >gi_1076415_pir__S30579 succinate--CoA ligase (GDP-forming) (EC 6.2.1.4) alpha chain - Arabidopsis thaliana (fragment) >gi_16510_emb_CAA48891_ (X69138) succinate--CoA ligase (GDP-forming) [Arabidopsis thaliana] 412300 Seq. No. uC-osflcyp099c12b1 Seq. ID Method BLASTN NCBI GI g487317 BLAST score 89 E value 3.0e-42Match length 101 % identity 97 NCBI Description Rice mRNA EN56, partial sequence Seq. No. 412301 uC-osflcyp099d02b1 Seq. ID BLASTX Method NCBI GI g4115938 BLAST score 170 6.0e-12 E value 87 Match length 53 % identity NCBI Description (AF118223) contains similarity several bacterial glutathione-regulated potassium efflux system proteins [Arabidopsis thaliana] 412302 Seq. No. Seq. ID uC-osflcyp099d05b1 Method BLASTX NCBI GI g2429290 BLAST score 155 E value 9.0e-11 Match length 33

```
NCBI Description (AF014469) peroxidase [Oryza sativa]
Seq. No.
                  412303
                  uC-osflcyp099d07b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2570511
BLAST score
                  235
                  3.0e-20
E value
Match length
                  53
                  89
% identity
NCBI Description (AF022738) chlorophyll a-b binding protein [Oryza sativa]
                  412304
Seq. No.
Seq. ID
                  uC-osflcyp099d08a1
Method
                  BLASTN
NCBI GI
                  g3885887
BLAST score
                  34
                  3.0e-10
E value
Match length
                  62
% identity
                  89
NCBI Description Oryza sativa high mobility group protein (HMG) mRNA,
                  complete cds
Seq. No.
                   412305
                  uC-osflcyp099d08b1
Seq. ID
Method
                  BLASTN
NCBI GI
                  q3885887
BLAST score
                  79
E value
                   4.0e-36
Match length
                  91
                  97
% identity
                  Oryza sativa high mobility group protein (HMG) mRNA,
NCBI Description
                   complete cds
Seq. No.
                   412306
Seq. ID
                  uC-osflcyp099d09b1
Method
                  BLASTN
                   g5042437
NCBI GI
                   37
BLAST score
E value
                   1.0e-11
                   37
Match length
                   100
% identity
NCBI Description Oryza sativa BAC T49B20 genomic sequence, complete sequence
Seq. No.
                   412307
Seq. ID
                   uC-osflcyp099d10a1
Method
                  BLASTN
                   g1304214
NCBI GI
                   169
BLAST score
E value
                   4.0e-90
                   233
Match length
                   97
% identity
NCBI Description Rice mRNA for precursor of 22 kDa protein of photosystem II
                   (PSII-S), complete cds
Seq. No.
                   412308
Seq. ID
                   uC-osflcyp099d10b1
```



```
Method
                  BLASTN
NCBI GI
                  g1304214
BLAST score
                  110
E value
                  3.0e-55
Match length
                  133
                  97
% identity
NCBI Description Rice mRNA for precursor of 22 kDa protein of photosystem II
                  (PSII-S), complete cds
Seq. No.
                  412309
Seq. ID
                  uC-osflcyp099e01b1
Method
                  BLASTX
NCBI GI
                  q3367534
BLAST score
                  285
E value
                  1.0e-25
Match length
                  91
% identity
                  62
NCBI Description
                  (AC004392) Strong similarity to coatamer alpha subunit
                   (HEPCOP) homolog gb_U24105 from Homo sapiens. [Arabidopsis
                  thaliana]
Seq. No.
                  412310
Seq. ID
                  uC-osflcyp099e02a1
Method
                  BLASTN
NCBI GI
                  q2267592
BLAST score
                  192
E value
                  1.0e-104
Match length
                  287
% identity
                  97
NCBI Description Oryza sativa glycine-rich RNA-binding protein mRNA,
                  complete cds
Seq. No.
                  412311
Seq. ID
                  uC-osflcyp099e03b1
Method
                  BLASTX
NCBI GI
                  q629849
BLAST score
                  212
E value
                  2.0e-17
Match length
                  50
% identity
                  74
NCBI Description pectate lyase (EC 4.2.2.2) - maize >gi_405535 (L20140)
                  homology with pectate lyase [Zea mays]
Seq. No.
                  412312
Seq. ID
                  uC-osflcyp099e04a1
                  BLASTX
Method
NCBI GI
                  g6015059
BLAST score
                  277
E value
                  2.0e-24
Match length
                  65
```

83 % identity

NCBI Description ELONGATION FACTOR 1-ALPHA (EF-1-ALPHA) >gi 2996096

(AF030517) translation elongation factor-1 alpha; EF-1

alpha [Oryza sativa]

Seq. No. 412313

Seq. ID uC-osflcyp099e04b1



Method BLASTX
NCBI GI g2662343
BLAST score 403
E value 2.0e-39
Match length 78
% identity 100

NCBI Description (D63581) EF-1 alpha [Oryza sativa]

Seq. No. 412314

Seq. ID uC-osflcyp099e06b1

Method BLASTX
NCBI GI 94079798
BLAST score 292
E value 3.0e-26
Match length 56
% identity 96

NCBI Description (AF052203) 23 kDa polypeptide of photosystem II [Oryza

sativa]

Seq. No. 412315

Seq. ID uC-osflcyp099e07a1

Method BLASTN
NCBI GI g5679685
BLAST score 102
E value 3.0e-50
Match length 130
% identity 97

NCBI Description Oryza sativa RPA gene for protein phosphatase 2A A subunit,

exons 1-12

Seq. No. 412316

Seq. ID uC-osflcyp099e07b1

Method BLASTX
NCBI GI g5679684
BLAST score 414
E value 6.0e-41
Match length 83
% identity 99

NCBI Description (AJ243828) phosphatase 2A regulatory A subunit [Oryza

sativa] >gi 5679686 emb CAB51804.1 (AJ243829) protein

phosphatase 2A A subunit [Oryza sativa]

Seq. No. 412317

Seq. ID uC-osflcyp099f01b1

Method BLASTX
NCBI GI g4539390
BLAST score 476
E value 9.0e-48
Match length 99
% identity 92

NCBI Description (AL035526) shaggy-like protein kinase etha (EC 2.7.1.-)

[Arabidopsis thaliana]

Seq. No. 412318

Seq. ID uC-osflcyp099f07b1

Method BLASTX NCBI GI g3978578

```
BLAST score
                  318
E value
                  3.0e-29
Match length
                  129
% identity
                  49
                 (AB020528) Polygalacturonase inhibitor [Poncirus
NCBI Description
                  trifoliata]
Seq. No.
                  412319
Seq. ID
                  uC-osflcyp099f08a1
Method
                  BLASTN
NCBI GI
                  g20367
BLAST score
                  183
E value
                  2.0e-98
Match length
                  261
                  96
% identity
NCBI Description Oryza sativa shoot GS1 mRNA for cytosolic glutamine
                  synthetase (EC 6.3.1.2) (clone lambda-GS28)
Seq. No.
                  412320
Seq. ID
                  uC-osflcyp099f08b1
Method
                  BLASTX
NCBI GI
                  g121349
BLAST score
                  520
E value
                  3.0e-53
Match length
                  98
                  100
% identity
NCBI Description GLUTAMINE SYNTHETASE SHOOT ISOZYME (GLUTAMATE--AMMONIA
                  LIGASE) (CLONE LAMBDA-GS28) >gi 20368 emb CAA32461
                  (X14245) cytosolic glutamine synthetase (AA 1-356) [Oryza
                  sativa]
                  412321
Seq. No.
Seq. ID
                  uC-osflcyp099f10b1
Method
                  BLASTX
NCBI GI
                  g218157
BLAST score
                  463
                  1.0e-46
E value
                  91
Match length
% identity
                  98
NCBI Description (D13512) cytoplasmic aldolase [Oryza sativa]
                  412322
Seq. No.
Seq. ID
                  uC-osflcyp099f11a1
Method
                  BLASTX
NCBI GI
                  q2058273
BLAST score
                  189
                  3.0e-14
E value
Match length
                  40
% identity
                  97
```

Seq. No. 412323

Seq. ID uC-osflcyp099f11b1

NCBI Description (D83527) YK426 [Oryza sativa]

Method BLASTN
NCBI GI g6016845
BLAST score 49

E value 3.0e-18



Match length 49 % identity 100

NCBI Description Oryza sativa genomic DNA, chromosome 1, clone:P0711E10

Seq. No. 412324

Seq. ID uC-osflcyp099g02b1

Method BLASTX
NCBI GI g940288
BLAST score 290
E value 3.0e-26
Match length 107
% identity 57

NCBI Description (L43510) protein localized in the nucleoli of pea nuclei;

ORF; putative [Pisum sativum]

Seq. No. 412325

Seq. ID uC-osflcyp099g03b1

Method BLASTX
NCBI GI g4107001
BLAST score 257
E value 1.0e-22
Match length 52
% identity 98

NCBI Description (D82035) OSK4 [Oryza sativa]

Seq. No. 412326

Seq. ID uC-osflcyp099g05b1

Method BLASTX
NCBI GI g2894281
BLAST score 164
E value 1.0e-11
Match length 80
% identity 44

NCBI Description (AL021838) ubiquitin carboxyl-terminal hydrolase

[Schizosaccharomyces pombe]

Seq. No. 412327

Seq. ID uC-osflcyp099h06a1

Method BLASTX
NCBI GI g2641619
BLAST score 191
E value 2.0e-14
Match length 40
% identity 93

NCBI Description (AF032468) ubiquitin-conjugating enzyme protein E2 [Zea

mays]

Seq. No. 412328

Seq. ID uC-osflcyp099h06b1

Method BLASTN
NCBI GI g2641618
BLAST score 63
E value 4.0e-27
Match length 79
% identity 95

NCBI Description Zea mays ubiquitin-conjugating enzyme protein E2 (ubc7)

mRNA, complete cds

Seq. No.

412334

```
412329
Seq. No.
Seq. ID
                  uC-osflcyp099h09a1
Method
                  BLASTX
NCBI GI
                  g2129825
                  239
BLAST score
                  5.0e-20
E value
Match length
                  56
% identity
                  86
                  dynamin-like protein phragmoplastin 12 - soybean
NCBI Description
                  >gi 1217994 (U25547) SDL [Glycine max]
                  412330
Seq. No.
Seq. ID
                  uC-osflcyp099h10a1
Method
                  BLASTN
NCBI GI
                  g769704
BLAST score
                  322
                  0.0e+00
E value
Match length
                  437
% identity
                  96
NCBI Description Oryza sativa mitochondrion genes for NADH dehydrogenase
                  subunits, ribosomal proteins and tRNA-fMet, partial cds
Seq. No.
                  412331
Seq. ID
                  uC-osflcyp099h10b1
Method
                  BLASTN
NCBI GI
                  q769704
BLAST score
                  73
E value
                  2.0e-33
                  77
Match length
                  99
% identity
NCBI Description Oryza sativa mitochondrion genes for NADH dehydrogenase
                  subunits, ribosomal proteins and tRNA-fMet, partial cds
Seq. No.
                  412332
Seq. ID
                  uC-osflcyp100a03a1
                  BLASTN
Method
NCBI GI
                  g968995
BLAST score
                  156
                  3.0e-82
E value
                  358
Match length
% identity
NCBI Description Oryza sativa clone glyceraldehyde-3-phosphate dehydrogenase
                   (Gpc) mRNA, complete cds
                  412333
Seq. No.
Seq. ID
                  uC-osflcyp100a06a1
Method
                  BLASTN
NCBI GI
                  g2773153
BLAST score
                  138
                  1.0e-71
E value
                  158
Match length
                  97
% identity
NCBI Description Oryza sativa abscisic acid- and stress-inducible protein
                  (Asr1) mRNA, complete cds
```

BLAST score

184

uC-osflcyp100a08a1 Seq. ID Method BLASTN NCBI GI q218171 59 BLAST score 8.0e-25 E value Match length 99 90 % identity NCBI Description Oryza sativa mRNA for type I light-harvesting chlorophyll a/b binding protein of photosystem II (LHCPII), complete 412335 Seq. No. uC-osflcyp100b06a1 Seq. ID Method BLASTN NCBI GI q2773153 BLAST score 52 5.0e-21 E value Match length 72 93 % identity NCBI Description Oryza sativa abscisic acid- and stress-inducible protein (Asr1) mRNA, complete cds Seq. No. 412336 Seq. ID uC-osflcyp100c11a1 Method BLASTN NCBI GI q1177319 BLAST score 161 E value 3.0e-85 Match length 372 % identity 98 NCBI Description O.sativa mRNA for Ca+2-binding EF hand protein 412337 Seq. No. Seq. ID uC-osflcyp100d11a1 Method BLASTN NCBI GI g1177319 BLAST score 37 1.0e-11 E value 77 Match length % identity 87 NCBI Description O.sativa mRNA for Ca+2-binding EF hand protein 412338 Seq. No. Seq. ID uC-osflcyp100f02a1 Method BLASTN NCBI GI g20280 131 BLAST score 2.0e-67 E value 186 Match length 95 % identity NCBI Description Rice gene for phenylalanine ammonia-lyase (EC 4.3.1.5) 412339 Seq. No. Seq. ID uC-osflcyp100h03a1 Method BLASTN NCBI GI q4158220

```
6.0e-99
E value
Match length
                   392
% identity
                    92
```

NCBI Description Oryza sativa mRNA for reversibly glycosylated polypeptide

412340 Seq. No.

uC-osflcyp101a01b1 Seq. ID

Method BLASTX NCBI GI q485126 BLAST score 190 E value 3.0e-14Match length 72 % identity 54

(U00052) Contains similarity to Pfam domain: PF00076 (rrm), Score=72.6, E-value=2.6e-18, N=1 [Caenorhabditis elegans] NCBI Description

Seq. No. 412341

Seq. ID uC-osflcyp101a03b1

Method BLASTX NCBI GI g1172818 BLAST score 262 E value 4.0e-23 Match length 53 % identity 94

NCBI Description 40S RIBOSOMAL PROTEIN S16 >gi_538428 (L36313) ribosomal protein S16 [Oryza sativa] >gi_1096552_prf__2111468A

ribosomal protein S16 [Oryza sativa]

Seq. No. 412342

Seq. ID uC-osflcyp101a04b1

Method BLASTX NCBI GI g3426037 BLAST score 383 7.0e-37 E value 148 Match length 52 % identity

NCBI Description (AC005168) putative ABC transporter protein [Arabidopsis

thaliana]

412343 Seq. No.

Seq. ID uC-osflcyp101a05b1

Method BLASTX NCBI GI g6006801 BLAST score 517 E value 1.0e-52 Match length 156 66 % identity

NCBI Description (AF156783) apyrase [Arabidopsis thaliana]

Seq. No. 412344

Seq. ID uC-osflcyp101a07a1

Method BLASTN NCBI GI q6006355 BLAST score 243 E value 1.0e-134 243 Match length 100 % identity

NCBI Description Oryza sativa genomic DNA, chromosome 6, clone:P0493C11 Seq. No. 412345 Seq. ID uC-osflcyp101a07b1 Method BLASTN NCBI GI g6006355 BLAST score 87 E value 1.0e-41 135 Match length % identity 91 NCBI Description Oryza sativa genomic DNA, chromosome 6, clone:P0493C11 Seq. No. 412346 Seq. ID uC-osflcyp101a08b1 Method BLASTX NCBI GI g1172818 BLAST score 247 E value 3.0e-21 Match length 52 % identity 94 NCBI Description 40S RIBOSOMAL PROTEIN S16 >gi_538428 (L36313) ribosomal protein S16 [Oryza sativa] >gi 1096552 prf 2111468A ribosomal protein S16 [Oryza sativa] Seq. No. 412347 Seq. ID uC-osflcyp101a09b1 Method BLASTN NCBI GI g607894 BLAST score 65 2.0e-28 E value 91 Match length % identity 93 NCBI Description Oryza sativa IR54 anther specific (RTS2) gene, complete cds Seq. No. 412348 Seq. ID uC-osflcyp101a10a1 Method BLASTN NCBI GI g886692 BLAST score 409 0.0e+00 E value Match length 425 % identity 99 NCBI Description O.sativa mRNA for lipid transfer protein, b1 Seq. No. 412349 Seq. ID uC-osflcyp101a10b1 Method BLASTN NCBI GI g510336 BLAST score 163 E value 1.0e-86 Match length 199 % identity 95 NCBI Description O.sativa lipid transfer protein gene, complete CDS Seq. No. 412350 Seq. ID uC-osflcyp101b02b1 Method BLASTX

Method

NCBI GI

BLASTN g3298475

```
NCBI GI
                   g82080
BLAST score
                   275
E value
                   2.0e-24
                   87
Match length
% identity
                   chlorophyll a/b-binding protein type III precursor - tomato
NCBI Description
                   >gi_226872_prf 1609235A chlorophyll a/b binding protein
                   [Lycopersicon esculentum]
Seq. No.
                   412351
Seq. ID
                   uC-osflcyp101b04a1
Method
                   BLASTN
NCBI GI
                   q2773153
BLAST score
                   271
E value
                   1.0e-151
Match length
                   283
% identity
                   99
NCBI Description Oryza sativa abscisic acid- and stress-inducible protein
                   (Asr1) mRNA, complete cds
Seq. No.
                   412352
Seq. ID
                   uC-osflcyp101b04b1
Method
                   BLASTN
NCBI GI
                   g2773153
BLAST score
                   77
E value
                   2.0e-35
Match length
                   145
% identity
                   90
NCBI Description Oryza sativa abscisic acid- and stress-inducible protein
                   (Asr1) mRNA, complete cds
Seq. No.
                   412353
Seq. ID
                  uC-osflcyp101b07a1
Method
                  BLASTX
NCBI GI
                   g4539390
BLAST score
                   258
E value
                   3.0e-22
Match length
                   61
% identity
                   74
NCBI Description
                  (AL035526) shaggy-like protein kinase etha (EC 2.7.1.-)
                   [Arabidopsis thaliana]
Seq. No.
                   412354
Seq. ID
                  uC-osflcyp101b09b1
Method
                  BLASTN
NCBI GI
                  g4322939
BLAST score
                  36
                  7.0e-11
E value
Match length
                  48
% identity
                  94
NCBI Description
                  Nicotiana tabacum DNA-binding protein 2 (WRKY2) mRNA,
                  complete cds
Seq. No.
                  412355
Seq. ID
                  uC-osflcyp101b12a1
```

```
BLAST score
E value
                   2.0e-24
Match length
                  73
% identity
                   97
NCBI Description Oryza sativa gene for ovp2, complete cds
                  412356
Seq. No.
Seq. ID
                  uC-osflcyp101b12b1
Method
                  BLASTN
NCBI GI
                  g3298475
BLAST score
                  59
                  8.0e-25
E value
Match length
                  111
                  89
% identity
NCBI Description Oryza sativa gene for ovp2, complete cds
                  412357
Seq. No.
Seq. ID
                  uC-osflcyp101c04a1
Method
                  BLASTN
NCBI GI
                  g218144
BLAST score
                  51
E value
                   4.0e-20
Match length
                  83
% identity
                  90
NCBI Description Rice mRNA for ATP/ADP translocator, complete cds
                  412358
Seq. No.
Seq. ID
                  uC-osflcyp101c05b1
                  BLASTX
Method
NCBI GI
                  g485517
BLAST score
                  212
E value
                   6.0e-17
Match length
                  63
% identity
                   68
NCBI Description ADP, ATP carrier protein - rice
Seq. No.
                   412359
Seq. ID
                  uC-osflcyp101c08b1
Method
                  BLASTX
NCBI GI
                  g4835763
BLAST score
                  393
E value
                  6.0e-38
Match length
                  110
% identity
NCBI Description (AC007202) T8K14.13 [Arabidopsis thaliana]
Seq. No.
                   412360
Seq. ID
                  uC-osflcyp101c10a1
Method
                  BLASTX
NCBI GI
                  q3334116
BLAST score
                  196
E value
                  5.0e-15
Match length
                  39
```

53637

>gi_1297066_emb_CAA65119_ (X95863) adenine nucleotide

NCBI Description ADP,ATP CARRIER PROTEIN 1 PRECURSOR (ADP/ATP TRANSLOCASE 1) (ADENINE NUCLEOTIDE TRANSLOCATOR 1) (ANT 1)

100

% identity

Seq. No.

412366



translocator [Triticum turgidum]

```
412361
Seq. No.
Seq. ID
                  uC-osflcyp101c10b1
Method
                  BLASTX
NCBI GI
                  g485517
                   468
BLAST score
                   6.0e-62
E value
Match length
                   126
                   100
% identity
NCBI Description ADP, ATP carrier protein - rice
Seq. No.
                   412362
                   uC-osflcyp101c12b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   q5262777
                   288
BLAST score
                   9.0e-26
E value
                   67
Match length
                   76
% identity
                  (AL080282) fatty acid hydroxylase-like protein [Arabidopsis
NCBI Description
                   thaliana]
                   412363
Seq. No.
                   uC-osflcyp101d03b1
Seq. ID
                   BLASTN
Method
                   q4769011
NCBI GI
                   96
BLAST score
                   6.0e-47
E value
                   116
Match length
                   96
% identity
NCBI Description Oryza sativa CER1 (CER1) mRNA, complete cds
                   412364
Seq. No.
                   uC-osflcyp101d05b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g6005948
BLAST score
                   151
E value
                   7.0e-10
                   72
Match length
% identity
                   40
                   WW domain binding protein 4 (formin binding protein 21)
NCBI Description
                   >gi 3550080 (AF071185) formin binding protein 21 [Homo
                   sapiens]
Seq. No.
                   412365
Seq. ID
                   uC-osflcyp101d08b1
Method
                   BLASTX
NCBI GI
                   q4894182
BLAST score
                   621
E value
                   8.0e-65
Match length
                   146
                   77
% identity
                   (AJ242551) 12-oxophytodienoate reductase [Lycopersicon
NCBI Description
                   esculentum]
```

NCBI GI

g303834

Seq. ID uC-osflcyp101d10b1 Method BLASTX NCBI GI q6005948 BLAST score 147 E value 4.0e-09 Match length 56 % identity 45 NCBI Description WW domain binding protein 4 (formin binding protein 21) >gi_3550080 (AF071185) formin binding protein 21 [Homo Seq. No. 412367 Seq. ID uC-osflcyp101e04b1 Method BLASTX NCBI GI q4158221 BLAST score 155 E value 9.0e-11 Match length 35 % identity NCBI Description (Y18624) reversibly glycosylated polypeptide [Oryza sativa] Seq. No. 412368 Seq. ID uC-osflcyp101e09b1 Method BLASTX NCBI GI g3150415 BLAST score 576 E value 2.0e-59 Match length 165 % identity 65 NCBI Description (AC004165) sec13-related protein [Arabidopsis thaliana] >gi_3420046 (AC004680) sec13-related protein [Arabidopsis thaliana] Seq. No. 412369 Seq. ID uC-osflcyp101e10a1 Method BLASTX NCBI GI q4158221 BLAST score 225 E value 2.0e-18 Match length 43 100 % identity NCBI Description (Y18624) reversibly glycosylated polypeptide [Oryza sativa] Seq. No. 412370 Seq. ID uC-osflcyp101f01a1 Method BLASTN NCBI GI q303834 BLAST score 120 E value 9.0e-61 Match length 256 % identity 93 NCBI Description Rice mRNA for 21kd polypeptide, complete cds Seq. No. 412371 Seq. ID uC-osflcyp101f01b1 Method BLASTN

Match length

% identity

45

93

NCBI Description catalase (EC 1.11.1.6) catA - rice

```
BLAST score
                   50
E value
                  1.0e-19
Match length
                  83
                  100
% identity
NCBI Description Rice mRNA for 21kd polypeptide, complete cds
Seq. No.
                  412372
Seq. ID
                  uC-osflcyp101f03b1
Method
                  BLASTN
NCBI GI
                  g5257255
BLAST score
                  132
E value
                  5.0e-68
Match length
                  316
                  97
% identity
NCBI Description Oryza sativa genomic DNA, chromosome 8, clone:P0026F07
Seq. No.
                  412373
Seq. ID
                  uC-osflcyp101f06b1
Method
                  BLASTX
NCBI GI
                  q1076348
BLAST score
                  145
E value
                  1.0e-09
Match length
                  45
% identity
                  64
NCBI Description myosin MYA1, class V - Arabidopsis thaliana
                  >gi_433663_emb_CAA82234_ (Z28389) myosin [Arabidopsis
                  thaliana]
Seq. No.
                  412374
Seq. ID
                  uC-osflcyp101f08a1
Method
                  BLASTN
NCBI GI
                  g6016845
BLAST score
                  159
                  4.0e-84
E value
Match length
                  279
% identity
                  90
NCBI Description Oryza sativa genomic DNA, chromosome 1, clone:P0711E10
Seq. No.
                  412375
Seq. ID
                  uC-osflcyp101g01b1
Method
                  BLASTX
NCBI GI
                  g2827536
BLAST score
                  244
E value
                  9.0e-21
Match length
                  100
% identity
                  47
NCBI Description (AL021633) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  412376
Seq. ID
                  uC-osflcyp101g07b1
Method
                  BLASTX
NCBI GI
                  g2130069
BLAST score
                  226
E value
                  4.0e-19
```

% identity

41

```
>gi 1261858 dbj BAA06232 (D29966) catalase [Oryza sativa]
Seq. No.
                  412377
Seq. ID
                  uC-osflcyp101g12b1
Method
                  BLASTX
NCBI GI
                  g3023816
BLAST score
                  517
E value
                  1.0e-53
Match length
                  113
% identity
                  93
NCBI Description GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC
                  >gi 968996 (U31676) glyceraldehyde-3-phosphate
                  dehydrogenase [Oryza sativa]
Seq. No.
                  412378
Seq. ID
                  uC-osflcyp101h02b1
Method
                  BLASTX
NCBI GI
                  g232031
BLAST score
                  276
E value
                  3.0e-28
Match length
                  77
% identity
                  90
NCBI Description ELONGATION FACTOR 1-BETA' (EF-1-BETA')
                  >gi_322851_pir__S29224 translation elongation factor eEF-1
                  beta' chain - rice >gi_218161_dbj_BAA02253_ (D12821)
                  elongation factor 1 beta' [Oryza sativa]
                  412379
Seq. No.
Seq. ID
                  uC-osflcyp101h04a1
Method
                  BLASTX
NCBI GI
                  g542191
BLAST score
                  162
E value
                  5.0e-11
Match length
                  56
% identity
                  62
NCBI Description floral homeotic protein ZAG1 - maize >gi 309574 (L18924)
                  homologue of Arabidopsis gene AGAMOUS [Zea mays]
                  412380
Seq. No.
Seq. ID
                  uC-osflcyp101h07b1
Method
                  BLASTX
NCBI GI
                  g4836883
BLAST score
                  257
                  3.0e-22
E value
Match length
                  90
% identity
NCBI Description (AC007260) lcl prt seq No definition line found
                  [Arabidopsis thaliana]
Seq. No.
                  412381
Seq. ID
                  uC-osflcyp101h08b1
Method
                  BLASTX
                  q4558552
NCBI GI
BLAST score
                  294
E value
                  1.0e-26
                  73
Match length
```

```
(AC007138) putative P-glycoprotein-like protein
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                  412382
                  uC-osflcyp101h09b1
Seq. ID
                  BLASTX
Method
NCBI GI
                  q3819164
                  585
BLAST score
E value
                  1.0e-60
                  138
Match length
                  79
% identity
                  (AJ012318) cytosolic chaperonin, delta-subunit [Glycine
NCBI Description
Seq. No.
                  412383
                  uC-osflcyp102b02a1
Seq. ID
                  BLASTX
Method
NCBI GI
                  q1170937
BLAST score
                  254
E value
                  8.0e-22
                  47
Match length
                  98
% identity
NCBI Description S-ADENOSYLMETHIONINE SYNTHETASE 1 (METHIONINE
                  ADENOSYLTRANSFERASE 1) (ADOMET SYNTHETASE 1)
                  >gi_450549_emb_CAA81481_ (Z26867) S-adenosyl methionine
                   synthetase [Oryza sativa]
                   412384
Seq. No.
                  uC-osflcyp102b04a1
Seq. ID
                  BLASTN
Method
NCBI GI
                   q450548
BLAST score
                   125
E value
                   8.0e-64
Match length
                   219
% identity
                   92
                  O.sativa (pRSAM-1) gene for S-adenosyl methionine
NCBI Description
                   synthetase
                   412385
Seq. No.
Seq. ID
                   uC-osflcyp102c03a1
Method
                   BLASTN
NCBI GI
                   g5922603
                   135
BLAST score
                   1.0e-69
E value
                   207
Match length
% identity
                   93
NCBI Description Oryza sativa genomic DNA, chromosome 1, clone:P0705D01
                   412386
Seq. No.
Seq. ID
                   uC-osflcyp102d01a1
Method
                   BLASTN
NCBI GI
                   g780371
                   152
BLAST score
                   4.0e-80
E value
Match length
                   195
% identity
                   96
NCBI Description Oryza sativa enolase mRNA, complete cds
```

Method

BLASTN

```
412387
Seq. No.
                  uC-osflcyp102d02a1
Seq. ID
Method
                  BLASTN
                  g6013290
NCBI GI
                  150
BLAST score
                  8.0e-79
E value
                  190
Match length
                  97
% identity
NCBI Description Oryza sativa polyubiquitin (RUBQ2) gene, complete cds
Seq. No.
                  412388
                  uC-osflcyp102g03a1
Seq. ID
Method
                  BLASTN
NCBI GI
                  q2894533
                  163
BLAST score
                  2.0e-86
E value
                  187
Match length
                  98
% identity
NCBI Description Oryza sativa mRNA for aquaporin, complete CDS
                  412389
Seq. No.
                  uC-osflcyp102g07a1
Seq. ID
                  BLASTN
Method
NCBI GI
                  q454881
BLAST score
                  171
                  2.0e-91
E value
                  179
Match length
                  99
% identity
NCBI Description Rice gene for thioredoxin h, complete cds
                  412390
Seq. No.
                  uC-osflcyp103b03a1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g20369
BLAST score
                  108
E value
                   6.0e-54
Match length
                  112
% identity
                  99
                  Oryza sativa shoot GS2 mRNA for chloroplastic glutamine
NCBI Description
                   synthetase (EC 6.3.1.2) (clone lambda-GS31)
                   >gi 2170909 dbj E02681 E02681 cDNA encoding precursor of
                   chloroplast localising glutamine synthetase
Seq. No.
                   412391
Seq. ID
                  uC-osflcyp103b06a1
Method
                  BLASTN
NCBI GI
                  g1136121
                  85
BLAST score
E value
                   3.0e-40
                  97
Match length
                   97
% identity
NCBI Description O.sativa mRNA for alpha-tubulin (clone OSTA-136)
                   412392
Seq. No.
Seq. ID
                   uC-osflcyp103b11a1
```

q2894533 NCBI GI BLAST score 111 2.0e-55 E value Match length 150 96 % identity NCBI Description Oryza sativa mRNA for aquaporin, complete CDS 412393 Seq. No. uC-osflcyp103e06a1 Seq. ID BLASTN Method NCBI GI q6013290 BLAST score 110 3.0e-55E value Match length 110 % identity 100 NCBI Description Oryza sativa polyubiquitin (RUBQ2) gene, complete cds 412394 Seq. No. uC-osflcyp103f05a1 Seq. ID Method BLASTN NCBI GI g6013290 42 BLAST score E value 7.0e-15 Match length 82 90 % identity NCBI Description Oryza sativa polyubiquitin (RUBQ2) gene, complete cds 412395 Seq. No. uC-osflcyp103h02a1 Seq. ID Method BLASTN q2894533 NCBI GI BLAST score 68 3.0e-30 E value Match length 88 % identity 94 NCBI Description Oryza sativa mRNA for aquaporin, complete CDS 412396 Seq. No. uC-osflcyp104a07a1 Seq. ID BLASTN Method g218209 NCBI GI 265 BLAST score 1.0e-147 E value 389 Match length 95 % identity Oryza sativa mRNA for the small subunit of NCBI Description ribulose-1,5-bisphosphate carboxylase, complete cds, clone posss2106

412397 Seq. No.

Seq. ID uC-osflcyp104b03a1

BLASTN Method NCBI GI q3248998 BLAST score 136 E value 3.0e-70 160 Match length 98 % identity

```
cds
                  412398
Seq. No.
                  uC-osflcyp104c12a1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g5852170
BLAST score
                  67
E value
                  3.0e-29
Match length
                  145
% identity
                  56
NCBI Description Oryza sativa indica(GLA4) genomic DNA, chromosome 4, BAC
                  clone:t17804
Seq. No.
                  412399
                  uC-osflcyp104g11a1
Seq. ID
Method
                  BLASTN
NCBI GI
                  q540532
BLAST score
                  124
E value
                  2.0e-63
Match length
                  156
                  97
% identity
NCBI Description Rice mRNA for G protein alpha subunit, complete cds
                  412400
Seq. No.
Seq. ID
                  uC-osflcyp104h01a1
                  BLASTN
Method
NCBI GI
                  q6006355
BLAST score
                  143
E value
                  8.0e-75
Match length
                  167
% identity
                  98
NCBI Description Oryza sativa genomic DNA, chromosome 6, clone:P0493C11
Seq. No.
                   412401
                  uC-osflcyp104h02a1
Seq. ID
                  BLASTN
Method
NCBI GI
                  q450548
BLAST score
                  60
E value
                   3.0e-25
                  108
Match length
                   91
% identity
NCBI Description O.sativa (pRSAM-1) gene for S-adenosyl methionine
                  synthetase
                   412402
Seq. No.
Seq. ID
                  uC-osflcyp104h03a1
                  BLASTN
Method
NCBI GI
                  q450548
BLAST score
                  47
E value
                   2.0e-17
Match length
                  63
                   94
% identity
NCBI Description O.sativa (pRSAM-1) gene for S-adenosyl methionine
                  synthetase
                   412403
Seq. No.
                                      53645
```

NCBI Description Oryza sativa translation elongation factor mRNA, partial

E value

Match length

% identity

```
uC-osflcyp104h08a1
Seq. ID
Method
                   BLASTN
NCBI GI
                   q450548
BLAST score
                   188
E value
                   1.0e-101
Match length
                   188
                   100
% identity
NCBI Description O.sativa (pRSAM-1) gene for S-adenosyl methionine
                   synthetase
Seq. No.
                   412404
Seq. ID
                   uC-osflcyp105a03a1
Method
                   BLASTN
NCBI GI
                   q450548
BLAST score
                   37
                   1.0e-11
E value
Match length
                   49
                   94
% identity
NCBI Description O.sativa (pRSAM-1) gene for S-adenosyl methionine
                   synthetase
                   412405
Seq. No.
Seq. ID
                   uC-osflcyp105a05a1
Method
                   BLASTX
NCBI GI
                   q120668
BLAST score
                   204
E value
                   7.0e-16
Match length
                   39
% identity
                   97
NCBI Description
                   GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC
                   >gi_82399_pir__A24159 glyceraldehyde-3-phosphate
dehydrogenase (EC 1.2.1.12), cytosolic - barley (fragment)
                   >gi 167044 (M36650) glyceraldehyde-3-phosphate
                   dehydrogenase [Hordeum vulgare] >gi 225347 prf 1301218A
                   dehydrogenase, glyceraldehydephosphate [Hordeum vulgare var.
                   distichum]
                   412406
Seq. No.
Seq. ID
                   uC-osflcyp105a08a1
Method
                   BLASTN
NCBI GI
                   g1911067
BLAST score
                   159
E value
                   5.0e-84
                   385
Match length
% identity
                   90
NCBI Description Oryza sativa gene for NADH-dependent glutamate synthase
                   412407
Seq. No.
Seq. ID
                   uC-osflcyp105a09a1
Method
                   BLASTX
NCBI GI
                   g1170937
BLAST score
                   262
```

NCBI Description S-ADENOSYLMETHIONINE SYNTHETASE 1 (METHIONINE ADENOSYLTRANSFERASE 1) (ADOMET SYNTHETASE 1)

8.0e-23

48

NCBI Description

2.7.2.3)

```
synthetase [Oryza sativa]
Seq. No.
                     412408
Seq. ID
                     uC-osflcyp105b03a1
Method
                     BLASTN
NCBI GI
                     q476751
BLAST score
                     45
E value
                     2.0e-16
                     77
Match length
% identity
                     95
                    Oryza sativa chloroplast rubisco large subunit (rbcL) mRNA,
NCBI Description
                     complete cds
                     412409
Seq. No.
                     uC-osflcyp105c06a1
Seq. ID
Method
                     BLASTX
NCBI GI
                     q1076800
                     163
BLAST score
E value
                     2.0e-11
                     43
Match length
                     91
% identity
NCBI Description L-ascorbate peroxidase (EC 1.11.1.11), cytosolic isozyme - maize >gi_600116_emb_CAA84406_ (Z34934) cytosolic ascorbate peroxidase [Zea mays] >gi_1096503_prf_2111423A ascorbate
                     peroxidase [Zea mays]
                     412410
Seq. No.
Seq. ID
                     uC-osflcyp105c08a1
Method
                     BLASTX
NCBI GI
                     g3668069
BLAST score
                     150
E value
                     1.0e-09
Match length
                     34
% identity
                     91
NCBI Description (U28007) Pto kinase interactor 1 [Lycopersicon esculentum]
Seq. No.
                     412411
Seq. ID
                     uC-osflcyp105d10a1
Method
                     BLASTN
NCBI GI
                     g20365
BLAST score
                     130
E value
                     9.0e-67
                     154
Match length
                     98
% identity
NCBI Description O.sativa RSs1 gene for sucrose synthase
                     412412
Seq. No.
Seq. ID
                     uC-osflcyp105e08a1
Method
                     BLASTN
NCBI GI
                     q21834
BLAST score
                     90
E value
                     8.0e-43
Match length
                     155
                     90
% identity
```

>gi_450549_emb_CAA81481_ (Z26867) S-adenosyl methionine

53647

Wheat mRNA for cytosolic phosphoglycerate kinase (EC

```
Seq. No.
Seq. ID
                  uC-osflcyp105e10a1
Method
                  BLASTN
NCBI GI
                  g1778820
BLAST score
                  94
                  3.0e-45
E value
Match length
                  147
% identity
                  90
NCBI Description Oryza sativa S-adenosyl-L-methionine synthetase (pOS-SAMS2)
                  mRNA, complete cds
                  412414
Seq. No.
Seq. ID
                  uC-osflcyp105e12a1
Method
                  BLASTX
                  g3913426
NCBI GI
BLAST score
                  213
                   5.0e-17
E value
Match length
                  39
% identity
                   97
NCBI Description S-ADENOSYLMETHIONINE DECARBOXYLASE PROENZYME (ADOMETDC)
                   (SAMDC) >gi 1532048 emb CAA69074 (Y07766)
                  S-adenosylmethionine decarboxylase [Oryza sativa]
                   412415
Seq. No.
                  uC-osflcyp105g01a1
Seq. ID
Method
                  BLASTN
NCBI GI
                   g2773153
BLAST score
                   365
E value
                   0.0e+00
                  397
Match length
% identity
                   98
NCBI Description Oryza sativa abscisic acid- and stress-inducible protein
                   (Asr1) mRNA, complete cds
Seq. No.
                   412416
                  uC-osflcyp105g05a1
Seq. ID
                  BLASTN
Method
                  g287398
NCBI GI
BLAST score
                   47
                   2.0e-17
E value
                   55
Match length
                   96
% identity
NCBI Description Oryza sativa mRNA for chilling tolerance related protein,
                   complete cds, clone:pBC591
Seq. No.
                   412417
Seq. ID
                   uC-osflcyp105h03a1
Method
                   BLASTX
NCBI GI
                   g1352347
                   259
BLAST score
E value
                   3.0e-22
                   59
Match length
                   85
% identity
NCBI Description ELONGATION FACTOR 1-BETA A1 (EF-1-BETA)
                   >gi 480620 pir S37103 translation elongation factor eEF-1
```

412413

beta-Al chain - Arabidopsis thaliana (cv. Colombia)

Seq. No.

Seq. ID Method

NCBI GI

E value Match length

BLAST score

% identity

412422

BLASTN

g1574943 45

1.0e-16

65 92

uC-osflcyp106a03a1

```
412418
Seq. No.
                  uC-osflcyp105h04a1
Seq. ID
Method
                  BLASTX
                  g1076758
NCBI GI
                  157
BLAST score
                  2.0e-10
E value
Match length
                  35
                  89
% identity
                 heat-shock protein precursor - rye >gi_2130093_pir__$65776
NCBI Description
                  heat-shock protein, 82K, precursor - rye
                  >gi_556673_emb_CAA82945_ (Z30243) heat-shock protein
                  [Secale cereale]
                  412419
Seq. No.
                  uC-osflcyp105h06a1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3885882
BLAST score
                  171
                  4.0e-12
E value
                  37
Match length
                  92
% identity
NCBI Description (AF093629) inorganic pyrophosphatase [Oryza sativa]
Seq. No.
                  412420
                  uC-osflcyp106a02a1
Seq. ID
                  BLASTN
Method
NCBI GI
                  g435648
BLAST score
                  139
                  4.0e-72
E value
                  155
Match length
                  99
% identity
NCBI Description Rice mRNA for gamma-Tip, complete cds
Seq. No.
                  412421
                  uC-osflcyp106a02b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1729971
BLAST score
                  155
E value
                   9.0e-11
Match length
                  53
                   68
% identity
NCBI Description TONOPLAST INTRINSIC PROTEIN, GAMMA (GAMMA TIP)
                   (AQUAPORIN-TIP) >gi 1076745 pir__S52004 gamma-Tip protein -
                   rice >gi_473997_dbj_BAA05017_ (D25534) gamma-Tip [Oryza
                   sativa]
```

>gi_398608_emb_CAA52751_ (X74733) elongation factor-1 beta

A1 [Arabidopsis thaliana]

NCBI GI

BLAST score

```
NCBI Description Oryza sativa polyubiquitin (Rubq1) mRNA, complete cds
Seq. No.
                  412423
                  uC-osflcyp106a03b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g625509
BLAST score
                  361
E value
                  1.0e-34
Match length
                  77
                  26
% identity
NCBI Description ubiquitin precursor - Arabidopsis thaliana (fragment)
Seq. No.
                  412424
Seq. ID
                  uC-osflcyp106a05b1
Method
                  BLASTX
NCBI GI
                  g3860018
BLAST score
                  184
                  7.0e-18
E value
Match length
                  103
% identity
                  49
NCBI Description (AF091090) unknown [Homo sapiens]
Seq. No.
                  412425
                  uC-osflcyp106a09b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q5903071
BLAST score
                  220
E value
                  1.0e-17
Match length
                  116
% identity
                  40
NCBI Description (AC008017) Unknown protein [Arabidopsis thaliana]
Seq. No.
                   412426
Seq. ID
                  uC-osflcyp106a11a1
Method
                  BLASTN
NCBI GI
                  g600766
BLAST score
                  201
                  1.0e-109
E value
                  377
Match length
                   91
% identity
NCBI Description Oryza sativa cyclophilin 2 (Cyp2) gene, complete cds
                   412427
Seq. No.
Seq. ID
                  uC-osflcyp106a11b1
Method
                  BLASTN
NCBI GI
                  g600768
BLAST score
                  35
E value
                  1.0e-10
                  39
Match length
                   97
% identity
NCBI Description Oryza sativa cyclophilin 2 (Cyp2) mRNA, complete cds
                   412428
Seq. No.
Seq. ID
                  uC-osflcyp106b05b1
Method
                  BLASTX
```

53650

g2493131

4.0e-38 E value Match length 91 88 % identity VACUOLAR ATP SYNTHASE SUBUNIT B ISOFORM 1 (V-ATPASE B NCBI Description SUBUNIT) >gi 167108 (L11862) vacuolar ATPase B subunit [Hordeum vulgare] Seq. No. 412429 Seq. ID uC-osflcyp106b07b1 Method BLASTX NCBI GI q5103807 BLAST score 552 E value 9.0e-57 Match length 136 % identity 71 NCBI Description (AC007591) Contains similarity to gb AF014403 type-2 phosphatidic acid phosphatase alpha- $\overline{2}$ (PAP2 a2) from Homo sapiens. ESTs gb_T88254 and gb_AA394650 come from this gene. [Arabidopsis thaliana] 412430 Seq. No. uC-osflcyp106b08b1 Seq. ID Method BLASTX NCBI GI q3668069 BLAST score 584 E value 2.0e-60 Match length 159 70 % identity NCBI Description (U28007) Pto kinase interactor 1 [Lycopersicon esculentum] Seq. No. 412431 uC-osflcyp106b10b1 Seq. ID Method BLASTX NCBI GI g3005931 BLAST score 457 E value 2.0e-45 117 Match length 68 % identity NCBI Description (AJ005016) ABC transporter [Homo sapiens] Seq. No. 412432 Seq. ID uC-osflcyp106c01b1 BLASTX Method NCBI GI g5263321 BLAST score 170 E value 6.0e-12 Match length 111 40 % identity (AC007727) Contains similarity to gb AF033823 moira protein NCBI Description

from Drosophila melanogaster and contains a PF 00249

Myb-like DNA-binding domain. EST gb Z25609 comes from this

gene. [Arabidopsis thaliana]

412433 Seq. No.

Seq. ID uC-osflcyp106c03b1

Method BLASTX NCBI GI g4836948

```
BLAST score
                   243
E value
                   4.0e-21
Match length
                   58
% identity
                   81
NCBI Description
                   (AC006085) Similar to human CGI-33 protein [Arabidopsis
                   412434
Seq. No.
Seq. ID
                   uC-osflcyp106c04a1
Method
                   BLASTN
NCBI GI
                   g20280
BLAST score
                   205
                   1.0e-111
E value
Match length
                   350
% identity
                   99
NCBI Description Rice gene for phenylalanine ammonia-lyase (EC 4.3.1.5)
Seq. No.
                   412435
                   uC-osflcyp106c04b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   q82496
                   555
BLAST score
E value
                   5.0e-57
Match length
                   138
% identity
                   78
NCBI Description phenylalanine ammonia-lyase (EC 4.3.1.5) - rice
Seq. No.
                   412436
                   uC-osflcyp106c05a1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g115802
BLAST score
                   229
E value
                   6.0e - 19
Match length
                   44
% identity
                   95
NCBI Description
                   CHLOROPHYLL A-B BINDING PROTEIN 36 PRECURSOR (LHCII TYPE I
                   CAB-36) (LHCP) >gi_100311_pir__S21827 chlorophyll a/b-binding protein (cab-36) - common tobacco
                   >qi 19827 emb CAA41188 (X58230) chlorophyll a/b binding
                   protein [Nicotiana tabacum]
                   412437
Seq. No.
Seq. ID
                   uC-osflcyp106c05b1
Method
                   BLASTX
NCBI GI
                   g3126854
BLAST score
                   477
E value
                   4.0e-48
                   93
Match length
% identity
NCBI Description (AF061577) chlorophyll a/b binding protein [Oryza sativa]
Seq. No.
                   412438
Seq. ID
                   uC-osflcyp106c06b1
Method
                   BLASTX
NCBI GI
                   g462195
BLAST score
                   495
E value
                   6.0e-50
```

Match length 114 85 % identity PROTEIN TRANSLATION FACTOR SUI1 HOMOLOG (GOS2 PROTEIN) NCBI Description >gi 100682 pir S21636 GOS2 protein - rice >gi_20238 emb_CAA36190_ (X51910) GOS2 [Oryza sativa] >gi_3789950 (AF094774) translation initiation factor [Oryza sativa] 412439 Seq. No. Seq. ID uC-osflcyp106c08b1 Method BLASTX NCBI GI g6102610 BLAST score 273 E value 5.0e-24 Match length 144 42 % identity NCBI Description (AF187317) CAF protein [Arabidopsis thaliana] Seq. No. 412440 uC-osflcyp106c09b1 Seq. ID Method BLASTN NCBI GI g2196541 BLAST score 72 8.0e-33 E value Match length 84 % identity 96 NCBI Description Oryza sativa glycine-rich protein mRNA, complete cds Seq. No. 412441 uC-osflcyp106c10b1 Seq. ID Method BLASTX NCBI GI q455399 BLAST score 464 E value 2.0e-46 Match length 94 97 % identity NCBI Description (D21068) dihydrolipoamide acetyltransferase [Oryza sativa] 412442 Seq. No. Seq. ID uC-osflcyp106c11b1 Method BLASTX NCBI GI g3063468 BLAST score 158 9.0e-11 E value Match length 46 % identity NCBI Description (AC003981) F22013.30 [Arabidopsis thaliana] 412443 Seq. No. Seq. ID uC-osflcyp106d04b1 Method BLASTX q4850400 NCBI GI BLAST score 231 E value 4.0e-19 Match length 54 % identity NCBI Description (AC007357) Similar to gb_M86917 oxysterol-binding protein



from Homo sapiens. [Arabidopsis thaliana]

Seq. No. 412444 uC-osflcyp106d05b1 Seq. ID Method BLASTN NCBI GI q20177 BLAST score 100 3.0e-49E value Match length 112 97 % identity NCBI Description Rice cab1R gene for light harvesting chlorophyll a/b-binding protein 412445 Seq. No. Seq. ID uC-osflcyp106d10a1 BLASTN Method NCBI GI g5091496 BLAST score 52 3.0e-20 E value Match length 135 95 % identity Oryza sativa genomic DNA, chromosome 6, clone P0680A03, NCBI Description complete sequence 412446 Seq. No. Seq. ID uC-osflcyp106d10b1 Method BLASTX NCBI GI q5091498 BLAST score 276 E value 1.0e-2453 Match length 100 % identity (AB023482) ESTs AU058067(E20733), AAU058070(E20873) NCBI Description correspond to a region of the predicted gene.; Similar to Populus tremuloides caffeoyl-CoA 3-O-methyltransferase mRNA, complete cds.(U27116) [Oryza sativa] 412447 Seq. No. Seq. ID uC-osflcyp106d11b1 Method BLASTX NCBI GI g4218121 BLAST score 229 7.0e-19 E value Match length 119 % identity 37 NCBI Description (AL035353) putative protein [Arabidopsis thaliana] 412448 Seq. No. Seq. ID uC-osflcyp106d12b1 Method BLASTX NCBI GI g120507 BLAST score 607 E value 3.0e-63 131 Match length % identity 87

53654

precursor (clone FM1) - maize (fragment)

NCBI Description FERRITIN 1 PRECURSOR >gi 82687 pir S22498 ferritin

```
>gi_22276_emb_CAA43663_ (X61391) ferritin [Zea mays]
                  412449
Seq. No.
                  uC-osflcyp106e01b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q5080790
BLAST score
                  179
                  1.0e-13
E value
Match length
                  59
                  59
% identity
                  (AC007576) Similar to mitochondrial carrier proteins
NCBI Description
                  [Arabidopsis thaliana]
                  412450
Seq. No.
Seq. ID
                  uC-osflcyp106e02b1
Method
                  BLASTX
NCBI GI
                  q4138343
BLAST score
                  480
E value
                  4.0e-65
Match length
                  156
% identity
                  72
NCBI Description (AJ011979) RNA-directed RNA polymerase [Petunia x hybrida]
                  412451
Seq. No.
                  uC-osflcyp106e03b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2618698
BLAST score
                  143
                  2.0e-09
E value
Match length
                  41
% identity
                  66
NCBI Description (AC002510) unknown protein [Arabidopsis thaliana]
                  412452
Seq. No.
Seq. ID
                  uC-osflcyp106e07b1
Method
                  BLASTX
NCBI GI
                  g421991
BLAST score
                  172
E value
                  8.0e-13
Match length
                  47
% identity
                  68
                  1,4-alpha-glucan branching enzyme (EC 2.4.1.18) sbel
NCBI Description
                  precursor - rice >gi 287404 dbj BAA01616 (D10838)
                  1,4-alpha-glucan branching enzyme [Oryza sativa]
Seq. No.
                  412453
                  uC-osflcyp106e11a1
Seq. ID
                  BLASTN
Method
NCBI GI
                  g20257
                  151
BLAST score
E value
                  3.0e-79
```

Seq. No. 412454

Match length

% identity

Seq. ID uC-osflcyp106e11b1

175

98

53655

NCBI Description O.sativa hsp82 gene for heat shock protein

Seq. No.

```
Method
                   BLASTX
NCBI GI
                   g547683
BLAST score
                   490
E value
                   1.0e-49
Match length
                   103
% identity
                   93
NCBI Description HEAT SHOCK COGNATE PROTEIN 80 >gi_170456 (M96549) heat
                   shock cognate protein 80 [Solanum lycopersicum]
                   >gi_445601_prf__1909348A heat shock protein hsp80
                   [Lycopersicon esculentum]
                   412455
Seq. No.
Seq. ID
                   uC-osflcyp106e12b1
Method
                   BLASTX
NCBI GI
                   q120670
BLAST score
                   282
E value
                   1.0e-25
Match length
                   57
                   96
% identity
NCBI Description
                   GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC 1
                   >gi_100879_pir__S06879 glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1.12) C - maize
                   >gi_295853_emb_CAA33620_ (X15596) GAPDH [Zea mays]
Seq. No.
                   412456
                   uC-osflcyp106f05b1
Seq. ID
Method
                   BLASTN
NCBI GI
                   q20181
BLAST score
                   84
E value
                   7.0e-40
Match length
                   100
% identity
                   96
NCBI Description Rice cab2R gene for light harvesting chlorophyll
                   a/b-binding protein
Seq. No.
                   412457
Seq. ID
                   uC-osflcyp106f06b1
                   BLASTX
Method
NCBI GI
                   q6056376
BLAST score
                   188
E value
                   1.0e-14
                   52
Match length
% identity
NCBI Description (AC009894) Similar to serine/threonine kinases [Arabidopsis
                   thaliana]
                   412458
Seq. No.
Seq. ID
                   uC-osflcyp106f09a1
Method
                   BLASTN
NCBI GI
                   g5042437
BLAST score
                   51
                   8.0e-20
E value
                   90
Match length
% identity
NCBI Description Oryza sativa BAC T49B20 genomic sequence, complete sequence
```

```
uC-osflcyp106f09b1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g5042437
BLAST score
                  63
E value
                  2.0e-27
Match length
                  95
                  92
% identity
NCBI Description Oryza sativa BAC T49B20 genomic sequence, complete sequence
                  412460
Seq. No.
Seq. ID
                  uC-osflcyp106f10b1
Method
                  BLASTX
NCBI GI
                  q1673366
BLAST score
                  435
E value
                  6.0e-43
Match length
                  142
% identity
                  (Z22673) cytosolic tRNA-Ala synthetase [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  412461
Seq. ID
                  uC-osflcyp106f12b1
Method
                  BLASTX
NCBI GI
                  g5419931
BLAST score
                  290
E value
                  4.0e-26
Match length
                  84
                  70
% identity
NCBI Description (AJ007496) protein phosphatase 2A catalytic subunit
                  [Nicotiana tabacum]
                  412462
Seq. No.
                  uC-osflcyp106g01b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q457682
BLAST score
                  194
                  2.0e-15
E value
Match length
                  44
                  89
% identity
NCBI Description (D25237) possible scar protein coding sequence [Oryza
                  sativa]
                  412463
Seq. No.
Seq. ID
                  uC-osflcyp106g03b1
Method
                  BLASTX
NCBI GI
                  g4586058
BLAST score
                  340
                  7.0e-32
E value
                  151
Match length
                  50
% identity
NCBI Description (AC007020) unknown protein [Arabidopsis thaliana]
                  412464
Seq. No.
Seq. ID
                  uC-osflcyp106g05a1
```

Method BLASTN
NCBI GI g1136121
BLAST score 273

```
1.0e-152
E value
Match length
                  381
                  96
% identity
NCBI Description O.sativa mRNA for alpha-tubulin (clone OSTA-136)
                  412465
Seq. No.
                  uC-osflcyp106g05b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1136122
BLAST score
                  774
E value
                  1.0e-82
Match length
                  147
% identity
                  97
NCBI Description (X91807) alfa-tubulin [Oryza sativa]
                  412466
Seq. No.
                  uC-osflcyp106g08b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1944205
BLAST score
                  154
E value
                  3.0e-10
Match length
                  56
% identity
                  54
NCBI Description (AB002820) RicMT [Oryza sativa]
Seq. No.
                  412467
Seq. ID
                  uC-osflcyp106h03b1
Method
                  BLASTX
NCBI GI
                  g4587611
BLAST score
                  354
                  1.0e-33
E value
                  93
Match length
                  72
% identity
NCBI Description (AC006951) putative 40S ribosomal protein S17 [Arabidopsis
                  thaliana]
Seq. No.
                   412468
                  uC-osflcyp106h04b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3309086
                  308
BLAST score
E value
                  2.0e-28
                  89
Match length
                   66
% identity
NCBI Description
                  (AF076253) calcineurin B-like protein 3 [Arabidopsis
                   thaliana] >gi 4938495 emb CAB43853.1 (AL078465)
                   calcineurin B-like protein 3 [Arabidopsis thaliana]
                   412469
Seq. No.
Seq. ID
                  uC-osflcyp106h05b1
                  BLASTX
Method
NCBI GI
                  g5729838
BLAST score
                  342
E value
                  4.0e-35
Match length
                  103
% identity
                  70
NCBI Description glioma-amplified sequence-41 >gi 4210496 (U61384) GAS41
```

Match length

NCBI Description

% identity

54

thaliana]

protein [Homo sapiens] Seq. No. 412470 Seq. ID uC-osflcyp106h07b1 Method BLASTN NCBI GI g5821066 BLAST score 35 E value 1.0e-10 Match length 51 92 % identity NCBI Description Oryza sativa gene for WHO4, complete cds 412471 Seq. No. Seq. ID uC-osflcyp106h08b1 Method BLASTX NCBI GI g3860319 BLAST score 150 E value 3.0e-10 Match length 34 % identity 76 NCBI Description (AJ012686) nucleolar protein [Cicer arietinum] Seq. No. 412472 Seq. ID uC-osflcyp106h10b1 Method BLASTX NCBI GI q115787 BLAST score 374 5.0e-36 E value 92 Match length % identity 84 CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I NCBI Description CAB-2) (LHCP) >gi_82461_pir__S03706 chlorophyll a/b-binding protein 2R precursor - rice >gi_20182_emb_CAA32109_ (X13909) chlorophyll a/b-binding preprotein (AA -28 to 235) [Oryza sativa] 412473 Seq. No. Seq. ID uC-osflcyp106h11b1 Method BLASTX NCBI GI g3786007 393 BLAST score E value 4.0e-38 138 Match length 51 % identity NCBI Description (AC005499) hypothetical protein [Arabidopsis thaliana] Seq. No. 412474 Seq. ID uC-osflcyp107a02b1 BLASTX Method NCBI GI q2160690 BLAST score 157 E value 1.0e-10

(U73526) B' regulatory subunit of PP2A [Arabidopsis



Seq. No. 412475 Seq. ID uC-osf

Geq. ID uC-osflcyp107a07b1

Method BLASTX
NCBI GI g2130073
BLAST score 632
E value 3.0e-66
Match length 128
% identity 98

NCBI Description fructose-bisphosphate aldolase (EC 4.1.2.13) isoenzyme C-1, cytosolic - rice >gi_786178 dbj BAA08845 (D50307) aldolase

C-1 [Oryza sativa] >gi 790970 dbj BAA08830 (D50301)

aldolase C-1 [Oryza sativa]

Seq. No. 412476

Seq. ID uC-osflcyp107a09b1

Method BLASTX
NCBI GI g2493650
BLAST score 449
E value 1.0e-44
Match length 124
% identity 77

NCBI Description RUBISCO SUBUNIT BINDING-PROTEIN BETA SUBUNIT (60 KD

CHAPERONIN BETA SUBUNIT) (CPN-60 BETA)

>gi 1167858 emb CAA93139_ (Z68903) chaperonin [Secale

cereale]

Seq. No. 412477

Seq. ID uC-osflcyp107b01b1

Method BLASTX
NCBI GI g5734733
BLAST score 347
E value 5.0e-33
Match length 95
% identity 65

NCBI Description (AC007259) Hypothetical protein [Arabidopsis thaliana]

Seq. No. 412478

Seq. ID uC-osflcyp107b03b1

Method BLASTX
NCBI GI g730456
BLAST score 346
E value 8.0e-33
Match length 72
% identity 90

NCBI Description 40S RIBOSOMAL PROTEIN S19

Seq. No. 412479

Seq. ID uC-osflcyp107b08b1

Method BLASTX
NCBI GI g1877397
BLAST score 716
E value 7.0e-76
Match length 147
% identity 88

NCBI Description (Y11591) shaggy-like kinase [Ricinus communis]

Seq. No. 412480

uC-osflcyp107b10b1 Seq. ID Method BLASTX NCBI GI a4512659 BLAST score 545 5.0e-56 E value Match length 121 83 % identity (AC006931) putative protein kinase [Arabidopsis thaliana] NCBI Description >gi_4544465_gb_AAD22372.1_AC006580_4 (AC006580) putative protein kinase [Arabidopsis thaliana] Seq. No. 412481 uC-osflcyp107c01b1 Seq. ID Method BLASTX NCBI GI q5733874 187 BLAST score E value 2.0e-14 Match length 67 46 % identity NCBI Description (AC007932) F11A17.8 [Arabidopsis thaliana] 412482 Seq. No. uC-osflcyp107c04b1 Seq. ID Method BLASTX NCBI GI q1814403 BLAST score 359 3.0e - 34E value 91 Match length 76 % identity NCBI Description (U84889) methionine synthase [Mesembryanthemum crystallinum] Seq. No. 412483 Seq. ID uC-osflcyp107c09b1 Method BLASTX NCBI GI g5738362 BLAST score 309 E value 1.0e-28 77 Match length 74 % identity NCBI Description (AL021637) putative protein [Arabidopsis thaliana] Seq. No. 412484 Seq. ID uC-osflcyp107c10b1 Method BLASTX NCBI GI g1814403 BLAST score 703 E value 2.0e-74 149 Match length 88 % identity (U84889) methionine synthase [Mesembryanthemum NCBI Description crystallinum]

Seq. No. 412485

Seq. ID uC-osflcyp107c11b1

Method BLASTN NCBI GI g886691

BLAST score 41 E value 3.0e-14 57 Match length 93 % identity NCBI Description O.sativa mRNA for lipid transfer protein, a15 Seq. No. 412486 Seq. ID uC-osflcyp107c12b1 Method BLASTX NCBI GI

Method BLASTX
NCBI GI g542179
BLAST score 597
E value 4.0e-62
Match length 115
% identity 99

NCBI Description alpha tubulin - maize >gi_629837_pir__S39998 tubulin alpha chain - maize (fragment) >gi_393401_emb_CAA52158_ (X73980)

alpha tubulin [Zea mays]

Seq. No. 412487

Seq. ID uC-osflcyp107d01b1

Method BLASTX
NCBI GI g3176691
BLAST score 329
E value 8.0e-31
Match length 97
% identity 68

NCBI Description (AC003671) Contains homology to serine/threonine protein kinase gb X99618 from Mycobacterium tuberculosis. ESTs

gb_F14403, gb_F14404, and gb_N96730 come from this gene.

[Arabidopsis thaliana]

Seq. No. 412488

Seq. ID uC-osflcyp107d03b1

Method BLASTX
NCBI GI g5732703
BLAST score 191
E value 5.0e-15
Match length 35
% identity 97

NCBI Description (AF159387) thioredoxin-like protein [Lolium perenne]

Seq. No. 412489

Seq. ID uC-osflcyp107d04b1

Method BLASTN
NCBI GI g1070353
BLAST score 82
E value 2.0e-38
Match length 98
% identity 96

NCBI Description H.vulgare mRNA for Hv14-3-3b

Seq. No. 412490

Seq. ID uC-osflcyp107d06b1

Method BLASTX
NCBI GI g3914005
BLAST score 162
E value 4.0e-12

Match length 59 78 % identity NCBI Description MITOCHONDRIAL LON PROTEASE HOMOLOG 1 PRECURSOR >gi 1816586 (U85494) LON1 protease [Zea mays] Seq. No. 412491 Seq. ID uC-osflcyp107d09b1 Method BLASTX NCBI GI q5733874 BLAST score 317 E value 4.0e-29 Match length 162 % identity 37 NCBI Description (AC007932) F11A17.8 [Arabidopsis thaliana] 412492 Seq. No. Seq. ID uC-osflcyp107d11b1 Method BLASTX NCBI GI g2407279 BLAST score 169 E value 6.0e-12 Match length 61 % identity 57 NCBI Description (AF017362) aldolase [Oryza sativa] Seq. No. 412493 Seq. ID uC-osflcyp107d12b1 Method BLASTX NCBI GI g3914005 BLAST score 752 E value 4.0e-80 Match length 154 97 % identity NCBI Description MITOCHONDRIAL LON PROTEASE HOMOLOG 1 PRECURSOR >gi_1816586 (U85494) LON1 protease [Zea mays] Seq. No. 412494

Seq. ID uC-osflcyp107e01b1

Method BLASTX NCBI GI g115787 BLAST score 224 E value 1.0e-18 Match length 64 78 % identity

NCBI Description CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I

CAB-2) (LHCP) >gi 82461 pir S03706 chlorophyll a/b-binding

protein 2R precursor - rice >gi 20182 emb CAA32109

(X13909) chlorophyll a/b-binding preprotein (AA -28 to 235)

[Oryza sativa]

Seq. No. 412495

Seq. ID uC-osflcyp107e09b1

BLASTX Method NCBI GI g1352830 BLAST score 589 E value 4.0e-61 Match length 124

% identity NCBI Description VACUOLAR ATP SYNTHASE CATALYTIC SUBUNIT A (V-ATPASE 69 KD SUBUNIT) >gi 1049253 (U36436) vacuolar ATPase 69 kDa subunit [Zea mays] Seq. No. 412496 Seq. ID uC-osflcyp107f01b1 Method BLASTX NCBI GI q2662343 577 BLAST score E value 1.0e-59 Match length 110 100 % identity NCBI Description (D63581) EF-1 alpha [Oryza sativa] 412497 Seq. No. Seq. ID uC-osflcyp107f06b1 Method BLASTX NCBI GI g3023713 BLAST score 240 E value 1.0e-20 Match length 51 92 % identity NCBI Description ENOLASE (2-PHOSPHOGLYCERATE DEHYDRATASE) (2-PHOSPHO-D-GLYCERATE HYDRO-LYASE) (OSE1) >gi_780372 (U09450) enolase [Oryza sativa] 412498 Seq. No. Seq. ID uC-osflcyp107f11b1 Method BLASTX NCBI GI g1235569 BLAST score 295 3.0e-27 E value Match length 56 98 % identity NCBI Description (X93301) NAD(P)H oxidase [Oryza sativa] 412499 Seq. No. Seq. ID uC-osflcyp107g01b1

BLASTN Method NCBI GI g20369 BLAST score 77 E value 9.0e-36 Match length 105 % identity 93

NCBI Description Oryza sativa shoot GS2 mRNA for chloroplastic glutamine

synthetase (EC 6.3.1.2) (clone lambda-GS31)

>gi 2170909 dbj E02681_E02681 cDNA encoding precursor of

chloroplast localising glutamine synthetase

412500 Seq. No.

Seq. ID uC-osflcyp107g05b1

BLASTN Method NCBI GI q3777597 BLAST score 173 E value 9.0e-93 Match length 173

NCBI GI

BLAST score

```
% identity
                    Oryza sativa clone LS273 30S ribosomal protein S17 (rps17)
NCBI Description
                    mRNA, nuclear gene encoding chloroplast protein, complete
                    412501
Seq. No.
                    uC-osflcyp107g06b1
Seq. ID
Method
                    BLASTX
NCBI GI
                    g1171008
BLAST score
                    514
                    4.0e-52
E value
Match length
                    140
% identity
                    64
                    POLLEN ALLERGEN PHL P 1 PRECURSOR (PHL P I)
NCBI Description
                    >gi_629812_pir__S44182 allergen Phl p I - common timothy
                    >gi_473360_emb_CAA55390_ (X78813) Phl p I allergen [Phleum
                    pratense]
                    412502
Seq. No.
                    uC-osflcyp107g08b1
Seq. ID
Method
                    BLASTX
NCBI GI
                    q70642
BLAST score
                    449
E value
                    8.0e-45
                    92
Match length
                    20
% identity
                    ubiquitin precursor - Arabidopsis thaliana
NCBI Description
                    >gi_17678_emb_CAA31331_ (X12853) polyubiquitin (AA 1 - 382)
[Arabidopsis thaliana] >gi_987519 (U33014) polyubiquitin
[Arabidopsis thaliana] >gi_226499_prf__1515347A
                    poly-ubiquitin [Arabidopsis thaliana]
                    412503
Seq. No.
                    uC-osflcyp107h03b1
Seq. ID
Method
                    BLASTX
NCBI GI
                    g5262759
BLAST score
                    772
E value
                    2.0e-82
Match length
                    173
% identity
NCBI Description (AL080283) putative protein [Arabidopsis thaliana]
Seq. No.
                    412504
                    uC-osflcyp107h07b1
Seq. ID
Method
                    BLASTX
NCBI GI
                    q4914411
BLAST score
                    325
                    2.0e-30
E value
                    105
Match length
% identity
                    64
NCBI Description (AL050352) putative protein [Arabidopsis thaliana]
Seq. No.
                    412505
                    uC-osflcyp107h08b1
Seq. ID
Method
                    BLASTX
```

53665

g2286153



E value 1.0e-33 Match length 80 % identity 86

NCBI Description (AF007581) cytoplasmic malate dehydrogenase [Zea mays]

Seq. No. 412506

Seq. ID uC-osflcyp107h09b1

Method BLASTX
NCBI GI g3650033
BLAST score 170
E value 2.0e-12
Match length 47
% identity 66

NCBI Description (AC005396) unknown protein [Arabidopsis thaliana]

Seq. No. 412507

Seq. ID uC-osflcyp107h10b1

Method BLASTX
NCBI GI g549063
BLAST score 280
E value 2.0e-25
Match length 55
% identity 96

NCBI Description TRANSLATIONALLY CONTROLLED TUMOR PROTEIN HOMOLOG (TCTP)

>gi_1072464_pir__A38958 IgE-dependent histamine-releasing
factor homolog - rice >gi_303835_dbj_BAA02151_ (D12626)

21kd polypeptide [Oryza sativa]

Seq. No. 412508

Seq. ID uC-osflcyp107h12b1

Method BLASTX
NCBI GI g3193296
BLAST score 205
E value 2.0e-16
Match length 69

% identity 57

NCBI Description (AF069298) similar to pectinesterase [Arabidopsis thaliana]

Seq. No. 412509

Seq. ID uC-osflcyp108a03b1

Method BLASTN
NCBI GI g4218534
BLAST score 42
E value 3.0e-14
Match length 46
% identity 98

NCBI Description Triticum sp. mRNA for GRAB1 protein

Seq. No. 412510

Seq. ID uC-osflcyp108a06b1

Method BLASTX
NCBI GI g1168260
BLAST score 297
E value 2.0e-48
Match length 138
% identity 64

NCBI Description ASPARTATE AMINOTRANSFERASE, MITOCHONDRIAL PRECURSOR

(TRANSAMINASE A) >gi_629503_pir__S47490 aspartate transaminase (EC 2.6.1.1) - Arabidopsis thaliana >gi_1361984_pir__S56657 aspartate transaminase (EC 2.6.1.1) precursor, chloroplast - Arabidopsis thaliana >gi_531555_emb_CAA56932_ (X81026) aspartate aminotransferase [Arabidopsis thaliana] >gi_1017411_emb_CAA62972_ (X91865) aspartate aminotransferase [Arabidopsis thaliana]

Seq. No. 412511

Seq. ID uC-osflcyp108a07b1

Method BLASTX
NCBI GI g2832628
BLAST score 250
E value 4.0e-27
Match length 114
% identity 58

NCBI Description (AL021711) putative protein [Arabidopsis thaliana]

Seq. No. 412512

Seq. ID uC-osflcyp108a09b1

Method BLASTX
NCBI GI g2244949
BLAST score 222
E value 5.0e-18
Match length 95
% identity 49

NCBI Description (Z97339) cytochrome c oxidoreductase like protein

[Arabidopsis thaliana]

Seq. No. 412513

Seq. ID uC-osflcyp108a12b1

Method BLASTX
NCBI GI g1084455
BLAST score 333
E value 3.0e-31
Match length 62
% identity 100

NCBI Description peptidylprolyl isomerase (EC 5.2.1.8) Cyp2 - rice >gi 600767 (L29469) cyclophilin 2 [Oryza sativa]

Seq. No. 412514

Seq. ID uC-osflcyp108b07b1

Method BLASTX
NCBI GI g115794
BLAST score 253
E value 3.0e-22
Match length 62
% identity 79

NCBI Description CHLOROPHYLL A-B BINDING PROTEIN 13 PRECURSOR (LHCII TYPE

III CAB-13) >gi_72748_pir__CDTO33 chlorophyll a/b-binding

protein type III precursor (cab-13) - tomato >gi_19277_emb_CAA42818_ (X60275) LHCII type III

[Lycopersicon esculentum]

Seq. No. 412515

Seq. ID uC-osflcyp108b08b1

```
Method
                  BLASTX
NCBI GI
                  g1666234
BLAST score
                  288
                  5.0e-26
E value
Match length
                  58
% identity
                  95
                 (U76193) actin [Pisum sativum] >gi 1724143 (U81049) actin
NCBI Description
                  [Pisum sativum]
Seq. No.
                  412516
                  uC-osflcyp108b10b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4519539
BLAST score
                  470
E value
                  5.0e-47
Match length
                  136
% identity
                  67
                  (AB016256) NAD-dependent sorbitol dehydrogenase [Malus
NCBI Description
                  domestica]
Seq. No.
                  412517
Seq. ID
                  uC-osflcyp108b11b1
Method
                  BLASTN
NCBI GI
                  g3126853
BLAST score
                  45
E value
                  3.0e-16
Match length
                  177
% identity
                  82
                  Oryza sativa chlorophyll a/b binding protein (RCABP89)
NCBI Description
                  mRNA, nuclear gene encoding chloroplast protein, complete
                  cds
                  412518
Seq. No.
Seq. ID
                  uC-osflcyp108c09b1
Method
                  BLASTX
NCBI GI
                  g2130069
BLAST score
                  685
E value
                  3.0e-72
Match length
                  139
                  91
% identity
NCBI Description catalase (EC 1.11.1.6) catA - rice
                  >gi 1261858_dbj_BAA06232_ (D29966) catalase [Oryza sativa]
Seq. No.
                  412519
Seq. ID
                  uC-osflcyp108c10b1
                  BLASTX
Method
NCBI GI
                  g2293480
BLAST score
                  353
E value
                  2.0e-33
Match length
                  92
% identity
NCBI Description (AF011331) glycine-rich protein [Oryza sativa]
```

Seq. No. 412520

Seq. ID uC-osflcyp108c11b1

Method BLASTN NCBI GI g2407274

% identity

94

```
BLAST score
                  132
                  3.0e-68
E value
                  156
Match length
                  96
% identity
NCBI Description Oryza sativa lipid transfer protein LPT III mRNA, complete
                  cds
Seq. No.
                  412521
Seq. ID
                  uC-osflcyp108d01b1
Method
                  BLASTX
NCBI GI
                  q4204859
BLAST score
                  175
E value
                  1.0e-14
Match length
                  105
% identity
                   48
NCBI Description (U55859) heat shock protein 80 [Triticum aestivum]
                   412522
Seq. No.
Seq. ID
                  uC-osflcyp108d11b1
Method
                  BLASTX
NCBI GI
                   g3913018
BLAST score
                  825
E value
                   1.0e-88
                  167
Match length
% identity
                   98
NCBI Description FRUCTOSE-BISPHOSPHATE ALDOLASE, CHLOROPLAST PRECURSOR
                   (ALDP) >gi 218155 dbj BAA02730 (D13513) chloroplastic
                   aldolase [Oryza sativa]
                   412523
Seq. No.
                   uC-osflcyp108d12b1
Seq. ID
                  BLASTX
Method
NCBI GI
                   q4580389
BLAST score
                   189
                   3.0e-14
E value
                  60
Match length
                   58
% identity
NCBI Description (AC007171) unknown protein [Arabidopsis thaliana]
                   412524
Seq. No.
Seq. ID
                   uC-osflcyp108e10b1
                   BLASTX
Method
NCBI GI
                   g2464852
BLAST score
                   201
E value
                   1.0e-15
                   100
Match length
                   45
% identity
NCBI Description (Z99707) putative protein [Arabidopsis thaliana]
Seq. No.
                   412525
                   uC-osflcyp108e11b1
Seq. ID
                   BLASTX
Method
                   q6006363
NCBI GI
BLAST score
                   446
E value
                   2.0e-44
                   93
Match length
```

NCBI Description (AP000559) ESTs AU078183(C62904),C73912(E21020) correspond to a region of the predicted gene.; Similar to water stress inducible protein (U74296) [Oryza sativa]

Seq. No. 412526

Seq. ID uC-osflcyp108f02b1

Method BLASTX
NCBI GI g3163946
BLAST score 212
E value 2.0e-17
Match length 41
% identity 98

NCBI Description (AJ005599) alpha-tubulin 1 [Eleusine indica]

Seq. No. 412527

Seq. ID uC-osflcyp108f03b1

Method BLASTX
NCBI GI g5091520
BLAST score 704
E value 2.0e-74
Match length 158
% identity 87

NCBI Description (AB023482) ESTs AU058081(E30812), AU058365(E50679),

AU030138(E50679) correspond to a region of the predicted gene.; Similar to Spinacia oleracea mRNA for proteasome

37kD subunit.(X96974) [Oryza sativa]

Seq. No. 412528

Seq. ID uC-osflcyp108f10b1

Method BLASTX
NCBI GI g4512667
BLAST score 379
E value 2.0e-36
Match length 100
% identity 72

NCBI Description (AC006931) putative MAP kinase [Arabidopsis thaliana]

Seq. No. 412529

Seq. ID uC-osflcyp108f11b1

Method BLASTX
NCBI GI g1632768
BLAST score 532
E value 2.0e-54
Match length 119
% identity 90

NCBI Description (D84408) calcium dependent protein kinase [Zea mays]

Seq. No. 412530

Seq. ID uC-osflcyp108g02b1

Method BLASTX
NCBI GI g3128168
BLAST score 221
E value 9.0e-18
Match length 56
% identity 61

NCBI Description (AC004521) putative carboxyl-terminal peptidase

[Arabidopsis thaliana]

Seq. No.

412536

412531 Seq. No. Seq. ID uC-osflcyp108g11b1 ${\tt BLASTX}$ Method NCBI GI g2245026 BLAST score 458 E value 1.0e-45 Match length 134 72 % identity NCBI Description (Z97341) hypothetical protein [Arabidopsis thaliana] 412532 Seq. No. Seq. ID uC-osflcyp108g12b1 Method BLASTX NCBI GI g3800993 BLAST score 152 E value 1.0e-09 Match length 147 % identity 31 (AF100669) contains similarity to prolyl oligopeptidase NCBI Description family (Pfam: Prolyl oligopep.hmm, score: 15.06) [Caenorhabditis elegans] Seq. No. 412533 Seq. ID uC-osflcyp108h03b1 Method BLASTN NCBI GI g4097337 BLAST score 149 E value 4.0e-78 Match length 246 % identity 96 NCBI Description Oryza sativa metallothionein-like protein mRNA, complete cds 412534 Seq. No. Seq. ID uC-osflcyp108h05b1 BLASTX Method NCBI GI g1006698 BLAST score 177 E value 2.0e-13 Match length 52 71 % identity (Z49766) rubisco subunit binding protein, beta subunit NCBI Description (60kD chaperonin beta subunit) (cpn-60 beta) [Pseudotsuga menziesii] 412535 Seq. No. Seq. ID uC-osflcyp108h07b1 Method BLASTX NCBI GI q4512667 183 BLAST score E value 4.0e-1451 Match length % identity NCBI Description (AC006931) putative MAP kinase [Arabidopsis thaliana]

NCBI Description

thaliana]



```
uC-osflcyp108h11b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1136122
BLAST score
                  460
E value
                  2.0e-48
Match length
                  111
% identity
                  82
NCBI Description (X91807) alfa-tubulin [Oryza sativa]
Seq. No.
                  412537
Seq. ID
                  uC-osflcyp109a01a1
Method
                  BLASTX
NCBI GI
                  q4587571
BLAST score
                  188
E value
                  4.0e-14
Match length
                  50
% identity
                  66
NCBI Description
                  (AC006550) Belongs to the PF 01027 Uncharacterized protein
                  family UPF0005 with 7 transmembrane domains. [Arabidopsis
                  thaliana]
                  412538
Seq. No.
Seq. ID
                  uC-osflcyp109a02a1
Method
                  BLASTX
NCBI GI
                  q487046
BLAST score
                  287
E value
                  2.0e-27
                  71
Match length
% identity
                  92
                  photosystem I chain II precursor - wood tobacco
NCBI Description
                  >gi_407769 dbj BAA02871 (D13718) PSI-D1 precursor
                  [Nicotiana sylvestris]
Seq. No.
                  412539
Seq. ID
                  uC-osflcyp109a02b1
Method
                  BLASTX
NCBI GI
                  g548603
BLAST score
                  481
E value
                  2.0e-48
Match length
                  143
% identity
                  71
NCBI Description PHOTOSYSTEM I REACTION CENTRE SUBUNIT II PRECURSOR
                  (PHOTOSYSTEM I 20 KD SUBUNIT) (PSI-D)
                  >gi_478404_pir__JQ2247 photosystem I chain D precursor -
                  barley >gi_167085 (M98254) PSI-D subunit [Hordeum vulgare]
Seq. No.
                  412540
Seq. ID
                  uC-osflcyp109a04a1
Method
                  BLASTX
NCBI GI
                  g3287693
BLAST score
                  247
E value
                  5.0e-21
Match length
                  59
% identity
```

53672

(AC003979) Similar to LIM17 gene product gb_1653769 from the genome of Synechocystis sp. qb D90916. [Arabidopsis

Seq. No. 412541 Seq. ID uC-osflcyp109a04b1 Method BLASTX NCBI GI g3287693 BLAST score 313 E value 1.0e-28 77 Match length 77 % identity (AC003979) Similar to LIM17 gene product gb_1653769 from NCBI Description the genome of Synechocystis sp. gb D90916. [Arabidopsis thaliana] 412542 Seq. No. Seq. ID uC-osflcyp109a05b1 Method BLASTX NCBI GI g2384671 BLAST score 416 E value 1.0e-40 Match length 101 % identity 80 NCBI Description (AF012657) putative potassium transporter AtKT2p [Arabidopsis thaliana] Seq. No. 412543 Seq. ID uC-osflcyp109a07a1 Method BLASTN NCBI GI g3819189 BLAST score 36 E value 1.0e-10 Match length 48 94 % identity NCBI Description Hordeum vulgare partial mRNA; clone cMWG0654 412544 Seq. No. Seq. ID uC-osflcyp109a07b1 Method BLASTX NCBI GI g3193302 BLAST score 311 E value 2.0e-28 Match length 133 % identity 52 NCBI Description (AF069298) contains similarity to a protein kinase domain (Pfam: pkinase.hmm, score: 166.20) and to legume lectins beta domain (Pfam: lectin legB.hmm, score: 139.32) [Arabidopsis thaliana] 412545 Seq. No. Seq. ID uC-osflcyp109a08b1 Method BLASTX NCBI GI g3297809 BLAST score 177 E value 9.0e-13 Match length 132 % identity NCBI Description (AL031032) putative protein [Arabidopsis thaliana]

Seq. ID

```
412546
Seq. No.
Seq. ID
                  uC-osflcyp109a10a1
Method
                  BLASTX
NCBI GI
                  g2130069
BLAST score
                  159
E value
                  1.0e-10
Match length
                  36
                  86
% identity
NCBI Description catalase (EC 1.11.1.6) catA - rice
                  >gi_1261858_dbj_BAA06232_ (D29966) catalase [Oryza sativa]
Seq. No.
Seq. ID
                  uC-osflcyp109a10b1
Method
                  BLASTX
NCBI GI
                  g2130069
BLAST score
                  730
E value
                  1.0e-77
Match length
                  140
% identity
                  97
NCBI Description catalase (EC 1.11.1.6) catA - rice
                  >gi 1261858 dbj BAA06232 (D29966) catalase [Oryza sativa]
Seq. No.
                  412548
Seq. ID
                  uC-osflcyp109b02b1
Method
                  BLASTN
NCBI GI
                  g22379
BLAST score
                  57
E value
                  5.0e-23
Match length
                  81
% identity
                  93
NCBI Description Z.mays mRNA for CAAT-box DNA binding protein subunit B
                  (NF-YB)
                  412549
Seq. No.
Seq. ID
                  uC-osflcyp109b03a1
Method
                  BLASTX
NCBI GI
                  g3914685
BLAST score
                  244
E value
                  1.0e-20
                  69
Match length
                  72
% identity
NCBI Description 60S RIBOSOMAL PROTEIN L17 >gi 2668748 (AF034948) ribosomal
                  protein L17 [Zea mays]
Seq. No.
                  412550
Seq. ID
                  uC-osflcyp109b03b1
Method
                  BLASTX
NCBI GI
                  q3914685
BLAST score
                  727
E value
                  4.0e-77
Match length
                  161
                  88
% identity
NCBI Description 60S RIBOSOMAL PROTEIN L17 >gi_2668748 (AF034948) ribosomal
                  protein L17 [Zea mays]
                  412551
Seq. No.
```

uC-osflcyp109b04b1

BLASTX Method NCBI GI g2119194 335 BLAST score E value 2.0e-31 99 Match length 70 % identity low-molecular-weight heat-shock protein - rice >gi 1815662 NCBI Description (U83670) low molecular mass heat shock protein Oshsp18.0 [Oryza sativa] Seq. No. 412552 Seq. ID uC-osflcyp109b06a1 Method BLASTX NCBI GI q5579090 BLAST score 264 7.0e-23 E value 116 Match length 46 % identity NCBI Description (AF099186) EH domain-containing protein EHD1 [Mus musculus] 412553 Seq. No. uC-osflcyp109b06b1 Seq. ID Method BLASTX NCBI GI q5732069 BLAST score 245 E value 1.0e-20 111 Match length % identity (AF147263) contains similarity to Pfam family PF00036 - EF NCBI Description hand; score=11.7, E=0.66, N=1 [Arabidopsis thaliana] 412554 Seq. No. uC-osflcyp109b08b1 Seq. ID Method BLASTX NCBI GI g3786001 BLAST score 218 E value 5.0e-18 53 Match length 74 % identity NCBI Description (AC005499) unknown protein [Arabidopsis thaliana] 412555 Seq. No. uC-osflcyp109b09a1 Seq. ID BLASTN Method NCBI GI q902935 BLAST score 40 E value 5.0e-13 Match length 68 90 % identity NCBI Description Oryza sativa FNR gene for ferredoxin-NADP+ reductase, complete cds (exon1-6)

Seq. No. 412556

Seq. ID uC-osflcyp109b09b1

Method BLASTX
NCBI GI g1620896
BLAST score 648

NCBI GI

BLAST score

q2293480

432

```
E value
                   7.0e-68
Match length
                  177
% identity
                  72
                  (D87956) protein involved in sexual development
NCBI Description
                   [Schizosaccharomyces pombe] >gi 2408048 emb CAB16251
                   (Z99164) hypothetical protein [Schizosaccharomyces pombe]
Seq. No.
                  412557
Seq. ID
                  uC-osflcyp109b10b1
Method
                  BLASTX
NCBI GI
                  q6094335
BLAST score
                  416
E value
                  9.0e-41
Match length
                  94
% identity
                  85
                  SPERMIDINE SYNTHASE (PUTRESCINE AMINOPROPYLTRANSFERASE)
NCBI Description
                   (SPDSY) >gi 3242659 dbj BAA29033 (AB015599) spermidine
                  synthase [Coffea arabica]
                  412558
Seq. No.
Seq. ID
                  uC-osflcyp109b11b1
Method
                  BLASTX
NCBI GI
                  q4335749
BLAST score
                  572
E value
                  4.0e-59
Match length
                  135
% identity
                  80
NCBI Description (AC006284) unknown protein [Arabidopsis thaliana]
Seq. No.
                  412559
Seq. ID
                  uC-osflcyp109b12a1
Method
                  BLASTX
                  g3287693
NCBI GI
BLAST score
                  162
                  3.0e-11
E value
                  50
Match length
% identity
                  64
NCBI Description
                  (AC003979) Similar to LIM17 gene product gb 1653769 from
                  the genome of Synechocystis sp. gb_D90916. [Arabidopsis
                  thaliana]
Seq. No.
                  412560
Seq. ID
                  uC-osflcyp109c01a1
Method
                  BLASTN
NCBI GI
                  q2331132
BLAST score
                  355
                  0.0e+00
E value
                  487
Match length
% identity
                  93
NCBI Description Oryza sativa glycine-rich protein (OSGRP2) mRNA, complete
Seq. No.
                  412561
Seq. ID
                  uC-osflcyp109c01b1
Method
                  BLASTX
```

E value 1.0e-42
Match length 84
% identity 100

NCBI Description (AF011331) glycine-rich protein [Oryza sativa]

Seq. No. 412562

Seq. ID uC-osflcyp109c02a1

Method BLASTX
NCBI GI g2340166
BLAST score 225
E value 3.0e-18
Match length 72
% identity 57

NCBI Description (AF008124) glutathione S-conjugate transporting ATPase

[Arabidopsis thaliana] >gi_2459949 (AF008125) multidrug

resistance-associated protein homolog [Arabidopsis

thaliana]

Seq. No. 412563

Seq. ID uC-osflcyp109c02b1

Method BLASTX
NCBI GI g2316024
BLAST score 474
E value 1.0e-47
Match length 123
% identity 75

NCBI Description (U96400) MRP-like ABC transporter [Arabidopsis thaliana]

Seq. No. 412564

Seq. ID uC-osflcyp109c07b1

Method BLASTX
NCBI GI g1710780
BLAST score 551
E value 2.0e-56
Match length 152
% identity 70

NCBI Description 40S RIBOSOMAL PROTEIN S9 (S7) >gi 1321917 emb CAA65433

(X96613) cytoplasmic ribosomal protein S7 [Podospora

anserina]

Seq. No. 412565

Seq. ID uC-osflcyp109c08a1

Method BLASTX
NCBI GI g3183094
BLAST score 291
E value 4.0e-26
Match length 81
% identity 69

NCBI Description ORNITHINE CARBAMOYLTRANSFERASE PRECURSOR (OTCASE)

(ORNITHINE TRANSCARBAMYLASE) >gi 971168 (U13684) ornithine

carbamoyltransferase [Pisum sativum]

Seq. No. 412566

Seq. ID uC-osflcyp109c08b1

Method BLASTX NCBI GI g3183094 BLAST score 316

```
5.0e-29
E value
Match length
                  71
% identity
                  82
                  ORNITHINE CARBAMOYLTRANSFERASE PRECURSOR (OTCASE)
NCBI Description
                   (ORNITHINE TRANSCARBAMYLASE) >gi 971168 (U13684) ornithine
                  carbamoyltransferase [Pisum sativum]
Seq. No.
                  412567
Seq. ID
                  uC-osflcyp109c10b1
Method
                  BLASTX
NCBI GI
                  g2618695
BLAST score
                  145
E value
                  6.0e-09
Match length
                  86
% identity
                  37
NCBI Description (AC002510) hypothetical protein [Arabidopsis thaliana]
                  412568
Seq. No.
Seq. ID
                  uC-osflcyp109c11a1
Method
                  BLASTX
NCBI GI
                  q1350820
BLAST score
                  248
E value
                  8.0e-29
Match length
                  92
% identity
                  75
                  30 KD RIBONUCLEOPROTEIN, CHLOROPLAST PRECURSOR
NCBI Description
                  >gi_280402_pir__S26203 RNA-binding protein 30 -
                  curled-leaved tobacco >gi 19708 emb CAA46234 (X65118) RNA
                  binding protein 30 [Nicotiana plumbaginifolia]
Seq. No.
                   412569
Seq. ID
                  uC-osflcyp109d01a1
                  BLASTX
Method
NCBI GI
                  g2331131
BLAST score
                  172
                  4.0e-12
E value
                  36
Match length
                  94
% identity
NCBI Description (AF010579) glycine-rich protein [Oryza sativa]
Seq. No.
                   412570
```

Seq. ID uC-osflcyp109d01b1

Method BLASTX
NCBI GI g2293480
BLAST score 431
E value 2.0e-42
Match length 85
% identity 98

NCBI Description (AF011331) glycine-rich protein [Oryza sativa]

Seq. No. 412571

Seq. ID uC-osflcyp109d05b1

Method BLASTX
NCBI GI g5903099
BLAST score 317
E value 4.0e-29
Match length 127

```
% identity
NCBI Description (AC008017) Unknown protein [Arabidopsis thaliana]
Seq. No.
                  412572
Seq. ID
                  uC-osflcyp109d07b1
Method
                  BLASTX
NCBI GI
                  g1708424
BLAST score
                  713
E value
                  2.0e-75
Match length
                  182
% identity
                  71
NCBI Description ISOFLAVONE REDUCTASE HOMOLOG >gi 1230614 (U48590)
                  isoflavone reductase-like protein [Lupinus albus]
Seq. No.
                  412573
                  uC-osflcyp109d09a1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g5441876
BLAST score
                  338
E value
                  0.0e+00
Match length
                  417
                  95
% identity
NCBI Description Oryza sativa genomic DNA, chromosome 2, clone:P0437H03
                  (contig b)
                  412574
Seq. No.
Seq. ID
                  uC-osflcyp109d09b1
Method
                  BLASTX
NCBI GI
                  g3128180
BLAST score
                  562
E value
                  1.0e-58
Match length
                  157
                  74
% identity
NCBI Description (AC004521) citrate synthetase [Arabidopsis thaliana]
Seq. No.
                  412575
Seq. ID
                  uC-osflcyp109d10a1
                  BLASTX
Method
NCBI GI
                  q2346966
BLAST score
                  179
E value
                  6.0e-13
Match length
                  65
% identity
                  52
                  (AB004871) CPC [Arabidopsis thaliana]
NCBI Description
                  >gi 4559383 gb AAD23043.1 AC006526 8 (AC006526) putative
                  DNA binding protein CPC [Arabidopsis thaliana]
                  412576
Seq. No.
Seq. ID
                  uC-osflcyp109d10b1
                  BLASTX
Method
NCBI GI
                  g2346966
BLAST score
                  187
E value
                  8.0e-14
                  66
Match length
% identity
                  53
NCBI Description
                  (AB004871) CPC [Arabidopsis thaliana]
                  >gi 4559383 gb AAD23043.1 AC006526 8 (AC006526) putative
```

DNA binding protein CPC [Arabidopsis thaliana]

```
Seq. No.
                  412577
                  uC-osflcyp109d11b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2501189
                  591
BLAST score
E value
                  4.0e-61
Match length
                  153
                  76
% identity
                  THIAMINE BIOSYNTHETIC ENZYME 1-1 PRECURSOR
NCBI Description
                  >gi_2130146_pir__S61419 thiamine biosynthetic enzyme thi1-1
                   - maize >gi_596078 (U17350) thiamine biosynthetic enzyme
                   [Zea mays]
                  412578
Seq. No.
                  uC-osflcyp109d12b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1129145
BLAST score
                  540
E value
                  3.0e-55
Match length
                  143
% identity
                   71
NCBI Description (X75329) acetyl-CoA C-acyltransferase [Mangifera indica]
Seq. No.
                  412579
Seq. ID
                  uC-osflcyp109e04b1
Method
                  BLASTX
NCBI GI
                  g1169585
BLAST score
                  516
E value
                   2.0e-52
Match length
                  112
% identity
                   87
NCBI Description FRUCTOSE-1, 6-BISPHOSPHATASE, CYTOSOLIC
                   (D-FRUCTOSE-1, 6-BISPHOSPHATE 1-PHOSPHOHYDROLASE) (FBPASE)
                  >gi 885894 (U20179) fructose 1,6-bisphosphatase [Brassica
                  napus]
                   412580
Seq. No.
Seq. ID
                  uC-osflcyp109e06b1
Method
                  BLASTX
NCBI GI
                  g2828293
                  290
BLAST score
                   3.0e-32
E value
Match length
                  142
% identity
                  54
NCBI Description (AL021687) putative protein [Arabidopsis thaliana]
Seq. No.
                   412581
Seq. ID
                  uC-osflcyp109e07a1
Method
                  BLASTX
NCBI GI
                   g3212861
BLAST score
                  323
E value
                   8.0e-30
Match length
                  75
% identity
NCBI Description (AC004005) unknown protein [Arabidopsis thaliana]
```

Seq. No.

412587

```
412582
Seq. No.
Seq. ID
                  uC-osflcyp109e07b1
Method
                  BLASTX
NCBI GI
                  g3212861
BLAST score
                  580
E value
                  6.0e-60
Match length
                  158
% identity
                  68
NCBI Description (AC004005) unknown protein [Arabidopsis thaliana]
                  412583
Seq. No.
Seq. ID
                  uC-osflcyp109e08b1
Method
                  BLASTX
NCBI GI
                  g6094335
BLAST score
                  348
E value
                  9.0e-33
                  80
Match length
% identity
                  82
                  SPERMIDINE SYNTHASE (PUTRESCINE AMINOPROPYLTRANSFERASE)
NCBI Description
                  (SPDSY) >gi_3242659_dbj_BAA29033_ (AB015599) spermidine
                  synthase [Coffea arabica]
                  412584
Seq. No.
Seq. ID
                  uC-osflcyp109e10b1
Method
                  BLASTX
NCBI GI
                  q1747294
BLAST score
                  465
E value
                  4.0e-71
Match length
                  170
% identity
                  84
NCBI Description (D45383) vacuolar H+-pyrophosphatase [Oryza sativa]
Seq. No.
                  412585
Seq. ID
                  uC-osflcyp109e11b1
Method
                  BLASTX
NCBI GI
                  g1171008
BLAST score
                  579
E value
                  8.0e-60
Match length
                  134
                  72
% identity
NCBI Description POLLEN ALLERGEN PHL P 1 PRECURSOR (PHL P I)
                  >gi_629812_pir__S44182 allergen Phl p I - common timothy
                  >gi_473360_emb_CAA55390_ (X78813) Phl p I allergen [Phleum
                  pratense]
Seq. No.
                  412586
Seq. ID
                  uC-osflcyp109e12b1
Method
                  BLASTX
NCBI GI
                  q3046696
BLAST score
                  340
E value
                  9.0e-32
                  76
Match length
% identity
NCBI Description (AL022224) CTP synthase like protein [Arabidopsis thaliana]
```

```
Seq. ID
                  uC-osflcyp109f01b1
Method
                  BLASTX
NCBI GI
                  g4586058
BLAST score
                  378
E value
                  2.0e-36
Match length
                  147
% identity
                  50
NCBI Description (AC007020) unknown protein [Arabidopsis thaliana]
                  412588
Seq. No.
Seq. ID
                  uC-osflcyp109f02b1
Method
                  BLASTX
NCBI GI
                  g3668089
BLAST score
                  525
E value
                  2.0e-53
Match length
                  160
% identity
                  66
NCBI Description (AC004667) unknown protein [Arabidopsis thaliana]
Seq. No.
                  412589
Seq. ID
                  uC-osflcyp109f03a1
Method
                  BLASTX
NCBI GI
                  q2497542
BLAST score
                  264
E value
                  5.0e-23
                  68
Match length
                  76
% identity
NCBI Description PYRUVATE KINASE ISOZYME G, CHLOROPLAST PRECURSOR
                  >gi_629696_pir__S44287 pyruvate kinase, plastid - common
                  tobacco >gi_482938_emb_CAA82223_ (Z28374) Pyruvate kinase;
                  plastid isozyme [Nicotiana tabacum]
Seq. No.
                  412590
Seq. ID
                  uC-osflcyp109f03b1
                  BLASTX
Method
NCBI GI
                  q2497542
BLAST score
                  656
E value
                  7.0e-69
Match length
                  162
% identity
                  81
NCBI Description PYRUVATE KINASE ISOZYME G, CHLOROPLAST PRECURSOR
                  >gi 629696 pir S44287 pyruvate kinase, plastid - common
                  tobacco >gi_482938_emb_CAA82223_ (Z28374) Pyruvate kinase;
                  plastid isozyme [Nicotiana tabacum]
Seq. No.
                  412591
Seq. ID
                  uC-osflcyp109f04b1
Method
                  BLASTX
NCBI GI
                  g3935184
BLAST score
                  213
E value
                  7.0e-17
Match length
                  162
% identity
NCBI Description (AC004557) F17L21.27 [Arabidopsis thaliana]
Seq. No.
                  412592
Seq. ID
                  uC-osflcyp109f06b1
```

Method BLASTX NCBI GI q4263717 BLAST score 369 E value 3.0e-35 Match length 129 % identity 64

(AC006223) putative inositol polyphosphate 5-phosphatase NCBI Description

[Arabidopsis thaliana]

412593 Seq. No.

Seq. ID uC-osflcyp109f10a1

Method BLASTX NCBI GI q4115925 BLAST score 145 E value 6.0e-09 Match length 38 74 % identity

(AF118222) contains similarity to RNA recognition motifs (Pfam: PF00076, Score=5.5e-23, N=2) [Arabidopsis thaliana] NCBI Description

>gi_4539439_emb_CAB40027.1_ (AL049523) RNA-binding protein
[Arabidopsis thaliana] >gi_4959384_gb_AAD34325.1_

(AF109721) RNA-binding protein [Arabidopsis thaliana]

Seq. No. 412594

Seq. ID uC-osflcyp109f10b1

Method BLASTX NCBI GI q4115925 BLAST score 581 E value 2.0e-60 Match length 165 % identity 44

(AF118222) contains similarity to RNA recognition motifs (Pfam: PF00076, Score=5.5e-23, N=2) [Arabidopsis thaliana] NCBI Description

>gi_4539439_emb_CAB40027.1_ (AL049523) RNA-binding protein
[Arabidopsis thaliana] >gi_4959384_gb_AAD34325.1_ (AF109721) RNA-binding protein [Arabidopsis thaliana]

412595 Seq. No.

uC-osflcyp109f11b1 Seq. ID

Method BLASTX NCBI GI g5596484 593 BLAST score E value 2.0e-61 Match length 165 % identity 69

NCBI Description (AL096882) beta-adaptin-like protein [Arabidopsis thaliana]

Seq. No. 412596

Seq. ID uC-osflcyp109f12b1

Method BLASTX NCBI GI g4337175 BLAST score 281 E value 1.0e-25 Match length 128 % identity 50

NCBI Description (AC006416) ESTs gb T20589, gb T04648, gb AA597906,

gb T04111, gb R84180, gb R65428, gb T44439, gb T76570,

```
Seq. No.
                  412597
Seq. ID
                  uC-osflcyp109g01b1
Method
                  BLASTX
NCBI GI
                  q1780757
BLAST score
                  255
E value
                  8.0e-22
Match length
                  66
% identity
                  68
NCBI Description
                  (Y10291) highly expressed in proliferating cells
                   [Arabidopsis thaliana]
Seq. No.
                  412598
Seq. ID
                  uC-osflcyp109q02b1
Method
                  BLASTX
NCBI GI
                  q2388911
BLAST score
                  380
E value
                  2.0e-36
Match length
                  144
                  49
% identity
NCBI Description (Z98974) hypothetical PSU1-like protein
                  [Schizosaccharomyces pombe]
Seq. No.
                  412599
Seq. ID
                  uC-osflcyp109g04b1
Method
                  BLASTX
NCBI GI
                  g4582459
BLAST score
                  506
E value
                  3.0e-60
Match length
                  172
                  72
% identity
NCBI Description (AC007071) putative RanBP7/importin protein [Arabidopsis
                  thaliana]
Seq. No.
                   412600
Seq. ID
                  uC-osflcyp109g09a1
Method
                  BLASTX
NCBI GI
                  g451193
BLAST score
                  193
E value
                  1.0e-14
Match length
                  50
                  76
% identity
NCBI Description (L28008) wali7 [Triticum aestivum]
                  >gi 1090845_prf__2019486B wali7 gene [Triticum aestivum]
                   412601
Seq. No.
Seq. ID
                  uC-osflcyp109g09b1
Method
                  BLASTX
NCBI GI
                  g451193
BLAST score
                  783
E value
                  1.0e-83
Match length
                  168
% identity
                   92
NCBI Description (L28008) wali7 [Triticum aestivum]
                  >gi 1090845 prf 2019486B wali7 gene [Triticum aestivum]
```

gb_R90004, gb_T45020, gb_T42457, gb_T20921, gb_AA042762 and gb_AA720210 come from this gene. [Arabidopsis thaliana]

Seq. No.

412607

Seq. No. 412602 Seq. ID uC-osflcyp109g10b1 Method BLASTX NCBI GI g399015 BLAST score 603 1.0e-62 E value Match length 119 % identity 100 NCBI Description ADP, ATP CARRIER PROTEIN PRECURSOR (ADP/ATP TRANSLOCASE) (ADENINE NUCLEOTIDE TRANSLOCATOR) (ANT) >gi_218145_dbj_BAA02161_ (D12637) ATP/ADP translocator [Oryza sativa] Seq. No. 412603 Seq. ID uC-osflcyp109g11a1 Method BLASTX NCBI GI g4835757 BLAST score 199 E value 2.0e-15 Match length 59 % identity 66 NCBI Description (AC007202) EST gb AA404917 comes from this gene. [Arabidopsis thaliana] Seq. No. 412604 Seq. ID uC-osflcyp109g11b1 Method BLASTX NCBI GI g4835757 BLAST score 245 E value 1.0e-20 Match length 114 % identity 49 NCBI Description (AC007202) EST gb AA404917 comes from this gene. [Arabidopsis thaliana] 412605 Seq. No. Seq. ID uC-osflcyp109g12a1 Method BLASTX NCBI GI g5725443 BLAST score 184 E value 1.0e-13 76 Match length % identity NCBI Description (AL109787) putative protein [Arabidopsis thaliana] 412606 Seq. No. Seq. ID uC-osflcyp109g12b1 Method BLASTX NCBI GI g5725443 BLAST score 330 E value 1.0e-30 151 Match length % identity NCBI Description (AL109787) putative protein [Arabidopsis thaliana]

NCBI GI

BLAST score

q1170937

725

```
uC-osflcyp109h01a1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4455232
BLAST score
                  206
E value
                  5.0e-28
Match length
                  108
                  57
% identity
NCBI Description (AL035523) putative protein [Arabidopsis thaliana]
Seq. No.
                  412608
Seq. ID
                  uC-osflcyp109h04b1
Method
                  BLASTX
NCBI GI
                  g3005590
BLAST score
                  370
E value
                  3.0e-37
Match length
                  118
% identity
                  67
                  (AF051326) dimethyladenosine transferase [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  412609
Seq. ID
                  uC-osflcyp109h05b1
Method
                  BLASTN
NCBI GI
                  q22336
BLAST score
                  42
E value
                  4.0e-14
                  74
Match length
% identity
                  89
NCBI Description Maize mRNA for an 18kDa heat shock protein
Seq. No.
                  412610
Seq. ID
                  uC-osflcyp109h07b1
Method
                  BLASTX
NCBI GI
                  q4850408
BLAST score
                  187
E value
                  8.0e-14
Match length
                  99
% identity
                  44
NCBI Description (AC007357) Contains PF 00097 Zinc finger (C3HC4) ring
                  finger motif. [Arabidopsis thaliana]
Seq. No.
                  412611
Seq. ID
                  uC-osflcyp109h08b1
Method
                  BLASTX
NCBI GI
                  q2832300
BLAST score
                  650
E value
                  3.0e-68
Match length
                  152
% identity
NCBI Description
                 (AF044285) adenosine-5'-phosphosulfate-kinase [Catharanthus
                  roseus]
Seq. No.
                  412612
Seq. ID
                  uC-osflcyp109h10b1
Method
                  BLASTX
```

% identity

98

```
E value
                  7.0e-77
Match length
                  138
                  99
% identity
                  S-ADENOSYLMETHIONINE SYNTHETASE 1 (METHIONINE
NCBI Description
                  ADENOSYLTRANSFERASE 1) (ADOMET SYNTHETASE 1)
                  >gi 450549 emb CAA81481\_ (Z26867) S-adenosyl methionine
                  synthetase [Oryza sativa]
Seq. No.
                  412613
Seq. ID
                  uC-osflcyp109h12a1
Method
                  BLASTX
NCBI GI
                  q1351017
BLAST score
                  168
E value
                  1.0e-11
                  39
Match length
                  79
% identity
NCBI Description 40S RIBOSOMAL PROTEIN S9 (S4) >gi 629697 pir S45375
                  ribosomal protein S4 - common tobacco (fragment)
                  >gi_443960_emb_CAA78463_ (Z14085) RIBOSOMAL PROTEIN S4
                  [Nicotiana tabacum]
Seq. No.
                  412614
Seq. ID
                  uC-osflcyp109h12b1
Method
                  BLASTX
NCBI GI
                  q131770
BLAST score
                  533
E value
                  2.0e-54
                  150
Match length
% identity
                  67
NCBI Description 40S RIBOSOMAL PROTEIN S9 (40S RIBOSOMAL PROTEIN 1024)
                  (VEGETATIVE SPECIFIC PROTEIN V12) >gi_70880_pir__R3D024
                  ribosomal protein S9.e - slime mold (Dictyostelium
                  discoideum) >gi_7353_emb_CAA29844_ (X06636) rp1024 protein
                  [Dictyostelium discoideum]
Seq. No.
                  412615
Seq. ID
                  uC-osflcyp110a01b1
Method
                  BLASTX
NCBI GI
                  g3334346
BLAST score
                  301
E value
                  3.0e-27
Match length
                  60
% identity
                  95
NCBI Description PROTEIN TRANSLATION FACTOR SUI1 HOMOLOG
                  >gi_2852445_dbj_BAA24697 (AB003378) SUI1 homolog [Salix
                  bakko]
                  412616
Seq. No.
Seq. ID
                  uC-osflcyp110a02b1
Method
                  BLASTX
NCBI GI
                  q4415992
BLAST score
                  537
E value
                  7.0e-89
Match length
                  169
```

53687

NCBI Description (AF059288) beta-tubulin 2 [Eleusine indica]



```
Seq. No.
                  412617
Seq. ID
                  uC-osflcyp110a06b1
Method
                  BLASTX
NCBI GI
                  g3913732
BLAST score
                  181
                  3.0e-25
E value
Match length
                  137
                  53
% identity
NCBI Description
                  HYDROXYACYLGLUTATHIONE HYDROLASE MITOCHONDRIAL ISOZYME
                  PRECURSOR (GLYOXALASE II) (GLX II) >gi 2570340 (U90928)
                  glyoxalase II mitochondrial isozyme [Arabidopsis thaliana]
                  412618
Seq. No.
Seq. ID
                  uC-osflcyp110a07b1
Method
                  BLASTX
NCBI GI
                  g4539437
BLAST score
                  491
E value
                  2.0e-49
Match length
                  167
% identity
                  61
NCBI Description (AL049523) putative protein [Arabidopsis thaliana]
Seq. No.
                  412619
Seq. ID
                  uC-osflcyp110a09b1
Method
                  BLASTX
NCBI GI
                  q451193
BLAST score
                  158
E value
                  2.0e-10
Match length
                  67
                  54
% identity
                  (L28008) wali7 [Triticum aestivum]
NCBI Description
                  >gi 1090845 prf 2019486B wali7 gene [Triticum aestivum]
Seq. No.
                   412620
Seq. ID
                  uC-osflcyp110a10b1
Method
                  BLASTX
                  q6091746
NCBI GI
BLAST score
                  630
E value
                  8.0e-66
Match length
                  145
% identity
                  79
NCBI Description (AC010797) putative sulfite oxidase [Arabidopsis thaliana]
                   412621
Seq. No.
Seq. ID
                  uC-osflcyp110a12b1
Method
                  BLASTX
NCBI GI
                  g1170937
                  227
BLAST score
                   7.0e-37
E value
                  104
Match length
% identity
                   78
NCBI Description S-ADENOSYLMETHIONINE SYNTHETASE 1 (METHIONINE
                  ADENOSYLTRANSFERASE 1) (ADOMET SYNTHETASE 1)
                   >gi_450549_emb_CAA81481_ (Z26867) S-adenosyl methionine
```

Seq. No. 412622

synthetase [Oryza sativa]

```
uC-osflcyp110b01b1
Seq. ID
                  BLASTX
Method
NCBI GI
                  g3738285
                  212
BLAST score
                  2.0e-27
E value
Match length
                  144
                  53
% identity
                 (AC005309) unknown protein [Arabidopsis thaliana]
NCBI Description
                  412623
Seq. No.
                  uC-osflcyp110b02a1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2618699
BLAST score
                  254
E value
                  1.0e-21
Match length
                  109
% identity
                  43
NCBI Description (AC002510) unknown protein [Arabidopsis thaliana]
Seq. No.
                  412624
Seq. ID
                  uC-osflcyp110b03b1
Method
                  BLASTX
NCBI GI
                  q2191140
BLAST score
                  233
E value
                   3.0e-19
Match length
                  130
                   46
% identity
NCBI Description (AF007269) contains weak similarity to MYB-related proteins
                   [Arabidopsis thaliana]
Seq. No.
                   412625
Seq. ID
                  uC-osflcyp110b05b1
Method
                  BLASTX
NCBI GI
                  g3334276
BLAST score
                   492
E value
                   1.0e-49
                  138
Match length
                   67
% identity
NCBI Description AUTOANTIGEN NGP-1 >gi_179285 gb AAC37588.1_ (L05425)
                  nucleolar GTPase [Homo sapiens]
                   412626
Seq. No.
Seq. ID
                  uC-osflcyp110b06b1
                  BLASTX
Method
NCBI GI
                   q3157949
BLAST score
                   180
E value
                   4.0e-13
                   61
Match length
                   56
% identity
                  (AC002131) Similar to glucan endo-1,3-beta-D-glucosidase
NCBI Description
                   precursor gb_Z28697 from Nicotiana tabacum. ESTs gb Z18185
                   and gb\_AA605\overline{3}62 come from this gene. [Arabidopsis thaliana]
```

Seq. No. 412627

Seq. ID uC-osflcyp110b07a1

Method BLASTX NCBI GI g2618699



```
BLAST score
                   2.0e-14
E value
Match length
                  85
                   42
% identity
                   412628
```

NCBI Description (AC002510) unknown protein [Arabidopsis thaliana]

Seq. No.

Seq. ID uC-osflcyp110b07b1

Method BLASTX NCBI GI g3122326 BLAST score 613 9.0e-64 E value 172 Match length 65 % identity

NCBI Description LEC14B PROTEIN >gi 1181604_dbj BAA11768_ (D83074) LEC14B

protein [Lithospermum erythrorhizon]

412629 Seq. No.

Seq. ID uC-osflcyp110b08b1

Method BLASTX NCBI GI g3834302 BLAST score 438 E value 3.0e-43 Match length 170 78 % identity

(AC005679) Similar to gb_D45384 vacuolar H+-pyrophosphatase NCBI Description

from Oryza sativa. ESTs gb F14272 and gb F14273 come from

this gene. [Arabidopsis thaliana]

Seq. No. 412630

uC-osflcyp110b10b1 Seq. ID

BLASTX Method NCBI GI g3641837 372 BLAST score E value 1.0e-35 128 Match length % identity 62

NCBI Description (AL023094) Nonclathrin coat protein gamma-like protein

[Arabidopsis thaliana]

412631 Seq. No.

Seq. ID uC-osflcyp110b12a1

BLASTX Method NCBI GI q1644427 BLAST score 315 6.0e-29 E value 84 Match length 71 % identity

NCBI Description (U74610) glyoxalase II [Arabidopsis thaliana]

412632 Seq. No.

uC-osflcyp110b12b1 Seq. ID

BLASTX Method NCBI GI q1644427 BLAST score 388 6.0e-41 E value 122 Match length

```
% identity
NCBI Description (U74610) glyoxalase II [Arabidopsis thaliana]
Seq. No.
                    412633
                    uC-osflcyp110c01b1
Seq. ID
                    BLASTX
Method
NCBI GI
                    q2341042
BLAST score
                    153
E value
                    8.0e-10
Match length
                    159
% identity
                    34
                    (AC000104) F19P19.26 [Arabidopsis thaliana]
NCBI Description
                    412634
Seq. No.
Seq. ID
                    uC-osflcyp110c02a1
Method
                    BLASTN
                    g2384757
NCBI GI
                    282
BLAST score
                    1.0e-157
E value
Match length
                    387
                    93
% identity
NCBI Description Oryza sativa GDP dissociation inhibitor protein OsGDI1
                    (OsGDI1) mRNA, complete cds
                    412635
Seq. No.
Seq. ID
                    uC-osflcyp110c03a1
Method
                    BLASTX
NCBI GI
                    q462195
BLAST score
                    449
E value
                    1.0e-44
                    97
Match length
% identity
                    91
                    PROTEIN TRANSLATION FACTOR SUI1 HOMOLOG (GOS2 PROTEIN)
NCBI Description
                    >gi_100682_pir__S21636 GOS2 protein - rice
>gi_20238_emb_CAA36190_ (X51910) GOS2 [Oryza sativa]
>gi_3789950 (AF094774) translation initiation factor [Oryza
                     satīva]
Seq. No.
                     412636
Seq. ID
                    uC-osflcyp110c03b1
Method
                    BLASTX
NCBI GI
                    g462195
BLAST score
                    290
```

E value 6.0e-26 Match length 70 % identity 81

NCBI Description PROTEIN TRANSLATION FACTOR SUI1 HOMOLOG (GOS2 PROTEIN)

>gi 100682 pir S21636 GOS2 protein - rice

>gi 20238 emb CAA36190 (X51910) GOS2 [Oryza sativa]

>gi 3789950 (AF094774) translation initiation factor [Oryza

satīva]

412637 Seq. No.

Seq. ID uC-osflcyp110c04b1

Method BLASTX NCBI GI q2494041 BLAST score 286

```
2.0e-25
E value
                   75
Match length
% identity
                   69
                   DIAMINOPIMELATE EPIMERASE (DAP EPIMERASE)
NCBI Description
                   >gi_1653875_dbj_BAA18785_ (D90917) diaminopimelate
                   epimerase [Synechocystis sp.]
Seq. No.
                   412638
Seq. ID
                   uC-osflcyp110c05b1
Method
                   BLASTX
NCBI GI
                   q5541704
BLAST score
                   339
E value
                   7.0e-34
Match length
                   89
% identity
                   (AL096860) 40S RIBOSOMAL PROTEIN S20 homolog [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   412639
Seq. ID
                   uC-osflcyp110c06a1
Method
                   BLASTX
NCBI GI
                   g1076741
BLAST score
                   531
E value
                   3.0e-54
Match length
                   93
% identity
                   100
                   chitinase (EC 3.2.1.14) precursor - rice
NCBI Description
                   >gi_2130070_pir__S65771 chitinase (EC 3.2.1.14) class I precursor - rice >gi_807955_emb_CAA60590_ (X87109)
                   chitinase [Oryza sativa]
                   412640
Seq. No.
Seq. ID
                   uC-osflcyp110c07b1
Method
                   BLASTX
NCBI GI
                   q100489
BLAST score
                   292
E value
                   4.0e-26
Match length
                   169
% identity
                   32
NCBI Description transposase Tam3 - garden snapdragon transposon Tam3
```

>gi_16064_emb_CAA38906_ (X55078) Tam3-transposase [Antirrhinum majus] >gi_3219237_dbj_BAA28817.1_ (AB013982) transposase [Antirrhinum majus] >gi_3219239_dbj_BAA28818.1_

(AB013983) transposase [Antirrhinum majus]

>gi 3219241_dbj_BAA28819.1_ (AB013984) transposase

[Antirrhinum majus] >gi_3219244_dbj_BAA28820.1 (AB013986) transposase [Antirrhinum majus] >gi 3219249 dbj BAA28821.1

(AB013990) transposase [Antirrhinum majus]

>gi 3219251 dbj BAA28822.1 (AB013991) transposase

[Antirrhinum majus] >gi 3219256 dbj BAA28823.1 (AB013995) transposase [Antirrhinum majus] >gi 3219259 dbj BAA28824.1

(AB013997) transposase [Antirrhinum majus]

412641 Seq. No.

Seq. ID uC-osflcyp110c08a1

Method BLASTN NCBI GI q2384757

Seq. ID

Method

BLAST score 46 E value 1.0e-16 Match length 138 % identity 83 Oryza sativa GDP dissociation inhibitor protein OsGDI1 NCBI Description (OsGDI1) mRNA, complete cds Seq. No. 412642 Seq. ID uC-osflcyp110c08b1 Method BLASTX NCBI GI q4115918 BLAST score 255 E value 8.0e-22 Match length 73 % identity 68 NCBI Description (AF118222) similar to nascent polypeptide associated complex alpha chain [Arabidopsis thaliana] Seq. No. Seq. ID 412643 uC-osflcyp110c09a1 Method BLASTX NCBI GI q462195 BLAST score 451 E value 9.0e - 45Match length 102 % identity 87 PROTEIN TRANSLATION FACTOR SUI1 HOMOLOG (GOS2 PROTEIN) NCBI Description >gi_100682_pir__S21636 GOS2 protein - rice
>gi_20238_emb_CAA36190_ (X51910) GOS2 [Oryza sativa] >gi 3789950 (AF094774) translation initiation factor [Oryza sativa] Seq. No. 412644 Seq. ID uC-osflcyp110c09b1 Method BLASTX NCBI GI g2911042 BLAST score 551 E value 2.0e-56 Match length 170 % identity 71 (AL021961) Phosphoglycerate dehydrogenase - like protein NCBI Description [Arabidopsis thaliana] Seq. No. 412645 Seq. ID uC-osflcyp110c10b1 Method BLASTX NCBI GI q3047117 BLAST score 445 E value 4.0e-44Match length 88 % identity 95 NCBI Description (AF058919) similar to ATP-dependent RNA helicases [Arabidopsis thaliana] Seq. No. 412646

53693

uC-osflcyp110c11b1

BLASTX

BLAST score

E value

431

2.0e-42

```
NCBI GI
                  q4582468
BLAST score
                  487
E value
                  4.0e-49
Match length
                  107
% identity
                  92
NCBI Description
                 (AC007071) putative 40S ribosomal protein; contains
                  C-terminal domain [Arabidopsis thaliana]
Seq. No.
                  412647
Seq. ID
                  uC-osflcyp110c12a1
Method
                  BLASTX
NCBI GI
                  g500615
BLAST score
                  537
E value
                  2.0e-61
Match length
                  116
% identity
                  99
NCBI Description (D16221) endochitinase [Oryza sativa]
Seq. No.
                  412648
Seq. ID
                  uC-osflcyp110d01b1
Method
                  BLASTX
NCBI GI
                  g3023713
BLAST score
                  387
E value
                  9.0e-69
Match length
                  151
% identity
                  90
NCBI Description ENOLASE (2-PHOSPHOGLYCERATE DEHYDRATASE)
                   (2-PHOSPHO-D-GLYCERATE HYDRO-LYASE) (OSE1) >gi 780372
                  (U09450) enolase [Oryza sativa]
                  412649
Seq. No.
Seq. ID
                  uC-osflcyp110d02a1
Method
                  BLASTX
NCBI GI
                  g3297808
BLAST score
                  324
                  7.0e-30
E value
                  111
Match length
                  35
% identity
NCBI Description (AL031032) putative protein [Arabidopsis thaliana]
Seq. No.
                  412650
Seq. ID
                  uC-osflcyp110d03a1
Method
                  BLASTN
NCBI GI
                  g2331130
BLAST score
                  205
E value
                  1.0e-111
                  264
Match length
% identity
                  99
NCBI Description Oryza sativa glycine-rich protein (OSGRP1) mRNA, complete
                  cds
Seq. No.
                  412651
Seq. ID
                  uC-osflcyp110d03b1
Method
                  BLASTX
NCBI GI
                  g2293480
```

```
Match length
                  85
% identity
                  98
NCBI Description (AF011331) glycine-rich protein [Oryza sativa]
Seq. No.
                  412652
                  uC-osflcyp110d04b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2129579
BLAST score
                  626
E value
                  7.0e-78
                  175
Match length
                  79
% identity
NCBI Description Dwarf1 protein - Arabidopsis thaliana >gi_516043 (U12400)
                  Dwarf1 [Arabidopsis thaliana]
                  412653
Seq. No.
                  uC-osflcyp110d05a1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1552379
BLAST score
                  155
E value
                  3.0e-10
Match length
                  60
% identity
                  47
NCBI Description (Y08155) pectin methylesterase [Silene latifolia ssp. alba]
Seq. No.
                  412654
Seq. ID
                  uC-osflcyp110d07a1
Method
                  BLASTX
NCBI GI
                  g3297808
BLAST score
                  310
                  3.0e-28
E value
Match length
                  111
                  33
% identity
NCBI Description (AL031032) putative protein [Arabidopsis thaliana]
Seq. No.
                  412655
Seq. ID
                  uC-osflcyp110d07b1
Method
                  BLASTX
NCBI GI
                  q5733874
BLAST score
                  202
E value
                  8.0e-16
                  101
Match length
% identity
                   41
NCBI Description (AC007932) F11A17.8 [Arabidopsis thaliana]
Seq. No.
                   412656
Seq. ID
                  uC-osflcyp110d08a1
                  BLASTX
Method
NCBI GI
                  g3297808
BLAST score
                  367
E value
                   9.0e - 35
Match length
                  128
% identity
NCBI Description (AL031032) putative protein [Arabidopsis thaliana]
Seq. No.
                   412657
                  uC-osflcyp110d08b1
Seq. ID
```



Method BLASTN
NCBI GI g4138731
BLAST score 36
E value 2.0e-10
Match length 88
% identity 85

NCBI Description Zea mays mRNA for proline-rich protein

Seq. No. 412658

Seq. ID uC-osflcyp110d12b1

Method BLASTX
NCBI GI g3080391
BLAST score 309
E value 4.0e-28
Match length 114
% identity 52

NCBI Description (AL022603) putative protein [Arabidopsis thaliana]

Seq. No. 412659

Seq. ID uC-osflcyp110e01a1

Method BLASTX
NCBI GI g1304215
BLAST score 329
E value 1.0e-30
Match length 93
% identity 51

NCBI Description (D84392) precursor of rice 22 kDa protein of photosystem II

(PSII-S) [Oryza sativa]

Seq. No. 412660

Seq. ID uC-osflcyp110e01b1

Method BLASTX
NCBI GI g1304215
BLAST score 539
E value 4.0e-55
Match length 127
% identity 64

NCBI Description (D84392) precursor of rice 22 kDa protein of photosystem II

(PSII-S) [Oryza sativa]

Seq. No. 412661

Seq. ID uC-osflcyp110e03b1

Method BLASTN
NCBI GI g2773153
BLAST score 474
E value 0.0e+00
Match length 489
% identity 99

NCBI Description Oryza sativa abscisic acid- and stress-inducible protein

(Asr1) mRNA, complete cds

Seq. No. 412662

Seq. ID uC-osflcyp110e04a1

Method BLASTX
NCBI GI g4455174
BLAST score 298
E value 7.0e-27

1

Match length 84 % identity 65

NCBI Description (AL035521) putative protein [Arabidopsis thaliana]

Seq. No. 412663

Seq. ID uC-osflcyp110e04b1

Method BLASTX
NCBI GI g4455174
BLAST score 213
E value 7.0e-17
Match length 56
% identity 66

NCBI Description (AL035521) putative protein [Arabidopsis thaliana]

Seq. No. 412664

Seq. ID uC-osflcyp110e06a1

Method BLASTN
NCBI GI g5231209
BLAST score 122
E value 8.0e-62
Match length 142
% identity 96

NCBI Description Oryza sativa subsp. indica serine/threonine protein

phosphatase PP2A-3 catalytic subunit (PP2A) gene, complete

cds

Seq. No. 412665

Seq. ID uC-osflcyp110e06b1

Method BLASTX
NCBI GI g5803029
BLAST score 261
E value 2.0e-22
Match length 132
% identity 39

NCBI Description ATP/GTP-binding protein >gi 1644402 (U73524) putative

ATP/GTP-binding protein [Homo sapiens]

Seq. No. 412666

Seq. ID uC-osflcyp110e07a1

Method BLASTN
NCBI GI g1304214
BLAST score 55
E value 3.0e-22
Match length 103
% identity 88

NCBI Description Rice mRNA for precursor of 22 kDa protein of photosystem II

(PSII-S), complete cds

Seq. No. 412667

Seq. ID uC-osflcyp110e07b1

Method BLASTX
NCBI GI g2583127
BLAST score 413
E value 2.0e-40
Match length 113
% identity 64

NCBI Description (AC002387) putative sialoglycoprotease [Arabidopsis



thaliana]

Seq. No. 412668

Seq. ID uC-osflcyp110e08b1

Method BLASTX
NCBI GI g1620753
BLAST score 360
E value 2.0e-34
Match length 81
% identity 80

NCBI Description (U72942) proteinase inhibitor [Oryza sativa]

>gi_2829212_gb_AAC00503_ (AF044059) proteinase inhibitor [Oryza sativa] >gi_6063551_dbj_BAA85411.1_ (AP000615) ESTs AU069800(E3445), AU078204(E11809) correspond to a region of the predicted gene.; similar to proteinase inhibitor.

(AF044059) [Oryza sativa]

Seq. No. 412669

Seq. ID uC-osflcyp110e10a1

Method BLASTX
NCBI GI g4455174
BLAST score 157
E value 1.0e-10
Match length 56
% identity 52

NCBI Description (AL035521) putative protein [Arabidopsis thaliana]

Seq. No. 412670

Seq. ID uC-osflcyp110e11b1

Method BLASTX
NCBI GI g3451068
BLAST score 438
E value 3.0e-43
Match length 141
% identity 65

NCBI Description (AL031326) putative protein [Arabidopsis thaliana]

Seq. No. 412671

Seq. ID uC-osflcyp110e12b1

Method BLASTN
NCBI GI g11957
BLAST score 181
E value 2.0e-97
Match length 185
% identity 50

NCBI Description Rice complete chloroplast genome

Seq. No. 412672

Seq. ID uC-osflcyp110f01b1

Method BLASTX NCBI GI g2493650 BLAST score 379

BLAST score 379 E value 2.0e-36 Match length 76 % identity 95

NCBI Description RUBISCO SUBUNIT BINDING-PROTEIN BETA SUBUNIT (60 KD

CHAPERONIN BETA SUBUNIT) (CPN-60 BETA)

>gi 1167858 emb CAA93139 (Z68903) chaperonin [Secale cereale] 412673 Seq. No. Seq. ID uC-osflcyp110f03b1 Method BLASTX NCBI GI g4539005 BLAST score 240 E value 5.0e-20 84 Match length 52 % identity NCBI Description (AL049481) putative oxidoreductase [Arabidopsis thaliana] Seq. No. 412674 Seq. ID uC-osflcyp110f05a1 Method BLASTX NCBI GI g2150002 BLAST score 608 E value 3.0e-63 Match length 166 % identity 67 NCBI Description (AF000940) ribonuclease [Hordeum vulgare] Seq. No. 412675 Seq. ID uC-osflcyp110f05b1 Method BLASTX NCBI GI g2150002 BLAST score 552 E value 1.0e-56 Match length 113 81 % identity NCBI Description (AF000940) ribonuclease [Hordeum vulgare] 412676 Seq. No. Seq. ID uC-osflcyp110f06a1 Method BLASTX NCBI GI g1136120 BLAST score 149 E value 3.0e-13 53 Match length 83 % identity NCBI Description (X91806) alpha-tubulin [Oryza sativa] Seq. No. 412677 Seq. ID uC-osflcyp110f07a1 Method BLASTX NCBI GI g6056374 BLAST score 280 E value 2.0e-25 Match length 115 % identity 51 NCBI Description (AC009894) Similar to serine/threonine kinases [Arabidopsis thaliana]

Seq. No. 412678

Seq. ID uC-osflcyp110f07b1

Method BLASTX

BLAST score

Match length

E value

568

139

2.0e-58

```
NCBI GI
                  q6056376
BLAST score
                  233
E value
                  1.0e-19
Match length
                  85
% identity
                  54
NCBI Description
                 (AC009894) Similar to serine/threonine kinases [Arabidopsis
                  thaliana]
Seq. No.
                  412679
Seq. ID
                  uC-osflcyp110f08b1
Method
                  BLASTN
NCBI GI
                  q6063530
BLAST score
                  212
E value
                  1.0e-115
                  404
Match length
                  95
% identity
NCBI Description Oryza sativa genomic DNA, chromosome 3, clone:P0043E01
Seq. No.
                  412680
Seq. ID
                  uC-osflcyp110f09a1
Method
                  BLASTN
NCBI GI
                  g2331130
BLAST score
                  216
E value
                  1.0e-118
Match length
                  268
% identity
                  99
NCBI Description Oryza sativa glycine-rich protein (OSGRP1) mRNA, complete
                  cds
                  412681
Seq. No.
Seq. ID
                  uC-osflcyp110f09b1
Method
                  BLASTX
NCBI GI
                  g2293480
BLAST score
                  449
E value
                  1.0e-44
Match length
                  89
                  98
% identity
NCBI Description (AF011331) glycine-rich protein [Oryza sativa]
                  412682
Seq. No.
Seq. ID
                  uC-osflcyp110f10a1
Method
                  BLASTX
NCBI GI
                  g4079798
BLAST score
                  202
E value
                  1.0e-15
Match length
                  69
% identity
                  64
NCBI Description
                 (AF052203) 23 kDa polypeptide of photosystem II [Oryza
                  sativa]
Seq. No.
                  412683
Seq. ID
                  uC-osflcyp110f10b1
Method
                  BLASTX
NCBI GI
                  q4079798
```

Method

BLASTX

```
% identity
NCBI Description (AF052203) 23 kDa polypeptide of photosystem II [Oryza
                   sativa]
Seq. No.
                   412684
Seq. ID
                  uC-osflcyp110f11a1
Method
                  BLASTX
NCBI GI
                  g4098272
BLAST score
                  296
E value
                  6.0e-27
Match length
                  68
                  97
% identity
NCBI Description (U76558) alpha-tubulin [Triticum aestivum]
Seq. No.
                   412685
Seq. ID
                  uC-osflcyp110f11b1
Method
                  BLASTX
NCBI GI
                  g1136120
BLAST score
                  521
E value
                  5.0e-53
Match length
                  135
% identity
                  76
NCBI Description (X91806) alpha-tubulin [Oryza sativa]
Seq. No.
                  412686
Seq. ID
                  uC-osflcyp110q02b1
Method
                  BLASTX
NCBI GI
                  g2198851
BLAST score
                  584
E value
                  1.0e-60
Match length
                  121
                  92
% identity
NCBI Description (AF007785) cystathionine gamma-synthase [Zea mays]
Seq. No.
                  412687
Seq. ID
                  uC-osflcyp110g03a1
Method
                  BLASTX
NCBI GI
                  g3860323
BLAST score
                  349
                  8.0e-33
E value
Match length
                  77
% identity
                  83
NCBI Description (AJ012688) hypothetical protein [Cicer arietinum]
Seq. No.
                  412688
Seq. ID
                  uC-osflcyp110g03b1
Method
                  BLASTX
NCBI GI
                  g3860323
BLAST score
                  349
                  7.0e-33
E value
Match length
                  77
                  83
% identity
NCBI Description (AJ012688) hypothetical protein [Cicer arietinum]
Seq. No.
                  412689
Seq. ID
                  uC-osflcyp110g04b1
```

NCBI GI

BLAST score

```
q3033384
NCBI GI
BLAST score
                  587
E value
                  1.0e-60
Match length
                  168
% identity
                  65
NCBI Description (AC004238) putative CTP synthase [Arabidopsis thaliana]
Seq. No.
                  412690
Seq. ID
                  uC-osflcyp110g05b1
Method
                  BLASTN
NCBI GI
                  q1944204
BLAST score
                  496
E value
                  0.0e + 00
Match length
                  500
% identity
                  100
NCBI Description Oryza sativa mRNA for RicMT, complete cds
Seq. No.
                  412691
Seq. ID
                  uC-osflcyp110g06a1
Method
                  BLASTX
NCBI GI
                  g1076820
BLAST score
                  377
E value
                  4.0e-36
Match length
                  81
% identity
                  90
NCBI Description phosphoglycerate mutase (EC 5.4.2.1) - maize
                  412692
Seq. No.
Seq. ID
                  uC-osflcyp110g06b1
Method
                  BLASTX
NCBI GI
                  g400803
BLAST score
                  641
E value
                  9.0e-69
Match length
                  145
                  90
% identity
NCBI Description 2,3-BISPHOSPHOGLYCERATE-INDEPENDENT PHOSPHOGLYCERATE MUTASE
                   (PHOSPHOGLYCEROMUTASE) (BPG-INDEPENDENT PGAM) (PGAM-I)
                  >gi 283033 pir A42807 phosphoglycerate mutase (EC
                   5.4.2.1), 2, 3-bisphosphoglycerate-independent - maize
                  >gi 168588 (M80912) 2,3-bisphosphoglycerate-independent
                  phosphoglycerate mutase [Zea mays]
Seq. No.
                  412693
Seq. ID
                  uC-osflcyp110g07a1
Method
                  BLASTX
NCBI GI
                  g2407279
BLAST score
                  367
E value
                  5.0e-35
                  71
Match length
                  99
% identity
NCBI Description (AF017362) aldolase [Oryza sativa]
Seq. No.
                  412694
Seq. ID
                  uC-osflcyp110g07b1
Method
                  BLASTX
```

53702

g3913018

5.0e-72 E value Match length 138 99 % identity NCBI Description FRUCTOSE-BISPHOSPHATE ALDOLASE, CHLOROPLAST PRECURSOR (ALDP) >gi 218155 dbj BAA02730 (D13513) chloroplastic aldolase [Oryza sativa] 412695 Seq. No. uC-osflcyp110g09a1 Seq. ID BLASTX Method NCBI GI q3169182 BLAST score 202 9.0e-16 E value 54 Match length 69 % identity NCBI Description (AC004401) unknown protein [Arabidopsis thaliana] 412696 Seq. No. uC-osflcyp110g09b1 Seq. ID Method BLASTX g3540195 NCBI GI BLAST score 443 6.0e-44E value 109 Match length 37 % identity (AC004260) Unknown protein [Arabidopsis thaliana] NCBI Description

Seq. No. 412697

uC-osflcyp110g11b1 Seq. ID

Method BLASTX NCBI GI q1888357 BLAST score 318 1.0e-59 E value Match length 170 59 % identity

NCBI Description (X98130) alpha-mannosidase [Arabidopsis thaliana]

>gi 1890154 emb CAA72432_ (Y11767) alpha-mannosidase

precursor [Arabidopsis thaliana]

Seq. No. 412698

Seq. ID uC-osflcyp110h01a1

Method BLASTX NCBI GI g1170937 BLAST score 194 9.0e-15 E value Match length 50 % identity 74

S-ADENOSYLMETHIONINE SYNTHETASE 1 (METHIONINE NCBI Description

ADENOSYLTRANSFERASE 1) (ADOMET SYNTHETASE 1)

>gi 450549 emb CAA81481 (Z26867) S-adenosyl methionine

synthetase [Oryza sativa]

412699 Seq. No.

Seq. ID uC-osflcyp110h01b1

Method BLASTX NCBI GI g1170937 BLAST score 462

% identity

78

```
E value
                  5.0e-46
Match length
                  86
                  99
% identity
                  S-ADENOSYLMETHIONINE SYNTHETASE 1 (METHIONINE
NCBI Description
                  ADENOSYLTRANSFERASE 1) (ADOMET SYNTHETASE 1)
                  >gi_450549_emb_CAA81481_ (Z26867) S-adenosyl methionine
                  synthetase [Oryza sativa]
Seq. No.
                  412700
Seq. ID
                  uC-osflcyp110h02b1
                  BLASTN
Method
NCBI GI
                  q4105602
BLAST score
                  217
E value
                  1.0e-118
                  217
Match length
                  100
% identity
NCBI Description Oryza sativa metallothionein (MTe) gene, complete cds
Seq. No.
                  412701
Seq. ID
                  uC-osflcyp110h03a1
Method
                  BLASTN
NCBI GI
                  g218144
BLAST score
                  285
                  1.0e-159
E value
Match length
                  368
                  95
% identity
NCBI Description Rice mRNA for ATP/ADP translocator, complete cds
                  412702
Seq. No.
Seq. ID
                  uC-osflcyp110h03b1
Method
                  BLASTX
NCBI GI
                  g3212879
BLAST score
                  169
                  1.0e-11
E value
Match length
                  69
                  52
% identity
NCBI Description (AC004005) putative ribosomal protein L7 [Arabidopsis
                  thaliana]
                  412703
Seq. No.
Seq. ID
                  uC-osflcyp110h04a1
Method
                  BLASTX
NCBI GI
                  g5726018
BLAST score
                  167
E value
                  1.0e-11
Match length
                  51
% identity
                  67
NCBI Description (AF090969) actin [Selaginella apoda]
Seq. No.
                  412704
Seq. ID
                  uC-osflcyp110h05b1
                  BLASTX
Method
NCBI GI
                  g3098603
BLAST score
                  607
E value
                  4.0e-70
Match length
                  167
```

Seq. ID

```
NCBI Description (AF052191) katanin p60 subunit [Strongylocentrotus
                  purpuratus]
                   412705
Seq. No.
Seq. ID
                  uC-osflcyp110h07a1
Method
                  BLASTX
NCBI GI
                  q1084455
BLAST score
                  362
E value
                  2.0e-34
Match length
                  75
                  93
% identity
NCBI Description
                  peptidylprolyl isomerase (EC 5.2.1.8) Cyp2 - rice
                  >gi 600767 (L29469) cyclophilin 2 [Oryza sativa]
Seq. No.
                   412706
Seq. ID
                  uC-osflcyp110h07b1
Method
                  BLASTX
NCBI GI
                  g1084455
BLAST score
                  532
E value
                  2.0e-54
Match length
                  114
% identity
                  89
NCBI Description
                  peptidylprolyl isomerase (EC 5.2.1.8) Cyp2 - rice
                  >gi 600767 (L29469) cyclophilin 2 [Oryza sativa]
                  412707
Seq. No.
Seq. ID
                  uC-osflcyp110h08b1
Method
                  BLASTX
NCBI GI
                  g445613
BLAST score
                  350
E value
                  6.0e-33
Match length
                  140
% identity
                  54
NCBI Description ribosomal protein L7 [Solanum tuberosum]
                  412708
Seq. No.
Seq. ID
                  uC-osflcyp110h09a1
Method
                  BLASTN
NCBI GI
                  g218144
BLAST score
                  349
E value
                  0.0e+00
Match length
                  405
% identity
                  97
NCBI Description Rice mRNA for ATP/ADP translocator, complete cds
                  412709
Seq. No.
Seq. ID
                  uC-osflcyp110h09b1
Method
                  BLASTX
NCBI GI
                  q485517
BLAST score
                  637
E value
                  1.0e-66
Match length
                  128
% identity
                  98
NCBI Description ADP, ATP carrier protein - rice
Seq. No.
                  412710
```

53705

uC-osflcyp110h10a1

Method BLASTX NCBI GI g122106 BLAST score 424 E value 1.0e-41 88 Match length 95 % identity NCBI Description HISTONE H4 >gi 70771 pir HSZM4 histone H4 - maize >gi 81642 pir S06904 histone H4 - Arabidopsis thaliana >gi 2119028 pir S60475 histone H4 - garden pea >gi 21795 emb CAA24924 (X00043) histone H4 [Triticum aestivum] >qi 166740 (M17132) histone H4 [Arabidopsis thaliana] >gi_166742 (M17133) histone H4 [Arabidopsis thaliana] >gi_168499 (M36659) histone H4 (H4C13) [Zea mays] >gi 168501 (M13370) histone H4 [Zea mays] >gi 168503 (M13377) histone H4 [Zea mays] >gi 498898 (U10042) histone H4 homolog [Pisum sativum] >gi 1806285 emb CAB01914 (Z79638) histone H4 homologue [Sesbania rostrata] >qi 3927823 (AC005727) histone H4 [Arabidopsis thaliana] >gi 4580385 gb AAD24364.1 AC007184 4 (AC007184) histone H4 [Arabidopsis thaliana] >gi 6009915 dbj BAA85120.1 (AB018245) histone H4-like protein [Solanum melongena] >gi 225838 prf 1314298A histone H4 [Arabidopsis thaliana]

Seq. No. 412711

Seq. ID uC-osflcyp110h10b1

Method BLASTX
NCBI GI g224293
BLAST score 410
E value 4.0e-40
Match length 82
% identity 100

NCBI Description histone H4 [Triticum aestivum]

Seq. No. 412712

Seq. ID uC-osflcyp110h11a1

Method BLASTX
NCBI GI g5702186
BLAST score 208
E value 2.0e-16
Match length 48
% identity 85

NCBI Description (AF106085) 4-coumarate: CoA ligase 2 [Arabidopsis thaliana]

>gi_5702188_gb_AAD47193.1_AF106086_1 (AF106086)
4-coumarate:CoA ligase 2 [Arabidopsis thaliana]

Seq. No. 412713

Seq. ID uC-osflcyp110h11b1

Method BLASTX
NCBI GI g5702186
BLAST score 436
E value 5.0e-43
Match length 124
% identity 70

NCBI Description (AF106085) 4-coumarate: CoA ligase 2 [Arabidopsis thaliana]

>gi_5702188_gb_AAD47193.1_AF106086_1 (AF106086)
4-coumarate:CoA ligase 2 [Arabidopsis thaliana]

Seq. No. 412714 Seq. ID uC-osflcyp111a02b1 Method BLASTX NCBI GI g3776559 BLAST score 181 2.0e-20 E value Match length 103 % identity 54 NCBI Description

NCBI Description (AC005388) Strong similarity to gene F14J9.26 gi_3482933

cdc2 protein kinase homolog from A. thaliana BAC

gb_AC003970. ESTs gb_Z35332 and gb_F19907 come from this

gene. [Arabidopsis thaliana]

Seq. No. 412715

Seq. ID uC-osflcyp111a03a1

Method BLASTX
NCBI GI g4646206
BLAST score 310
E value 2.0e-28
Match length 72
% identity 74

NCBI Description (AC007230) Contains similarity to gb_D13630 KIAA0005 gene

from Homo sapiens. ESTs gb_T45345, gb_T21086, gb_R90360, gb_T20468, gb_T45191 and gb_AI100459 come from this gene.

[Arabidopsis thaliana]

Seq. No. 412716

Seq. ID uC-osflcyp111a03b1

Method BLASTX
NCBI GI g4646206
BLAST score 534
E value 1.0e-55
Match length 167
% identity 63

NCBI Description (AC007230) Contains similarity to gb_D13630 KIAA0005 gene

from Homo sapiens. ESTs gb_T45345, gb_T21086, gb_R90360, gb_T20468, gb_T45191 and gb_AI100459 come from this gene.

[Arabidopsis thaliana]

Seq. No. 412717

Seq. ID uC-osflcyp111a04b1

Method BLASTX
NCBI GI g3859568
BLAST score 453
E value 4.0e-45
Match length 82
% identity 100

NCBI Description (AF098752) unknown [Oryza sativa]

Seq. No. 412718

Seq. ID uC-osflcyp111a05b1

Method BLASTX
NCBI GI g6102610
BLAST score 233
E value 2.0e-19

Match length 127 % identity 37

Seq. No.

Seq. ID

412724

uC-osflcyp111a10b1



```
NCBI Description (AF187317) CAF protein [Arabidopsis thaliana]
Seq. No.
                  412719
                  uC-osflcyp111a07a1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g303858
BLAST score
                  362
E value
                  0.0e+00
Match length
                  414
                  97
% identity
NCBI Description
                  Rice mRNA for brain specific protein (S94 gene), complete
                  412720
Seq. No.
Seq. ID
                  uC-osflcyp111a07b1
Method
                  BLASTX
NCBI GI
                  g543711
BLAST score
                  518
E value
                  4.0e-59
Match length
                  129
                  93
% identity
NCBI Description
                 14-3-3-LIKE PROTEIN S94 >gi 419796 pir S30927 14-3-3
                  protein homolog - rice >gi_303859_dbj_BAA03711_ (D16140)
                  brain specific protein [Oryza sativa]
Seq. No.
                  412721
Seq. ID
                  uC-osflcyp111a08a1
Method
                  BLASTX
NCBI GI
                  g4432864
BLAST score
                  282
E value
                  5.0e-25
Match length
                  81
                  70
% identity
NCBI Description (AC006300) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  412722
Seq. ID
                  uC-osflcyp111a08b1
                  BLASTX
Method
NCBI GI
                  q4432864
BLAST score
                  510
E value
                  9.0e-52
                  149
Match length
% identity
                  61
NCBI Description (AC006300) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  412723
Seq. ID
                  uC-osflcyp111a09b1
Method
                  BLASTX
NCBI GI
                  q3047104
BLAST score
                  181
E value
                  3.0e-13
                  61
Match length
% identity
NCBI Description (AF058919) No definition line found [Arabidopsis thaliana]
```



Method BLASTX
NCBI GI g1705629
BLAST score 698
E value 8.0e-74
Match length 150
% identity 89

NCBI Description CATALASE ISOZYME B (CAT-B) >gi_516839_dbj_BAA05494_

(D26484) catalase [Oryza sativa]

Seq. No. 412725

Seq. ID uC-osflcyp111a11b1

Method BLASTX
NCBI GI g1652856
BLAST score 227
E value 1.0e-18
Match length 130
% identity 40

NCBI Description (D90909) hypothetical protein [Synechocystis sp.]

Seq. No. 412726

Seq. ID uC-osflcyp111a12b1

Method BLASTX
NCBI GI g1806140
BLAST score 180
E value 5.0e-13
Match length 79
% identity 51

NCBI Description (X97314) cdc2MsC [Medicago sativa]

Seq. No. 412727

Seq. ID uC-osflcyp111b01a1

Method BLASTX

NCBI GI g3928090

BLAST score 196

E value 5.0e-15

Match length 65
% identity 60

NCBI Description (AC005770) putative MTN3 protein [Arabidopsis thaliana]

Seq. No. 412728

Seq. ID uC-osflcyp111b01b1

Method BLASTX
NCBI GI g4539359
BLAST score 179
E value 6.0e-13
Match length 125
% identity 38

NCBI Description (AL049525) putative protein [Arabidopsis thaliana]

Seq. No. 412729

Seq. ID uC-osflcyp111b02a1

Method BLASTX
NCBI GI g1084455
BLAST score 261
E value 1.0e-22
Match length 50
% identity 100

```
NCBI Description peptidylprolyl isomerase (EC 5.2.1.8) Cyp2 - rice
                  >gi 600767 (L29469) cyclophilin 2 [Oryza sativa]
                  412730
Seq. No.
Seq. ID
                  uC-osflcyp111b02b1
Method
                  BLASTX
NCBI GI
                  g1084455
BLAST score
                  374
E value
                  2.0e-69
Match length
                  133
                  98
% identity
                  peptidylprolyl isomerase (EC 5.2.1.8) Cyp2 - rice
NCBI Description
                  >gi 600767 (L29469) cyclophilin 2 [Oryza sativa]
                  412731
Seq. No.
Seq. ID
                  uC-osflcyp111b04a1
Method
                  BLASTN
NCBI GI
                  g3885887
BLAST score
                  136
E value
                  2.0e-70
                  196
Match length
% identity
                  94
NCBI Description Oryza sativa high mobility group protein (HMG) mRNA,
                  complete cds
                  412732
Seq. No.
Seq. ID
                  uC-osflcyp111b04b1
                  BLASTX
Method
NCBI GI
                  g6102610
BLAST score
                  264
E value
                  7.0e-23
Match length
                  130
% identity
                  41
NCBI Description (AF187317) CAF protein [Arabidopsis thaliana]
                  412733
Seq. No.
Seq. ID
                  uC-osflcyp111b05b1
Method
                  BLASTX
NCBI GI
                  g2499115
BLAST score
                  603
E value
                  1.0e-62
Match length
                  168
% identity
                  65
NCBI Description VACUOLAR ASSEMBLY PROTEIN VPS41 HOMOLOG >gi 1835788
                  (U86662) VPS41 [Lycopersicon esculentum]
                  412734
Seq. No.
                  uC-osflcyp111b06b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4895215
BLAST score
                  201
                  1.0e-15
E value
Match length
                  69
% identity
NCBI Description
                 (AC007660) putative 1-phosphatidylinositol-4,5-biphosphate
```

phosphodiesterase [Arabidopsis thaliana]



Seq. No. 412735

Seq. ID uC-osflcyp111b07b1

Method BLASTX
NCBI GI g3395938
BLAST score 174
E value 1.0e-24
Match length 75
% identity 80

NCBI Description (AF076924) polypyrimidine tract-binding protein homolog

[Arabidopsis thaliana]

Seq. No. 412736

Seq. ID uC-osflcyp111b10a1

Method BLASTN
NCBI GI g3885887
BLAST score 468
E value 0.0e+00
Match length 484
% identity 99

NCBI Description Oryza sativa high mobility group protein (HMG) mRNA,

complete cds

Seq. No. 412737

Seq. ID uC-osflcyp111b10b1

Method BLASTX
NCBI GI g3885888
BLAST score 202
E value 1.0e-15
Match length 111
% identity 44

NCBI Description (AF093632) high mobility group protein [Oryza sativa]

Seq. No. 412738

Seq. ID uC-osflcyp111b11b1

Method BLASTX
NCBI GI g3668069
BLAST score 206
E value 5.0e-16
Match length 103
% identity 45

NCBI Description (U28007) Pto kinase interactor 1 [Lycopersicon esculentum]

Seq. No. 412739

Seq. ID uC-osflcyp111c01b1

Method BLASTX
NCBI GI g3986695
BLAST score 606
E value 5.0e-63
Match length 131
% identity 92

NCBI Description (AF101423) ribosomal protein L12 [Cichorium intybus]

Seq. No. 412740

Seq. ID uC-osflcyp111c03a1

Method BLASTN NCBI GI g6069643

BLAST score 37

```
4.0e-11
E value
                  53
Match length
                  92
% identity
NCBI Description Oryza sativa genomic DNA, chromosome 6, clone:P0514G12
                  412741
Seq. No.
Seq. ID
                  uC-osflcyp111c04b1
Method
                  BLASTX
NCBI GI
                  g3393062
BLAST score
                  673
                  8.0e-71
E value
Match length
                  171
                  73
% identity
NCBI Description (Y17386) putative In2.1 protein [Triticum aestivum]
                  412742
Seq. No.
                  uC-osflcyp111c05a1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2829892
BLAST score
                  308
E value
                  4.0e-28
Match length
                  102
                  54
% identity
NCBI Description (AC002311) putative pectinesterase [Arabidopsis thaliana]
                  412743
Seq. No.
Seq. ID
                  uC-osflcyp111c06b1
                  BLASTX
Method
NCBI GI
                  g3075488
BLAST score
                  514
E value
                  3.0e-52
                  126
Match length
                  79
% identity
NCBI Description (AF058796) chlorophyll a/b-binding protein [Oryza sativa]
                  412744
Seq. No.
Seq. ID
                  uC-osflcyp111c07a1
Method
                  BLASTX
NCBI GI
                  g6094002
BLAST score
                  193
E value
                  1.0e-14
                  45
Match length
                  84
% identity
NCBI Description 60S RIBOSOMAL PROTEIN L12 >gi 2677830 (U93168) ribosomal
                  protein L12 [Prunus armeniaca]
                  412745
Seq. No.
Seq. ID
                  uC-osflcyp111c07b1
Method
                  BLASTX
NCBI GI
                  g1173187
BLAST score
                  578
                  8.0e-60
E value
                  115
Match length
% identity
NCBI Description
                  40S RIBOSOMAL PROTEIN S23 (S12) >gi 1362041 pir S56673
                  ribosomal protein S23.e, cytosolic (clone RJ3) - garden
```

53712

strawberry >gi 643074 (U19940) putative 40S ribosomal

Seq. No.

Seq. ID

412751

uC-osflcyp111d04b1

protein s12 [Fragaria x ananassa]

412746 Seq. No. uC-osflcyp111c08b1 Seq. ID BLASTN Method NCBI GI g4097337 BLAST score 260 1.0e-144 E value Match length 345 100 % identity Oryza sativa metallothionein-like protein mRNA, complete NCBI Description 412747 Seq. No. Seq. ID uC-osflcyp111c11a1 BLASTX Method q5679314 NCBI GI 569 BLAST score 1.0e-58 E value Match length 121 % identity NCBI Description (AF164021) receptor kinase [Oryza sativa] 412748 Seq. No. uC-osflcyp111c11b1 Seq. ID Method BLASTX a5679314 NCBI GI 829 BLAST score 4.0e-89 E value Match length 172 % identity 91 NCBI Description (AF164021) receptor kinase [Oryza sativa] 412749 Seq. No. Seq. ID uC-osflcyp111c12b1 Method BLASTX NCBI GI q3603353 568 BLAST score 1.0e-58 E value 153 Match length 73 % identity NCBI Description (AF074843) peroxisomal targeting signal type 1 receptor [Arabidopsis thaliana] 412750 Seq. No. uC-osflcyp111d03b1 Seq. ID Method BLASTX g4406761 NCBI GI 569 BLAST score E value 1.0e-58 Match length 124 81 % identity NCBI Description (AC006836) putative ubiquinone biosynthesis protein [Arabidopsis thaliana]



```
BLASTX
Method
NCBI GI
                  q4587515
                  435
BLAST score
E value
                  6.0e-43
                  160
Match length
                  51
% identity
                  (AC007060) EST gb_Z37678 comes from this gene. [Arabidopsis
NCBI Description
                  thaliana]
                  412752
Seq. No.
Seq. ID
                  uC-osflcyp111d07a1
                  BLASTN
Method
                  q5670155
NCBI GI
                  37
BLAST score
E value
                  2.0e-11
                  49
Match length
                   94
% identity
NCBI Description Oryza sativa subsp. japonica BAC clone 34K24, complete
                   sequence
Seq. No.
                   412753
                   uC-osflcyp111d08b1
Seq. ID
                  BLASTX
Method
NCBI GI
                   g1706260
                   439
BLAST score
                   1.0e-47
E value
                   119
Match length
                   91
% identity
NCBI Description CYSTEINE PROTEINASE 1 PRECURSOR >gi_2118131_pir__S59597
                   cysteine proteinase 1 precursor - maize
                   >qi 643597 dbj BAA08244 (D45402) cysteine proteinase [Zea
                   mays]
                   412754
Seq. No.
Seq. ID
                   uC-osflcyp111d09b1
```

Method BLASTX g4768968 NCBI GI 284 BLAST score 3.0e-25 E value 103 Match length % identity 64

(AF140219) nuclear cap-binding protein; CBP20 [Arabidopsis NCBI Description

thaliana]

412755 Seq. No.

Seq. ID uC-osflcyp111d10a1

Method BLASTX g4836888 NCBI GI 208 BLAST score 2.0e-16 E value 128 Match length % identity 46

NCBI Description (AC007369) Unknown protein [Arabidopsis thaliana]

412756 Seq. No.

Seq. ID uC-osflcyp111d10b1

Method BLASTX

```
NCBI GI
                  q2894599
BLAST score
                  264
E value
                  3.0e - 29
Match length
                  128
                  56
% identity
                 (AL021889) putative protein [Arabidopsis thaliana]
NCBI Description
                  412757
Seq. No.
Seq. ID
                  uC-osflcyp111d11b1
Method
                  BLASTX
NCBI GI
                  q556409
BLAST score
                  415
E value
                  1.0e-40
Match length
                  139
% identity
                  68
NCBI Description (L34551) transcriptional activator protein [Oryza sativa]
                  412758
Seq. No.
                  uC-osflcyp111d12b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3126854
BLAST score
                  530
E value
                  4.0e-70
Match length
                  153
% identity
                  89
NCBI Description (AF061577) chlorophyll a/b binding protein [Oryza sativa]
Seq. No.
                  412759
Seq. ID
                  uC-osflcyp111e01b1
Method
                  BLASTX
NCBI GI
                  g3281853
BLAST score
                  187
E value
                   5.0e-14
Match length
                  106
% identity
                   64
NCBI Description (AL031004) putative protein [Arabidopsis thaliana]
                   412760
Seq. No.
Seq. ID
                  uC-osflcyp111e02b1
Method
                  BLASTN
NCBI GI
                  g871495
BLAST score
                  367
E value
                  0.0e+00
                  409
Match length
% identity
                   84
NCBI Description O.sativa mRNA for AT hook-containing protein (1866 bp)
                   412761
Seq. No.
Seq. ID
                  uC-osflcyp111e04b1
Method
                  BLASTX
NCBI GI
                   g5541667
BLAST score
                  751
E value
                   6.0e-80
Match length
                  170
% identity
                   82
NCBI Description (AL096859) putative protein [Arabidopsis thaliana]
```

Seq. ID

```
Seq. No.
                   412762
Seq. ID
                   uC-osflcyp111e05b1
Method
                   BLASTX
NCBI GI
                   g2055262
BLAST score
                   642
E value
                   1.0e-73
Match length
                   137
                   97
% identity
NCBI Description (AB003194) chitinase IIb [Oryza sativa]
Seq. No.
                   412763
                   uC-osflcyp111e06a1
Seq. ID
Method
                   BLASTN
NCBI GI
                   q20181
BLAST score
                   137
E value
                   8.0e-71
Match length
                   161
                   96
% identity
NCBI Description Rice cab2R gene for light harvesting chlorophyll
                   a/b-binding protein
Seq. No.
                   412764
Seq. ID
                   uC-osflcyp111e06b1
Method
                   BLASTX
NCBI GI
                   g1173187
BLAST score
                   575
E value
                   2.0e-59
Match length
                   113
% identity
                   95
                   40S RIBOSOMAL PROTEIN S23 (S12) >gi_1362041_pir__S56673 ribosomal protein S23.e, cytosolic (clone RJ3) - garden
NCBI Description
                   strawberry >gi 643074 (U19940) putative 40S ribosomal
                   protein s12 [Fragaria x ananassa]
Seq. No.
                   412765
Seq. ID
                   uC-osflcyp111e07a1
Method
                   BLASTN
NCBI GI
                   g2331130
BLAST score
                   190
E value
                   1.0e-102
                   206
Match length
                   99
% identity
NCBI Description Oryza sativa glycine-rich protein (OSGRP1) mRNA, complete
                   cds
                   412766
Seq. No.
Seq. ID
                   uC-osflcyp111e07b1
                   BLASTX
Method
NCBI GI
                   g2293480
BLAST score
                   373
                   9.0e-38
E value
                   86
Match length
% identity
NCBI Description (AF011331) glycine-rich protein [Oryza sativa]
Seq. No.
                   412767
```

53716

uC-osflcyp111e08a1

Method BLASTN
NCBI GI g2331130
BLAST score 94
E value 2.0e-45
Match length 148
% identity 97
NCBI Description Oryza sa

NCBI Description Oryza sativa glycine-rich protein (OSGRP1) mRNA, complete

cds

Seq. No. 412768

Seq. ID uC-osflcyp111e08b1

Method BLASTX
NCBI GI g4827050
BLAST score 262
E value 1.0e-22
Match length 92
% identity 52

NCBI Description ubiquitin specific protease 14 (tRNA-guanine

transglycosylase) >gi_1729927_sp_P54578_TGT_HUMAN QUEUINE TRNA-RIBOSYLTRANSFERASE (TRNA-GUANINE TRANSGLYCOSYLASE) (GUANINE INSERTION ENZYME) >gi 940182 (U30888) tRNA-Guanine

Transglycosylase [Homo sapiens]

Seq. No. 412769

Seq. ID uC-osflcyp111e09b1

Method BLASTX
NCBI GI g3859568
BLAST score 289
E value 8.0e-26
Match length 56
% identity 98

NCBI Description (AF098752) unknown [Oryza sativa]

Seq. No. 412770

Seq. ID uC-osflcyp111e10a1

Method BLASTX
NCBI GI g671740
BLAST score 326
E value 4.0e-30
Match length 61
% identity 100

NCBI Description (X84730) ribulose-bisphosphate carboxylase [synthetic

construct]

Seq. No. 412771

Seq. ID uC-osflcyp111e10b1

Method BLASTX
NCBI GI g132105
BLAST score 648
E value 6.0e-68
Match length 143
% identity 87

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR

(RUBISCO SMALL SUBUNIT C) >gi 68094 pir RKRZS9

ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_ (D00643) small subunit of ribulose-1,5-bisphosphate

,

carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa] >gi 226375 prf 1508256A ribulose bisphosphate carboxylase S [Oryza sativa]

412772 Seq. No.

Seq. ID uC-osflcyp111e11a1

Method BLASTX NCBI GI g4512125 BLAST score 243 1.0e-20 E value 45 Match length 100 % identity

(AF133340) putative chlorophyll a/b-binding protein NCBI Description

[Phalaenopsis sp. 'KCbutterfly']

412773 Seq. No.

Seq. ID uC-osflcyp111e11b1

Method BLASTX NCBI GI g115787 389 BLAST score E value 1.0e-60 Match length 140 % identity 89

CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I NCBI Description

CAB-2) (LHCP) >gi_82461_pir__S03706 chlorophyll a/b-binding protein 2R precursor - rice >gi_20182_emb_CAA32109_

(X13909) chlorophyll a/b-binding preprotein (AA -28 to 235)

[Oryza sativa]

412774 Seq. No.

Seq. ID uC-osflcyp111e12a1

BLASTN Method NCBI GI g5295936 BLAST score 399 0.0e + 00E value 407 Match length 100 % identity

NCBI Description Oryza sativa genomic DNA, chromosome 6, clone:P0681F10,

complete sequence

412775 Seq. No.

Seq. ID uC-osflcyp111e12b1

Method BLASTN NCBI GI g5295936 BLAST score 469 0.0e+00 E value 484 Match length 99 % identity

Oryza sativa genomic DNA, chromosome 6, clone:P0681F10, NCBI Description

complete sequence

412776 Seq. No.

Seq. ID uC-osflcyp111f01a1

Method BLASTN NCBI GI q3983664 BLAST score 359

Seq. No.

412782

```
0.0e + 00
E value
                  423
Match length
% identity
                  96
NCBI Description Oryza sativa mRNA for importin-beta2, partial cds
                  412777
Seq. No.
                  uC-osflcyp111f01b1
Seq. ID
                  BLASTX
Method
NCBI GI
                  q3983665
BLAST score
                  391
E value
                   7.0e-38
Match length
                  139
                   66
% identity
NCBI Description (AB011271) importin-beta2 [Oryza sativa]
                   412778
Seq. No.
                  uC-osflcyp111f02b1
Seq. ID
                  BLASTX
Method
NCBI GI
                   q3047104
BLAST score
                   240
                   4.0e-20
E value
Match length
                   90
% identity
                   56
NCBI Description (AF058919) No definition line found [Arabidopsis thaliana]
Seq. No.
                   412779
                   uC-osflcyp111f03a1
Seq. ID
                   BLASTN
Method
NCBI GI
                   g5410347
BLAST score
                   70
E value
                   7.0e-31
Match length
                   142
                   87
% identity
NCBI Description Sorghum bicolor BAC clone 110K5, partial sequence
Seq. No.
                   412780
                   uC-osflcyp111f03b1
Seq. ID
                   BLASTN
Method
                   g5410347
NCBI GI
                   95
BLAST score
E value
                   1.0e-45
                   303
Match length
                   86
% identity
NCBI Description Sorghum bicolor BAC clone 110K5, partial sequence
Seq. No.
                   412781
                   uC-osflcyp111f05b1
Seq. ID
                   BLASTX
Method
                   g3319345
NCBI GI
                   152
BLAST score
E value
                   1.0e-09
                   53
Match length
                   49
% identity
NCBI Description (AF077407) contains similarity to maize transposon MuDR
                   (GB:M76978) [Arabidopsis thaliana]
```

E value

6.0e-54

```
uC-osflcyp111f06b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4972097
BLAST score
                  211
E value
                  1.0e-16
                  77
Match length
                  45
% identity
NCBI Description (AL078468) putative protein [Arabidopsis thaliana]
                  412783
Seq. No.
                  uC-osflcyp111f07a1
Seq. ID
                  BLASTX
Method
NCBI GI
                  q4713951
BLAST score
                  148
E value
                  5.0e-10
Match length
                  55
                  45
% identity
NCBI Description (AC007293) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  412784
                  uC-osflcyp111f07b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q730456
BLAST score
                  398
                  1.0e-55
E value
Match length
                  114
% identity
                  98
NCBI Description 40S RIBOSOMAL PROTEIN S19
                  412785
Seq. No.
                  uC-osflcyp111f10b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4538920
BLAST score
                  192
E value
                  2.0e-14
Match length
                  49
                  80
% identity
NCBI Description (AL049483) nitrogen fixation like protein [Arabidopsis
                  thaliana]
                   412786
Seq. No.
Seq. ID
                  uC-osflcyp111f11a1
                  BLASTX
Method
                  g5833467
NCBI GI
BLAST score
                  230
                   5.0e-19
E value
Match length
                  61
                   70
% identity
NCBI Description (AF158602) monodehydroascorbate reductase [Zantedeschia
                   aethiopica]
Seq. No.
                   412787
Seq. ID
                  uC-osflcyp111f11b1
                  BLASTX
Method
NCBI GI
                   g4704613
                   529
BLAST score
```

Seq. No.

412793

```
125
Match length
% identity
NCBI Description
                  (AF109695) monodehydroascorbate reductase [Brassica juncea]
                  412788
Seq. No.
                  uC-osflcyp111f12a1
Seq. ID
Method
                  BLASTX
                  q4006978
NCBI GI
BLAST score
                  153
E value
                   6.0e-10
Match length
                  53
% identity
                   49
NCBI Description (AJ131335) pollen allergen (group II) [Cynodon dactylon]
                  412789
Seq. No.
                  uC-osflcyp111f12b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4006978
                  201
BLAST score
E value
                  2.0e-15
                  87
Match length
% identity
                  44
NCBI Description (AJ131335) pollen allergen (group II) [Cynodon dactylon]
                   412790
Seq. No.
Seq. ID
                  uC-osflcyp111g01b1
Method
                  BLASTX
NCBI GI
                   q4309726
BLAST score
                  158
                   1.0e-10
E value
Match length
                   127
% identity
NCBI Description (AC006439) hypothetical protein [Arabidopsis thaliana]
                   412791
Seq. No.
Seq. ID
                   uC-osflcyp111g02a1
Method
                   BLASTX
NCBI GI
                   q4510402
BLAST score
                   362
                   1.0e-34
E value
Match length
                   112
% identity
                   62
NCBI Description (AC006587) putative AP2 domain [Arabidopsis thaliana]
                   412792
Seq. No.
Seq. ID
                   uC-osflcyp111g04a1
Method
                   BLASTX
NCBI GI
                   g2117937
BLAST score
                  513
                   5.0e-53
E value
Match length
                   125
% identity
                   85
                  UTP--glucose-1-phosphate uridylyltransferase (EC 2.7.7.9) -
NCBI Description
                  barley >gi_1212996_emb_CAA62689_ (X91347) UDP-glucose
                  pyrophosphorylase [Hordeum vulgare]
```

```
Seq. ID
                   uC-osflcyp111g04b1
Method
                   BLASTX
NCBI GI
                   g2117937
BLAST score
                   684
                   4.0e-72
E value
Match length
                   160
% identity
                   81
NCBI Description
                   UTP--glucose-1-phosphate uridylyltransferase (EC 2.7.7.9) -
                   barley >gi 1212996 emb CAA62689 (X91347) UDP-glucose
                   pyrophosphorylase [Hordeum vulgare]
                   412794
Seq. No.
Seq. ID
                   uC-osflcyp111g07a1
Method
                   BLASTX
NCBI GI
                   g3334409
BLAST score
                   238
E value
                   6.0e-20
Match length
                   60
% identity
                   77
NCBI Description
                   VACUOLAR ATP SYNTHASE SUBUNIT E (V-ATPASE E SUBUNIT)
                   >gi_2129765_pir__S71261 V-type proton-ATPase - Arabidopsis thaliana >gi_1143394_emb_CAA63086_ (X92117) V-type
                   proton-ATPase [Arabidopsis thaliana]
Seq. No.
                   412795
Seq. ID
                   uC-osflcyp111q07b1
Method
                   BLASTX
NCBI GI
                   g5565981
BLAST score
                   290
E value
                   8.0e-37
Match length
                   117
                   77
% identity
NCBI Description (AF152600) unknown [Zea mays]
Seq. No.
                   412796
Seq. ID
                   uC-osflcyp111g08b1
Method
                   BLASTX
NCBI GI
                   g1742959
BLAST score
                   485
E value
                   5.0e-49
Match length
                   122
                   75
% identity
NCBI Description
                  (Z71450) CLC-d chloride channel protein [Arabidopsis
                   thaliana]
                   412797
Seq. No.
Seq. ID
                   uC-osflcyp111g10a1
Method
                   BLASTX
NCBI GI
                   g231706
BLAST score
                   519
E value
                   8.0e-53
Match length
                   100
% identity
                   99
NCBI Description
                   CELL DIVISION CONTROL PROTEIN 2 HOMOLOG 1
                   >gi 100667 pir S22440 protein kinase (EC 2.7.1.37) cdc2
                   homolog 1 - rice >gi_20343_emb_CAA42922_ (X60374) Rcdc2-1
```

[Oryza sativa] >gi_228924_prf__1814443A cdc2

protein:ISOTYPE=cdc2Os-1 [Oryza sativa] Seq. No. 412798 Seq. ID uC-osflcyp111g10b1 Method BLASTX NCBI GI g231706 BLAST score 258 E value 1.0e-22 74 Match length % identity 85 NCBI Description CELL DIVISION CONTROL PROTEIN 2 HOMOLOG 1 >gi 100667 pir S22440 protein kinase (EC 2.7.1.37) cdc2 homolog 1 - rice >gi_20343_emb_CAA42922_ (X60374) Rcdc2-1 [Oryza sativa] >gi_228924_prf_1814443A cdc2 protein:ISOTYPE=cdc2Os-1 [Oryza sativa] 412799 Seq. No. Seq. ID uC-osflcyp111g11b1 Method BLASTX NCBI GI g4455194

Method BLASTX
NCBI GI g4455194
BLAST score 257
E value 5.0e-22
Match length 67
% identity 70

NCBI Description (AL035440) putative protein [Arabidopsis thaliana]

Seq. No. 412800
Seq. ID uC-osflcyp111h02a1
Method BLASTX
NCBI GI g226263
BLAST score 229
E value 5.0e-19
Match length 43

% identity 100

NCBI Description chlorophyll a/b binding protein [Glycine max]

Seq. No. 412801

Seq. ID uC-osflcyp111h02b1

Method BLASTX
NCBI GI g3036942
BLAST score 210
E value 6.0e-17
Match length 39
% identity 100

NCBI Description (AB012636) light harvesting chlorophyll a/b-binding protein

[Nicotiana sylvestris]

Seq. No. 412802

Seq. ID uC-osflcyp111h03a1

Method BLASTN
NCBI GI g1532047
BLAST score 196
E value 1.0e-106
Match length 228

Match length 228 % identity 97

NCBI Description O.sativa mRNA for S-adenosylmethionine decarboxylase

412803 Seq. No. uC-osflcyp111h03b1 Seq. ID Method BLASTX NCBI GI q2911067 BLAST score 381 5.0e-49E value 141 Match length 73 % identity (AL021960) UV-damaged DNA-binding protein-like [Arabidopsis NCBI Description thaliana] 412804 Seq. No. uC-osflcyp111h04a1 Seq. ID BLASTX Method q5257277 NCBI GI BLAST score 344 2.0e-32 E value 81 Match length 85 % identity (AP000364) ESTs C98431(E0144), C71728(E0144) correspond to a NCBI Description region of the predicted gene.; Similar to Medicago sativa S-adenosyl-L-methionine. (U20736) [Oryza sativa] 412805 Seq. No. uC-osflcyp111h04b1 Seq. ID BLASTX Method NCBI GI q5257277 458 BLAST score 5.0e-58 E value 128 Match length % identity 94 (AP000364) ESTs C98431(E0144), C71728(E0144) correspond to a NCBI Description region of the predicted gene.; Similar to Medicago sativa S-adenosyl-L-methionine. (U20736) [Oryza sativa] Seq. No. 412806 uC-osflcyp111h05a1 Seq. ID BLASTN Method NCBI GI q2967681 BLAST score 86 2.0e-40 E value Match length 208 92 % identity NCBI Description Oryza sativa strain Malkolam microsatellite OS1E6 412807 Seq. No. Seq. ID uC-osflcyp111h05b1 Method BLASTX NCBI GI g5931629 BLAST score 186 1.0e-13 E value Match length 66 % identity 58

NCBI Description (AJ011609) squamosa promoter binding protein-like 5 [Arabidopsis thaliana] >gi_5931631_emb_CAB56572.1_ (AJ011610) squamosa promoter binding protein-like 5

[Arabidopsis thaliana]

Method

BLASTX

```
412808
Seq. No.
Seq. ID
                  uC-osflcyp111h06b1
Method
                  BLASTX
NCBI GI
                  g1946368
BLAST score
                  331
                  8.0e-31
E value
                  131
Match length
% identity
NCBI Description (U93215) unknown protein [Arabidopsis thaliana]
                  412809
Seq. No.
                  uC-osflcyp111h07b1
Seq. ID
                  BLASTX
Method
NCBI GI
                  q3047124
                  274
BLAST score
                  4.0e-24
E value
                  121
Match length
% identity
NCBI Description (AF058919) No definition line found [Arabidopsis thaliana]
                  412810
Seq. No.
                  uC-osflcyp111h08a1
Seq. ID
Method
                  BLASTX
                   q3913426
NCBI GI
BLAST score
                   287
                   1.0e-25
E value
                   55
Match length
                   98
% identity
NCBI Description S-ADENOSYLMETHIONINE DECARBOXYLASE PROENZYME (ADOMETDC)
                   (SAMDC) >gi_1532048_emb_CAA69074_ (Y07766)
                   S-adenosylmethionine decarboxylase [Oryza sativa]
                   412811
Seq. No.
Seq. ID
                   uC-osflcyp111h08b1
Method
                   BLASTX
                   q2129921
NCBI GI
                   179
BLAST score
                   5.0e-13
E value
                   51
Match length
% identity
                   67
NCBI Description hypothetical protein 1 - Madagascar periwinkle >gi_758694
                   (U12573) putative [Catharanthus roseus]
                   412812
Seq. No.
                   uC-osflcyp111h09b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   q4680675
                   154
BLAST score
                   5.0e-10
E value
Match length
                   120
                   34
% identity
NCBI Description (AF132952) CGI-18 protein [Homo sapiens]
                   412813
Seq. No.
Seq. ID
                   uC-osflcyp111h10a1
```

```
q5531937
NCBI GI
                  283
BLAST score
E value
                   4.0e-25
Match length
                  62
                   90
% identity
                  (AF113522) acetoacetyl CoA thiolase [Zea mays]
NCBI Description
                   412814
Seq. No.
Seq. ID
                  uC-osflcyp111h10b1
                  BLASTX
Method
NCBI GI
                   g1542941
BLAST score
                   481
                   2.0e-48
E value
Match length
                   130
% identity
                   76
                  (X78116) Acetoacetyl-coenzyme A thiolase [Raphanus sativus]
NCBI Description
                   412815
Seq. No.
                   uC-osflcyp111h12a1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3789942
BLAST score
                   414
E value
                   1.0e-40
Match length
                   83
                   20
% identity
                   (AF093505) polyubiquitin [Saccharum hybrid cultivar
NCBI Description
                   H32-8560]
Seq. No.
                   412816
Seq. ID
                   uC-osflcyp111h12b1
Method
                   BLASTX
                   g3789942
NCBI GI
BLAST score
                   414
E value
                   2.0e-40
Match length
                   83
% identity
                   20
                  (AF093505) polyubiquitin [Saccharum hybrid cultivar
NCBI Description
                   H32-8560]
                   412817
Seq. No.
                   uC-osflcyp112a01a1
Seq. ID
                   BLASTN
Method
                   g540534
NCBI GI
BLAST score
                   46
E value
                   3.0e-17
Match length
                   114
                   85
% identity
NCBI Description Rice mRNA for q group of receptor for activated C-kinase,
                   complete cds
Seq. No.
                   412818
                   uC-osflcyp112a01b1
Seq. ID
                   BLASTX
Method
NCBI GI
                   g1346109
BLAST score
                   562
                   5.0e-58
E value
                   111
Match length
```

% identity GUANINE NUCLEOTIDE-BINDING PROTEIN BETA SUBUNIT-LIKE NCBI Description PROTEIN (GPB-LR) (RWD) >gi 540535 dbj BAA07404_ (D38231) RWD [Oryza sativa] 412819 Seq. No. uC-osflcyp112a03b1 Seq. ID Method BLASTN NCBI GI q3986152 BLAST score 135 4.0e-70 E value Match length 147 % identity 99 Oryza sativa gene for plastidic ATP sulfurylase, complete NCBI Description 412820 Seq. No. uC-osflcyp112a04b1 Seq. ID Method BLASTN NCBI GI g4680189 BLAST score 41 E value 1.0e-13 Match length 76 % identity 89 NCBI Description Oryza sativa subsp. indica putative dnaJ-like protein, putative myb-related protein, putative farnesyl pyrophosphate synthase, and hypothetical protein genes, complete cds Seq. No. 412821 uC-osflcyp112a08a1 Seq. ID Method BLASTN NCBI GI g607894 41 BLAST score E value 3.0e-14 53 Match length 96 % identity NCBI Description Oryza sativa IR54 anther specific (RTS2) gene, complete cds 412822 Seq. No. Seq. ID uC-osflcyp112a08b1 Method BLASTN NCBI GI q607894 BLAST score 64 1.0e-27

E value Match length 76 96 % identity

NCBI Description Oryza sativa IR54 anther specific (RTS2) gene, complete cds

412823 Seq. No.

uC-osflcyp112b01a1 Seq. ID

BLASTN Method NCBI GI q3370779 BLAST score 107 E value 4.0e-53 Match length 163 % identity 94

NCBI Description Oryza sativa mRNA for chitinase, complete cds Seq. No. 412824 uC-osflcyp112b01b1 Seq. ID Method BLASTX NCBI GI g3370780 BLAST score 643 E value 2.0e-67 Match length 124 % identity 98 NCBI Description (AB016497) chitinase [Oryza sativa] 412825 Seq. No. uC-osflcyp112b10b1 Seq. ID Method BLASTX NCBI GI g2982458 BLAST score 293 E value 3.0e-26 Match length 105 % identity 55 NCBI Description (AL022223) putative protein [Arabidopsis thaliana] Seq. No. 412826 Seq. ID uC-osflcyp112c01a1 Method BLASTX NCBI GI q5731756 BLAST score 217 2.0e-17 E value Match length 89 51 % identity NCBI Description (AL109819) putative protein [Arabidopsis thaliana] Seq. No. 412827 Seq. ID uC-osflcyp112c02a1 BLASTN Method NCBI GI q303854 BLAST score 85 E value 7.0e-40 Match length 191 87 % identity NCBI Description Rice mRNA for ribosomal protein L7A, complete cds 412828 Seq. No. Seq. ID uC-osflcyp112c02b1 Method BLASTX NCBI GI q548774 501 BLAST score E value 9.0e-51 Match length 119 % identity 83

NCBI Description 60S RIBOSOMAL PROTEIN L7A >gi_542158_pir__S38360 ribosomal

protein L7a - rice >gi_303855_dbj_BAA02156_ (D12631)

ribosomal protein L7A [Oryza sativa]

Seq. No. 412829

Seq. ID uC-osflcyp112c04a1

Method BLASTX



```
NCBI GI g3386611
BLAST score 188
E value 5.0e-14
Match length 86
% identity 40
NCBI Description (AC00466
```

NCBI Description (AC004665) unknown protein [Arabidopsis thaliana]

Seq. No. 412830

Seq. ID uC-osflcyp112c06b1

Method BLASTX
NCBI GI g629775
BLAST score 630
E value 7.0e-66
Match length 140
% identity 86

NCBI Description beta-ketoacyl-ACP synthase - barley (fragment)

Seq. No. 412831

Seq. ID uC-osflcyp112c07b1

Method BLASTX
NCBI GI g2662343
BLAST score 160
E value 3.0e-21
Match length 63
% identity 82

NCBI Description (D63581) EF-1 alpha [Oryza sativa]

Seq. No. 412832

Seq. ID uC-osflcyp112c08a1

Method BLASTX
NCBI GI g4115936
BLAST score 346
E value 1.0e-32
Match length 85
% identity 78

NCBI Description (AF118223) No definition line found [Arabidopsis thaliana]

Seq. No. 412833

Seq. ID uC-osflcyp112c08b1

Method BLASTX
NCBI GI g4115936
BLAST score 258
E value 8.0e-29
Match length 102
% identity 58

NCBI Description (AF118223) No definition line found [Arabidopsis thaliana]

Seq. No. 412834

Seq. ID uC-osflcyp112c09b1

Method BLASTX
NCBI GI g2570515
BLAST score 636
E value 1.0e-66
Match length 135
% identity 93

NCBI Description (AF022740) glycolate oxidase [Oryza sativa]

NCBI GI

```
Seq. No.
                   412835
Seq. ID
                   uC-osflcyp112c10b1
Method
                   BLASTX
NCBI GI
                   g113360
BLAST score
                   400
E value
                   1.0e-53
Match length
                   136
% identity
                   86
NCBI Description ALCOHOL DEHYDROGENASE 1 >gi_100652_pir__JQ0474 alcohol dehydrogenase (EC 1.1.1.1) 1 - rice >gi_20165_emb_CAA34363_
                   (X16296) alcohol dehydrogenase 1 [Oryza sativa]
                   412836
Seq. No.
Seq. ID
                   uC-osflcyp112c12b1
Method
                   BLASTX
NCBI GI
                   g3603353
                   224
BLAST score
E value
                   2.0e-18
Match length
                   98
                   53
% identity
NCBI Description (AF074843) peroxisomal targeting signal type 1 receptor
                   [Arabidopsis thaliana]
                   412837
Seq. No.
Seq. ID
                   uC-osflcyp112d01a1
Method
                   BLASTX
NCBI GI
                   g231924
BLAST score
                   174
E value
                   2.0e-12
Match length
                   43
% identity
                   81
NCBI Description CYTOCHROME C1, HEME PROTEIN PRECURSOR (CLONE PC181)
Seq. No.
                   412838
Seq. ID
                   uC-osflcyp112d02b1
Method
                   BLASTX
NCBI GI
                   q6002641
BLAST score
                   231
                   3.0e-19
E value
Match length
                   118
% identity
                   42
NCBI Description (AF094825) RNA-binding protein homolog [Brassica napus]
Seq. No.
                   412839
Seq. ID
                   uC-osflcyp112d05b1
Method
                   BLASTX
NCBI GI
                   q4090943
BLAST score
                   603
E value
                   1.0e-62
Match length
                   175
% identity
                   69
NCBI Description (AF029984) COP1 homolog [Lycopersicon esculentum]
Seq. No.
                   412840
Seq. ID
                   uC-osflcyp112d06b1
Method
                   BLASTX
```

53730

g3047116

BLAST score 208 E value 2.0e-16 Match length 61 67 % identity NCBI Description (AF058919) No definition line found [Arabidopsis thaliana] Seq. No. 412841 Seq. ID uC-osflcyp112d07b1 Method BLASTX NCBI GI g3885334 BLAST score 660 E value 3.0e-69 Match length 178 % identity 73 (AC005623) putative argonaute protein [Arabidopsis NCBI Description thaliana] 412842 Seq. No. Seq. ID uC-osflcyp112d08b1 Method BLASTX NCBI GI g2245000 BLAST score 223 E value 4.0e-18 Match length 85 % identity 58 NCBI Description (Z97341) LET1 like protein [Arabidopsis thaliana] 412843 Seq. No. Seq. ID uC-osflcyp112d09b1 Method BLASTX NCBI GI g5731756 BLAST score 595 E value 1.0e-61 Match length 154 74 % identity NCBI Description (AL109819) putative protein [Arabidopsis thaliana] Seq. No. 412844 Seq. ID uC-osflcyp112d10b1 Method BLASTX NCBI GI g4337174 BLAST score 574 E value 4.0e-59 Match length 181 % identity 60 NCBI Description (AC006416) Similar to gi 1573829 HI0816 aminopeptidase P homolog (pepP) from Haemophilus influenzae genome gb U32764. [Arabidopsis thaliana] 412845 Seq. No. Seq. ID uC-osflcyp112d12a1

Method BLASTN NCBI GI g11957 BLAST score 43 E value 2.0e-15 Match length 87 % identity 87

NCBI Description Rice complete chloroplast genome Seq. No. 412846 Seq. ID uC-osflcyp112d12b1 Method BLASTX NCBI GI g3126854 BLAST score 231 E value 3.0e-19 99 Match length 54 % identity NCBI Description (AF061577) chlorophyll a/b binding protein [Oryza sativa] Seq. No. 412847 Seq. ID uC-osflcyp112e02b1 Method BLASTN NCBI GI g2645165 BLAST score 35 E value 3.0e-10 Match length 39 % identity 97 NCBI Description Oryza sativa mRNA, similar to ribosomal protein Seq. No. 412848 Seq. ID uC-osflcyp112e03b1 Method BLASTX NCBI GI q1321661 BLAST score 247 E value 3.0e-21Match length 49 100 % identity NCBI Description (D45423) ascorbate peroxidase [Oryza sativa] 412849 Seq. No. Seq. ID uC-osflcyp112e04b1 Method BLASTX NCBI GI g5733877 BLAST score 467 E value 1.0e-46 Match length 154 % identity 58 NCBI Description (AC007932) F11A17.13 [Arabidopsis thaliana] Seq. No. 412850 Seq. ID uC-osflcyp112e05b1 Method BLASTX NCBI GI g1632822 BLAST score 784 E value 8.0e-84 Match length 176 87 % identity NCBI Description (Y08962) transmembrane protein [Oryza sativa] >gi_1667594 (U77297) transmembrane protein [Oryza sativa] Seq. No. 412851

Seq. ID uC-osflcyp112e06b1

Method BLASTX NCBI GI g1170507



BLAST score 843 E value 1.0e-90 Match length 171 % identity 94

NCBI Description EUKARYOTIC INITIATION FACTOR 4A-3 (EIF-4A-3)

>gi_100276_pir__S22579 translation initiation factor eIF-4A
- curled-leaved tobacco >gi_19699_emb_CAA43514_ (X61206)
nicotiana eukaryotic translation initiation factor 4A

[Nicotiana plumbaginifolia]

Seq. No. 412852

Seq. ID uC-osflcyp112e09a1

Method BLASTX
NCBI GI g1350986
BLAST score 289
E value 6.0e-26
Match length 60
% identity 97

NCBI Description 40S RIBOSOMAL PROTEIN S3A (CYCO7 PROTEIN)

>gi_483431_dbj_BAA05059_ (D26060) cyc07 [Oryza sativa]

Seq. No. 412853

Seq. ID uC-osflcyp112e09b1

Method BLASTX
NCBI GI g1350986
BLAST score 373
E value 2.0e-36
Match length 81
% identity 94

NCBI Description 40S RIBOSOMAL PROTEIN S3A (CYC07 PROTEIN)

>gi_483431_dbj_BAA05059 (D26060) cyc07 [Oryza sativa]

Seq. No. 412854

Seq. ID uC-osflcyp112e10a1

Method BLASTN
NCBI GI 94680335
BLAST score 38
E value 6.0e-12
Match length 82
% identity 87

NCBI Description Oryza sativa subsp. indica BAC clone 16F19 php20725 region,

complete sequence

Seq. No. 412855

Seq. ID uC-osflcyp112e11b1

Method BLASTX
NCBI GI g4006868
BLAST score 381
E value 1.0e-36
Match length 173
% identity 51

NCBI Description (Z99707) putative protein [Arabidopsis thaliana]

Seq. No. 412856

Seq. ID uC-osflcyp112e12b1

Method BLASTX NCBI GI g3834314



BLAST score 357 E value 9.0e-34 Match length 116 % identity 62

NCBI Description (AC005679) Similar to gene pi010 glycosyltransferase gi_2257490 from S. pombe clone 1750 gb_AB004534. ESTs

gb_T46079 and gb_AA394466 come from this gene. [Arabidopsis

thaliana]

Seq. No. 412857

Seq. ID uC-osflcyp112f01b1

Method BLASTX
NCBI GI g2605887
BLAST score 156
E value 6.0e-11
Match length 60
% identity 60

NCBI Description (AF029242) dormancy-associated protein [Pisum sativum]

Seq. No. 412858

Seq. ID uC-osflcyp112f04b1

Method BLASTX
NCBI GI g2997589
BLAST score 731
E value 1.0e-77
Match length 152
% identity 92

NCBI Description (AF020813) glucose-6-phosphate/phosphate-translocator

precursor [Zea mays]

Seq. No. 412859

Seq. ID uC-osflcyp112f08b1

Method BLASTX
NCBI GI g129591
BLAST score 378
E value 2.0e-36
Match length 112
% identity 71

NCBI Description PHENYLALANINE AMMONIA-LYASE >gi_295824_emb_CAA34226_

(X16099) phenylalanine ammonia-Tyase [Oryza sativa]

Seq. No. 412860

Seq. ID uC-osflcyp112f11a1

Method BLASTN
NCBI GI g493709
BLAST score 372
E value 0.0e+00
Match length 400
% identity 98

NCBI Description Rice mRNA for beta-tubulin, complete cds

Seq. No. 412861

Seq. ID uC-osflcyp112f11b1

Method BLASTX
NCBI GI g1174600
BLAST score 879
E value 6.0e-95

```
Match length
                   169
% identity
                   97
NCBI Description
                   TUBULIN BETA CHAIN >gi_493710_dbj_BAA06382_ (D30717)
                   beta-tubulin [Oryza sativa]
Seq. No.
                   412862
Seq. ID
                   uC-osflcyp112f12b1
Method
                   BLASTX
NCBI GI
                   q3287688
BLAST score
                   343
E value
                   4.0e-32
Match length
                   112
% identity
NCBI Description
                  (AC003979) Contains similarity to ycf37 gene product
                   gb_1001425 from Synechocystis sp. genome gb_D63999. ESTs
                   gb_T43026, gb_R64902, gb_Z18169 and gb_N37374 come from
                   this gene. [Arabidopsis thaliana]
Seq. No.
                   412863
Seq. ID
                  uC-osflcyp112g02b1
Method
                  BLASTX
NCBI GI
                  q5803266
BLAST score
                  340
                  2.0e-32
E value
Match length
                  66
% identity
                  (AP000399) ESTs AU078063(S15496), C97608(C60475),
NCBI Description
                  C28255(C60475) correspond to a region of the predicted
                  gene; similar to plastid transketolase 2 (Y15782) [Oryza
                  sativa]
Seq. No.
                  412864
Seq. ID
                  uC-osflcyp112g04a1
Method
                  BLASTX
NCBI GI
                  g1531756
BLAST score
                  209
E value
                  2.0e-16
Match length
                  41
% identity
                  93
NCBI Description
                  (X82413) proline-rich-like protein [Asparagus officinalis]
Seq. No.
                  412865
Seq. ID
                  uC-osflcyp112q05a1
Method
                  BLASTN
NCBI GI
                  q1304214
BLAST score
                  276
E value
                  1.0e-154
Match length
                  347
% identity
                  95
NCBI Description
                 Rice mRNA for precursor of 22 kDa protein of photosystem II
                  (PSII-S), complete cds
```

Seq. No. 412866

Seq. ID uC-osflcyp112g05b1

Method BLASTX
NCBI GI g1304215
BLAST score 358

2.0e-53 E value Match length 117 % identity 73 NCBI Description (D84392) precursor of rice 22 kDa protein of photosystem II (PSII-S) [Oryza sativa] Seq. No. 412867 Seq. ID uC-osflcyp112g06a1 Method BLASTX NCBI GI g2960364 BLAST score 280 E value 7.0e-25 Match length 90 % identity 59 NCBI Description (AJ224986) cinnamoyl CoA reductase [Populus balsamifera subsp. trichocarpa] Seq. No. 412868 Seq. ID uC-osflcyp112g06b1 Method BLASTX NCBI GI g2960364 BLAST score 353 E value 2.0e-33 Match length 130 % identity 57 (AJ224986) cinnamoyl CoA reductase [Populus balsamifera NCBI Description subsp. trichocarpa] Seq. No. 412869 Seq. ID uC-osflcyp112g09b1 Method BLASTX NCBI GI g129591 BLAST score 381 E value 8.0e-37 94 Match length 80 % identity NCBI Description PHENYLALANINE AMMONIA-LYASE >gi_295824_emb_CAA34226_ (X16099) phenylalanine ammonia-lyase [Oryza sativa] 412870 Seq. No. Seq. ID uC-osflcyp112g11a1 Method BLASTX NCBI GI g122084 BLAST score 218 E value 1.0e-17 Match length 45 % identity 98 HISTONE H3 >gi_70754_pir__HSBH3 histone H3 - barley NCBI Description

 $(fragment) > gi_167061 (M34928)$ histone H3 protein [Hordeum

vulgare] >gi_225348_prf__1301219A histone H3 [Hordeum

vulgare var. distichum]

Seq. No. 412871

Seq. ID uC-osflcyp112g11b1

Method BLASTX NCBI GI g488573 BLAST score 434

Match length

174

```
E value
                   7.0e-43
Match length
                   88
% identity
                   100
NCBI Description (U09463) histone H3.2 [Medicago sativa]
Seq. No.
                   412872
Seq. ID
                   uC-osflcyp112h03b1
Method
                   BLASTX
NCBI GI
                   g5880464
BLAST score
                   145
E value
                   1.0e-09
Match length
                   40
% identity
                   62
NCBI Description
                  (AF088901) actin bundling protein ABP135 [Lilium
                   longiflorum]
Seq. No.
                   412873
Seq. ID
                   uC-osflcyp112h04b1
Method
                   BLASTX
NCBI GI
                   g5732049
BLAST score
                   172
E value
                   4.0e-12
Match length
                   65
% identity
                   58
                  (AF147262) contains similarity to Pfam family PF00400 -WD
NCBI Description
                   domain, G-beta repeat; score=37.6, E=2.9e-07, N=3
                   [Arabidopsis thaliana]
Seq. No.
                   412874
Seq. ID
                   uC-osflcyp112h05a1
Method
                  BLASTX
NCBI GI
                   g5381253
BLAST score
                  298
E value
                   5.0e-27
Match length
                  74
% identity
                   74
NCBI Description (AB027752) peroxidase [Nicotiana tabacum]
Seq. No.
                   412875
Seq. ID
                  uC-osflcyp112h08a1
Method
                  BLASTX
NCBI GI
                  g1076668
BLAST score
                  299
E value
                  5.0e-27
Match length
                  60
% identity
                  92
NCBI Description
                  NADH dehydrogenase (EC 1.6.99.3) - potato
                  >gi_639834_emb_CAA58823 (X83999) NADH dehydrogenase
                  [Solanum tuberosum]
Seq. No.
                  412876
Seq. ID
                  uC-osflcyp112h10b1
Method
                  BLASTN
NCBI GI
                  g488161
BLAST score
                  58
E value
                  6.0e-24
```

```
% identity
NCBI Description Rice ribosomal external intergenic spacer DNA
                   412877
Seq. No.
Seq. ID
                   uC-osflcyp115a02a1
Method
                   BLASTX
NCBI GI
                   g1304215
BLAST score
                   325
E value
                   6.0e-30
Match length
                   94
% identity
                   48
NCBI Description (D84392) precursor of rice 22 kDa protein of photosystem II
                   (PSII-S) [Oryza sativa]
Seq. No.
                   412878
Seq. ID
                   uC-osflcyp115a03a1
Method
                   BLASTX
NCBI GI
                  g3953458
                  216
BLAST score
E value
                   2.0e-17
Match length
                  77
% identity
                   58
NCBI Description (AC002328) F20N2.3 [Arabidopsis thaliana]
Seq. No.
                   412879
Seq. ID
                  uC-osflcyp115a04a1
Method
                  BLASTX
NCBI GI
                  g2982455
BLAST score
                  334
E value
                  1.0e-32
Match length
                  87
% identity
                  83
NCBI Description (AL022223) putative uracil phosphoribosyl transferase
                   [Arabidopsis thaliana]
Seq. No.
                  412880
Seq. ID
                  uC-osflcyp115a05a1
Method
                  BLASTN
NCBI GI
                  g5918186
BLAST score
                  93
                  2.0e-44
E value
Match length
                  229
% identity
                  85
NCBI Description Hordeum vulgare mRNA for hordeum vulgare (barley)
                  ribophorin I, partial
Seq. No.
                  412881
Seq. ID
                  uC-osflcyp115a06a1
Method
                  BLASTN
NCBI GI
                  g2331130
BLAST score
                  205
E value
                  1.0e-111
Match length
                  205
% identity
                  100
NCBI Description Oryza sativa glycine-rich protein (OSGRP1) mRNA, complete
```



Seq. ID uC-osflcyp115a09a1

Method BLASTX
NCBI GI g3885888
BLAST score 161
E value 8.0e-11
Match length 32
% identity 100

NCBI Description (AF093632) high mobility group protein [Oryza sativa]

Seq. No. 412883

Seq. ID uC-osflcyp115a10a1

Method BLASTN
NCBI GI g20289
BLAST score 455
E value 0.0e+00
Match length 497
% identity 98

NCBI Description O.sativa DNA for phyB1 gene

Seq. No. 412884

Seq. ID uC-osflcyp115a11a1

Method BLASTN
NCBI GI g4105602
BLAST score 308
E value 1.0e-173
Match length 340
% identity 98

NCBI Description Oryza sativa metallothionein (MTe) gene, complete cds

Seq. No. 412885

Seq. ID uC-osflcyp115a12a1

Method BLASTN
NCBI GI g2331130
BLAST score 174
E value 3.0e-93
Match length 186
% identity 99

NCBI Description Oryza sativa glycine-rich protein (OSGRP1) mRNA, complete

cds

Seq. No. 412886

Seq. ID uC-osflcyp115b01a1

Method BLASTX
NCBI GI g1170937
BLAST score 260
E value 2.0e-22
Match length 47
% identity 100

NCBI Description S-ADENOSYLMETHIONINE SYNTHETASE 1 (METHIONINE

ADENOSYLTRANSFERASE 1) (ADOMET SYNTHETASE 1)

>gi_450549 emb CAA81481 (Z26867) S-adenosyl methionine

synthetase [Oryza sativa]

Seq. No. 412887

Seq. ID uC-osflcyp115b03a1

Method BLASTX

E value

5.0e-35

```
NCBI GI
                   g4731573
BLAST score
                  237
E value
                  1.0e-19
Match length
                  89
                   55
% identity
NCBI Description (AF123265) remorin 1 [Lycopersicon esculentum]
Seq. No.
                  412888
Seq. ID
                  uC-osflcyp115b12a1
Method
                  BLASTX
NCBI GI
                  g5031281
BLAST score
                  157
E value
                  2.0e-10
Match length
                  36
% identity
                  81
NCBI Description (AF139499) unknown [Prunus armeniaca]
Seq. No.
                  412889
Seq. ID
                  uC-osflcyp115c03a1
Method
                  BLASTN
NCBI GI
                  g1632821
BLAST score
                  69
E value
                  1.0e-30
Match length
                  165
% identity
                  85
                  O.sativa mRNA for transmembrane protein
NCBI Description
                  >gi_1667593_gb_U77297 OSU77297 Oryza sativa transmembrane
                  protein mRNA, complete cds
Seq. No.
                  412890
Seq. ID
                  uC-osflcyp115c09a1
Method
                  BLASTN
NCBI GI
                  g857573
BLAST score
                  358
E value
                  0.0e + 00
Match length
                  400
% identity
                  98
NCBI Description Oryza sativa vacuolar H+-ATPase (vatp-P1) mRNA, complete
                  cds
Seq. No.
                  412891
Seq. ID
                  uC-osflcyp115d01a1
Method
                  BLASTX
NCBI GI
                  g129591
BLAST score
                  332
E value
                  8.0e-31
Match length
                  61
% identity
                  100
NCBI Description PHENYLALANINE AMMONIA-LYASE >gi_295824_emb_CAA34226
                  (X16099) phenylalanine ammonia-Tyase [Oryza sativa]
Seq. No.
                  412892
Seq. ID
                  uC-osflcyp115d05a1
Method
                  BLASTN
NCBI GI
                  q5257255
BLAST score
                  77
```

```
430
Match length
% identity
                   87
NCBI Description Oryza sativa genomic DNA, chromosome 8, clone:P0026F07
Seq. No.
                   412893
Seq. ID
                   uC-osflcyp115e02a1
Method
                  BLASTX
NCBI GI
                   g2114207
BLAST score
                   401
E value
                   6.0e-39
Match length
                   76
% identity
                   100
NCBI Description (D86744) glutaredoxin [Oryza sativa]
Seq. No.
                   412894
Seq. ID
                  uC-osflcyp115e04a1
Method
                  BLASTX
NCBI GI
                  g1808694
BLAST score
                  352
E value
                   3.0e-33
Match length
                  83
% identity
                   81
NCBI Description (Y10787) hypothetical protein [Sporobolus stapfianus]
Seq. No.
                  412895 .
Seq. ID
                  uC-osflcyp115f03a1
Method
                  BLASTX
NCBI GI
                  g2194125
BLAST score
                  368
E value
                   4.0e-35
Match length
                  85
% identity
                  76
NCBI Description (AC002062) ESTs gb_R30459,gb_N38441 come from this gene.
                   [Arabidopsis thaliana]
Seq. No.
                  412896
Seq. ID
                  uC-osflcyp115f10a1
Method
                  BLASTN
NCBI GI
                  g3582315
BLAST score
                  44
E value
                  2.0e-15
Match length
                  56
% identity
                  95
NCBI Description Arabidopsis thaliana chromosome II BAC T27A16 genomic
                  sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                  412897
Seq. ID
                  uC-osflcyp115g03a1
Method
                  BLASTX
NCBI GI
                  g3738285
```

NCBI GI g3738285
BLAST score 274
E value 4.0e-24
Match length 73
% identity 70

NCBI Description (AC005309) unknown protein [Arabidopsis thaliana]

Seq. No. 412898

```
Seq. ID
                   uC-osflcyp115g07a1
Method
                   BLASTX
NCBI GI
                   g1402878
BLAST score
                   162
E value
                    6.0e-11
Match length
                   71
% identity
                    45
NCBI Description (X98130) unknown [Arabidopsis thaliana]
Seq. No.
                   412899
Seq. ID
                   uC-osflcyp115g08a1
Method
                   BLASTX
NCBI GI
                   q400803
BLAST score
                   197
E value
                   3.0e-15
Match length
                   42
% identity
                   90
NCBI Description 2,3-BISPHOSPHOGLYCERATE-INDEPENDENT PHOSPHOGLYCERATE MUTASE
                   (PHOSPHOGLYCEROMUTASE) (BPG-INDEPENDENT PGAM) (PGAM-I) >gi_283033_pir__A42807 phosphoglycerate mutase (EC
                   5.4.2.1), \overline{2}, 3-bisphosphoglycerate-independent - maize
                   >gi_168588 (M80912) 2,3-bisphosphoglycerate-independent
                   phosphoglycerate mutase [Zea mays]
Seq. No.
                   412900
Seq. ID
                   uC-osflcyp115h01a1
Method
                   BLASTX
NCBI GI
                   g3294467
BLAST score
                   381
E value
                   9.0e-37
Match length
                   77
% identity
                   97
NCBI Description (U89341) phosphoglucomutase 1 [Zea mays]
Seq. No.
                   412901
Seq. ID
                   uC-osflcyp115h02a1
Method
                   BLASTX
NCBI GI
                   g2493123
BLAST score
                   236
E value
                   1.0e-19
Match length
                   46
% identity
                   100
NCBI Description
                   VACUOLAR ATP SYNTHASE CATALYTIC SUBUNIT A (V-ATPASE 69 KD
                   SUBUNIT) >gi 1051258 (U36939) vacuolar ATPase catalytic
                   subunit [Hordeum vulgare]
Seq. No.
                   412902
Seq. ID
                   uC-osflcyp115h04a1
Method
                   BLASTX
NCBI GI
                   g4680338
BLAST score
                   260
                   2.0e-22
E value
Match length
                   88
% identity
NCBI Description
                   (AF128457) hypothetical protein [Oryza sativa subsp.
```

indica]

Seq. ID uC-osflcyp115h10a1

Method BLASTN
NCBI GI g4138731
BLAST score 42
E value 4.0e-14
Match length 134
% identity 58

NCBI Description Zea mays mRNA for proline-rich protein

Seq. No. 412904

Seq. ID uC-osflcyp115h11a1

Method BLASTX
NCBI GI 94455210
BLAST score 287
E value 1.0e-25
Match length 65
% identity 83

NCBI Description (AL035440) putative aspartate-tRNA ligase [Arabidopsis

thaliana]

Seq. No. 412905

Seq. ID uC-osflcyp116a08a1

Method BLASTN
NCBI GI g3560532
BLAST score 44
E value 2.0e-15
Match length 118

% identity 94
NCBI Description Oryza sativa 24-methylene lophenol C24(1)methyltransferase

mRNA, complete cds

Seq. No. 412906

Seq. ID uC-osflcyp116a11a1

Method BLASTN
NCBI GI g1261857
BLAST score 381
E value 0.0e+00
Match length 412
% identity 98

NCBI Description Rice CatA gene for catalase, complete cds

Seq. No. 412907

Seq. ID uC-osflcyp116a12a1

Method BLASTX
NCBI GI g2062389
BLAST score 268
E value 2.0e-23
Match length 56
% identity 84

NCBI Description (U77657) pathogenesis-related thaumatin-like protein [Oryza

sativa]

Seq. No. 412908

Seq. ID uC-osflcyp116b01a1

Method BLASTX NCBI GI g6093980

```
BLAST score
E value
                   2.0e-11
Match length
                   58
% identity
                   50
NCBI Description
                   CHLOROPLAST 50S RIBOSOMAL PROTEIN L1
                   >gi_3602937_gb_AAC35598_ (AF041468) ribosomal protein L1
                   [Guillardia theta]
Seq. No.
                   412909
Seq. ID
                   uC-osflcyp116b09a1
Method
                   BLASTX
NCBI GI
                   g2501021
BLAST score
                   193
E value
                   1.0e-14
Match length
                   47
% identity
                   79
NCBI Description LYSYL-TRNA SYNTHETASE (LYSINE--TRNA LIGASE) (LYSRS)
                   >gi_1652562_dbj_BAA17483_ (D90906) lysyl-tRNA synthetase
                   [Synechocystis sp.]
Seq. No.
                   412910
Seq. ID
                   uC-osflcyp116b10a1
Method
                   BLASTX
NCBI GI
                   g322854
BLAST score
                   195
E value
                   6.0e-15
Match length
                   74
% identity
                   58
NCBI Description pollen-specific protein - rice >gi_20310_emb_CAA78897_
                   (Z16402) pollen specific gene [Oryza satīva]
Seq. No.
                   412911
Seq. ID
                  uC-osflcyp116b12a1
Method
                  BLASTX
NCBI GI
                  g4741952
BLAST score
                  188
E value
                  3.0e-14
Match length
                  67
% identity
                  60
NCBI Description
                  (AF134126) Lhcb3 protein [Arabidopsis thaliana]
                  >gi_5002210_gb_AAD37362.1_AF143691_1 (AF143691) type III
                  chlorophyll a/b binding protein [Arabidopsis thaliana]
Seq. No.
                  412912
Seq. ID
                  uC-osflcyp116c03a1
Method
                  BLASTX
NCBI GI
                  q439879
BLAST score
                  169
E value
                  8.0e-12
Match length
                  38
% identity
                  79
NCBI Description
                  (L15194) [Golden delicious apple fruit expressed mRNA,
                  complete cds.], gene product [Malus domestica]
```

Seq. ID uC-osflcyp116c06a1

Method BLASTX

```
NCBI GI
                    g3122572
BLAST score
                    187
E value
                    6.0e-14
Match length
                    57
% identity
                    65
NCBI Description
                   NADH-UBIQUINONE OXIDOREDUCTASE 75 KD SUBUNIT PRECURSOR
                    (COMPLEX I-75KD) (CI-75KD) (76 KD MITOCHONDRIAL COMPLEX I
                   SUBUNIT) >gi_1084434_pir__S52737 NADH dehydrogenase (ubiquinone) (EC 1.6.5.3) 76K chain precursor - potato
                    >gi_758340_emb_CAA59818_ (X85808) 76 kDa mitochondrial
                    complex I subunit [Solanum tuberosum]
Seq. No.
                    412914
Seq. ID
                   uC-osflcyp116c08a1
Method
                   BLASTX
NCBI GI
                   g2982297
BLAST score
                   171
E value
                    4.0e-12
Match length
                   36
% identity
                   94
NCBI Description (AF051233) KIAA0107-like protein [Picea mariana]
Seq. No.
                   412915
Seq. ID
                   uC-osflcyp116c12a1
Method
                   BLASTX
NCBI GI
                   q1170937
BLAST score
                   153
E value
                   5.0e-10
Match length
                   33
% identity
                   82
                   S-ADENOSYLMETHIONINE SYNTHETASE 1 (METHIONINE
NCBI Description
                   ADENOSYLTRANSFERASE 1) (ADOMET SYNTHETASE 1)
                   >gi_450549_emb_CAA81481_ (Z26867) S-adenosyl methionine
                   synthetase [Oryza sativa]
Seq. No.
                   412916
Seq. ID
                   uC-osflcyp116d01a1
Method
                   BLASTN
NCBI GI
                   q6006355
BLAST score
                   37
E value
                   3.0e-11
Match length
                   77
% identity
                   87
NCBI Description Oryza sativa genomic DNA, chromosome 6, clone:P0493C11
Seq. No.
                   412917
Seq. ID
                   uC-osflcyp116d02a1
Method
                   BLASTN
NCBI GI
                   q20367
BLAST score
                   252
E value
                   1.0e-139
Match length
                   326
% identity
                   98
```

synthetase (EC 6.3.1.2) (clone lambda-GS28)

NCBI Description Oryza sativa shoot GS1 mRNA for cytosolic glutamine

NCBI GI

BLAST score

```
Seq. ID
                   uC-osflcyp116d07a1
Method
                   BLASTN
NCBI GI
                   g20276
BLAST score
                   41
E value
                   2.0e-13
Match length
                   97
% identity
                   86
NCBI Description O.sativa oryzacystatin-II gene
Seq. No.
                   412919
Seq. ID
                   uC-osflcyp116d11a1
Method
                   BLASTX
NCBI GI
                   g1854378
BLAST score
                   494
E value
                   8.0e-50
Match length
                   126
% identity
                   74
NCBI Description (AB001338) Sucrose-Phosphate Synthase [Saccharum
                   officinarum]
Seq. No.
                   412920
Seq. ID
                   uC-osflcyp116d12a1
Method
                   BLASTX
NCBI GI
                   q5738378
BLAST score
                   266
E value
                   4.0e-23
Match length
                   85
% identity
                   65
NCBI Description (AL080253) putative protein [Arabidopsis thaliana]
Seq. No.
                   412921
Seq. ID
                  uC-osflcyp116e01a1
Method
                  BLASTN
NCBI GI
                   g4730883
BLAST score
                   372
E value
                   0.0e+00
Match length
                   455
% identity
                   95
NCBI Description Oryza sativa gene for alanine aminotransferase, complete
                   cds
Seq. No.
                   412922
Seq. ID
                  uC-osflcyp116e03a1
Method
                  BLASTN
NCBI GI
                  g2331130
BLAST score
                  108
E value
                  9.0e-54
Match length
                  204
% identity
                  92
NCBI Description Oryza sativa glycine-rich protein (OSGRP1) mRNA, complete
                  cds
Seq. No.
                  412923
Seq. ID
                  uC-osflcyp116e06a1
Method
                  BLASTX
```

53746

q2702279

```
E value
                       1.0e-09
   Match length
                      52
   % identity
   NCBI Description
                      (AC003033) putative phosphate transporter [Arabidopsis
                      thaliana] >gi_2780345_dbj_BAA24280_ (AB000093) inorganic phosphate transporter [Arabidopsis thaliana] >gi_2914691
                      (AC003974) putative phosphate transporter [Arabidopsis
                      thaliana]
   Seq. No.
                      412924
   Seq. ID
                      uC-osflcyp116e07a1
   Method
                      BLASTX
   NCBI GI
                      q548774
   BLAST score
                      392
   E value
                      7.0e-38
   Match length
                      93
   % identity
                      84
   NCBI Description 60S RIBOSOMAL PROTEIN L7A >gi_542158_pir__S38360 ribosomal
                      protein L7a - rice >gi 303855 dbj BAA02156 (D12631)
                      ribosomal protein L7A [Oryza sativa]
   Seq. No.
                      412925
   Seq. ID
                      uC-osflcyp116e09a1
  Method
                      BLASTX
NCBI GI
                      q3822223
  BLAST score
                      191
  E value
                      2.0e-14
  Match length
                      114
   % identity
                      32
  NCBI Description (AF077955) branched-chain alpha keto-acid dehydrogenase E1
                      alpha subunit [Arabidopsis thaliana]
  Seq. No.
                      412926
  Seq. ID
                      uC-osflcyp116e11a1
  Method
                      BLASTX
  NCBI GI
                      g1170937
  BLAST score
                      267
  E value
                      3.0e-23
  Match length
                      50
  % identity
  NCBI Description S-ADENOSYLMETHIONINE SYNTHETASE 1 (METHIONINE
                      ADENOSYLTRANSFERASE 1) (ADOMET SYNTHETASE 1)
                      >gi_450549_emb_CAA81481_ (Z26867) S-adenosyl methionine
                      synthetase [Oryza sativa]
  Seq. No.
                      412927
  Seq. ID
                      uC-osflcyp116f08a1
  Method
                     BLASTX
  NCBI GI
                     g2129742
  BLAST score
                     216
                      2.0e-17
  E value
  Match length
                      56
  % identity
  NCBI Description
                     stress-induced protein OZI1 precursor - Arabidopsis
                     thaliana >gi_790583 (U20347) mRNA corresponding to this
                     gene accumulates in response to ozone stress and pathogen
```

(bacterial) infection; putative pathogenesis-related

NCBI Description

protein [Arabidopsis thaliana] >gi_2252869 (AF013294) No
definition line found [Arabidopsis thaliana]

Seq. No. 412928 Seq. ID uC-osflcyp116f09a1 Method BLASTX NCBI GI q3885886 BLAST score 205 E value 4.0e-16 Match length 54 % identity 74 NCBI Description (AF093631) Rieske Fe-S precursor protein [Oryza sativa] Seq. No. 412929 Seq. ID uC-osflcyp116q01a1 Method BLASTX NCBI GI g2754849 BLAST score 175 E value 1.0e-12 Match length 45 % identity 78 (AF039000) putative serine-glyoxylate aminotransferase NCBI Description [Fritillaria agrestis] Seq. No. 412930 Seq. ID uC-osflcyp116q12a1 Method BLASTX NCBI GI g1261917 BLAST score 197 E value 4.0e-15 Match length 46 % identity 78 NCBI Description (X96979) lipid transfer protein 7a2b [Hordeum vulgare] Seq. No. 412931 Seq. ID uC-osflcyp116h05a1 Method BLASTX NCBI GI g129916 BLAST score 195 E value 7.0e-15 Match length 42 % identity 98 NCBI Description PHOSPHOGLYCERATE KINASE, CYTOSOLIC >gi_66911_pir__TVWTGY phosphoglycerate kinase (EC 2.7.2.3), cytosolic - wheat >gi_21835_emb_CAA33302_ (X15232) phosphoglycerate kinase (AA 1 - 401) [Triticum aestivum] Seq. No. 412932 Seq. ID uC-osflcyp116h10a1 Method BLASTX NCBI GI g129916 BLAST score 352 E value 3.0e-33 Match length 94 % identity 79

PHOSPHOGLYCERATE KINASE, CYTOSOLIC >gi_66911_pir__TVWTGY phosphoglycerate kinase (EC 2.7.2.3), cytosolic - wheat

Method

NCBI GI

BLAST score

```
>gi_21835_emb_CAA33302_ (X15232) phosphoglycerate kinase
                   (AA 1 - 401) [Triticum aestivum]
                   412933
Seq. No.
Seq. ID
                   uC-osflcyp116h11a1
Method
                   BLASTX
NCBI GI
                   q2213867
BLAST score
                   238
E value
                   3.0e-30
Match length
                   114
% identity
                   67
NCBI Description (AF003124) fructose-biphosphate aldolase [Mesembryanthemum
                  crystallinum]
Seq. No.
                   412934
Seq. ID
                  uC-osflcyp117a01a1
Method
                  BLASTX
NCBI GI
                  g2088650
BLAST score
                  149
E value
                   1.0e-09
Match length
                  57
% identity
                   51
NCBI Description (AF002109) peroxisomal ATP/ADP carrier protein isolog
                   [Arabidopsis thaliana]
Seq. No.
                  412935
Seq. ID
                  uC-osflcyp117a08a1
Method
                  BLASTX
NCBI GI
                  g1170937
BLAST score
                  373
E value
                  1.0e-35
Match length
                  73
% identity
                  93
                  S-ADENOSYLMETHIONINE SYNTHETASE 1 (METHIONINE
NCBI Description
                  ADENOSYLTRANSFERASE 1) (ADOMET SYNTHETASE 1)
                  >gi_450549_emb_CAA81481_ (Z26867) S-adenosyl methionine
                  synthetase [Oryza sativa]
Seq. No.
                  412936
Seq. ID
                  uC-osflcyp117a10a1
Method
                  BLASTX
NCBI GI
                  g3258570
BLAST score
                  239
E value
                  5.0e-20
Match length
                  90
% identity
                  59
NCBI Description (U89959) Unknown protein [Arabidopsis thaliana]
Seq. No.
                  412937
Seq. ID
                  uC-osflcyp117a12a1
```

E value 2.0e-99
Match length 178
% identity 98

BLASTX

g129231

917

NCBI Description ORYZAIN ALPHA CHAIN PRECURSOR >gi_67644_pir__KHRZOA oryzain

```
(EC 3.4.22.-) alpha precursor - rice
>gi_218181_dbj_BAA14402_ (D90406) oryzain alpha precursor
[Oryza sativa]

412938
uC-osflcyp117b03a1
```

Method BLASTX
NCBI GI 9729135
BLAST score 256
E value 4.0e-22
Match length 53
% identity 91

Seq. No.

Seq. ID

NCBI Description CAFFEIC ACID 3-O-METHYLTRANSFERASE (S-ADENOSYSL-L-METHIONINE:CAFFEIC ACID

3-O-METHYLTRANSFERASE) (COMT) >gi_283034_pir__S28612 catechol O-methyltransferase (EC 2.1.1.6) - maize >gi_168532 (M73235) O-methyltransferase [Zea mays]

Seq. No. 412939

Seq. ID uC-osflcyp117b07a1

Method BLASTX
NCBI GI g2160322
BLAST score 394
E value 5.0e-38
Match length 78
% identity 96

NCBI Description (D16139) cytokinin binding protein CBP57 [Nicotiana

sylvestris]

Seq. No. 412940

Seq. ID uC-osflcyp117b09a1

Method BLASTX
NCBI GI g829283
BLAST score 284
E value 2.0e-25
Match length 67
% identity 82

NCBI Description (Z15018) heat shock protein hsp82 [Oryza sativa]

Seq. No. 412941

Seq. ID uC-osflcyp117c02a1

Method BLASTX
NCBI GI g4097579
BLAST score 164
E value 3.0e-11
Match length 37
% identity 84

NCBI Description (U64922) NTGP1 [Nicotiana tabacum]

Seq. No. 412942

Seq. ID uC-osflcyp117c08a1

Method BLASTX
NCBI GI 94097579
BLAST score 143
E value 9.0e-09
Match length 35
% identity 80

```
NCBI Description (U64922) NTGP1 [Nicotiana tabacum]
                  412943
Seq. No.
Seq. ID
                  uC-osflcyp117c09a1
Method
                  BLASTX
NCBI GI
                  g2952328
BLAST score
                  803
E value
                  5.0e-86
Match length
                  163
% identity
NCBI Description (AF049889) 1-aminocyclopropane-1-carboxylate oxidase [Oryza
                  sativa]
                  412944
Seq. No.
Seq. ID
                  uC-osflcyp117c11a1
Method
                  BLASTX
NCBI GI
                  q2952328
BLAST score
                  584
E value
                  2.0e-60
Match length
                  138
% identity
                  83
NCBI Description (AF049889) 1-aminocyclopropane-1-carboxylate oxidase [Oryza
                  sativa]
Seq. No.
                  412945
Seq. ID
                  uC-osflcyp117c12a1
Method
                  BLASTX
NCBI GI
                  q3915254
BLAST score
                  219
E value
                  2.0e-17
Match length
                  87
% identity
                  60
NCBI Description VACUOLAR ATP SYNTHASE 16 KD PROTEOLIPID SUBUNIT (V-ATPASE
                  16 KD PROTEOLIPID SUBUNIT)
Seq. No.
                  412946
Seq. ID
                  uC-osflcyp117d03a1
Method
                  BLASTN
NCBI GI
                  q2331130
BLAST score
                  123
E value
                  1.0e-62
Match length
                  247
% identity
                  88
NCBI Description Oryza sativa glycine-rich protein (OSGRP1) mRNA, complete
Seq. No.
                  412947
Seq. ID
                  uC-osflcyp117d05a1
Method
                  BLASTX
NCBI GI
                  g2914700
BLAST score
                  154
E value
                  4.0e-10
Match length
                  70
% identity
                  49
NCBI Description
                  (AC003974) tRNA-processing protein SEN3-like [Arabidopsis
```

thaliana]

```
Seq. No.
                   412948
Seq. ID
                   uC-osflcyp117d09a1
Method
                   BLASTX
NCBI GI
                   g5002357
BLAST score
                   242
E value
                   3.0e-20
                   70
Match length
% identity
                   69
                  (AF150957) heat-shock protein ClpP [Azospirillum
NCBI Description
                   brasilense]
Seq. No.
                   412949
Seq. ID
                   uC-osflcyp117d10a1
Method
                   BLASTX
NCBI GI
                   q5103846
BLAST score
                   245
E value
                   1.0e-20
Match length
                   80
% identity
                   56
NCBI Description (AC007591) F9L1.43 [Arabidopsis thaliana]
Seq. No.
                   412950
Seq. ID
                   uC-osflcyp117d11a1
Method
                   BLASTX
NCBI GI
                   q3328221
BLAST score
                   590
E value
                   5.0e-61
Match length
                   122
% identity
                   91
NCBI Description (AF076920) thioredoxin peroxidase [Secale cereale]
Seq. No.
                   412951
Seq. ID
                   uC-osflcyp117e07a1
Method
                   BLASTN
NCBI GI
                   g3819201
BLAST score
                   36
E value
                   1.0e-10
Match length
                   60
% identity
                   90
NCBI Description Hordeum vulgare partial mRNA; clone cMWG0680.uni
Seq. No.
                   412952
Seq. ID
                   uC-osflcyp117e09a1
Method
                   BLASTN
NCBI GI
                   g416266
                  82
BLAST score
E value
                   3.0e-38
Match length
                  225
% identity
                   84
NCBI Description Rice mRNA for oxygen-evolving protein, partial sequence
Seq. No.
                   412953
Seq. ID
                  uC-osflcyp117e11a1
Method
                  BLASTX
NCBI GI
                  q1076820
BLAST score
                  425
                  1.0e-41
E value
```

```
Match length
                  89
% identity
                  91
NCBI Description phosphoglycerate mutase (EC 5.4.2.1) - maize
Seq. No.
                  412954
Seq. ID
                  uC-osflcyp117f02a1
Method
                  BLASTN
NCBI GI
                  q5777612
BLAST score
                  203
E value
                  1.0e-110
Match length
                  296
% identity
                  98
NCBI Description Oryza sativa chromosome 4 BAC q3037-207F1 complete genome
Seq. No.
                  412955
Seq. ID
                  uC-osflcyp117f05a1
Method
                  BLASTX
NCBI GI
                  g2443755
BLAST score
                  329
E value
                  1.0e-30
Match length
                  71
                  87
% identity
NCBI Description (AF020433) cyclophilin [Arabidopsis thaliana]
Seq. No.
                  412956
Seq. ID
                  uC-osflcyp117f06a1
Method
                  BLASTX
NCBI GI
                  q3023713
BLAST score
                  300
E value
                  4.0e-27
Match length
                  63
% identity
                  94
NCBI Description ENOLASE (2-PHOSPHOGLYCERATE DEHYDRATASE)
                  (2-PHOSPHO-D-GLYCERATE HYDRO-LYASE) (OSE1) >gi 780372
                  (U09450) enolase [Oryza sativa]
Seq. No.
                  412957
Seq. ID
                  uC-osflcyp117f11a1
Method
                  BLASTX
NCBI GI
                  g3256035
BLAST score
                  289
E value
                  9.0e-26
Match length
                  124
% identity
                  44
NCBI Description (Y14274) putative serine/threonine protein kinase [Sorghum
                  bicolor]
                  412958
Seq. No.
Seq. ID
                  uC-osflcyp117g02a1
Method
                  BLASTX
NCBI GI
                  g6017123
BLAST score
                  177
E value
                  5.0e-13
Match length
                  52
% identity
NCBI Description (AC009895) unknown protein [Arabidopsis thaliana]
```

E value

1.0e-38

```
412959
Seq. No.
                  uC-osflcyp117g04a1
Seq. ID
Method
                  BLASTN
NCBI GI
                  q6016845
BLAST score
                  80
E value
                  7.0e-37
Match length
                  272
                  83
% identity
NCBI Description Oryza sativa genomic DNA, chromosome 1, clone:P0711E10
                  412960
Seq. No.
Seq. ID
                  uC-osflcyp117g05a1
Method
                  BLASTX
NCBI GI
                  q1084455
BLAST score
                  149
                  1.0e-09
E value
                   31
Match length
                   97
% identity
                  peptidylprolyl isomerase (EC 5.2.1.8) Cyp2 - rice
NCBI Description
                  >gi 600767 (L29469) cyclophilin 2 [Oryza sativa]
                   412961
Seq. No.
                  uC-osflcyp117g08a1
Seq. ID
Method
                  BLASTX
NCBI GI
                   q6017123
BLAST score
                   203
                   5.0e-16
E value
                   56
Match length
                   70
% identity
NCBI Description (AC009895) unknown protein [Arabidopsis thaliana]
                   412962
Seq. No.
                   uC-osflcyp117g09a1
Seq. ID
Method
                   BLASTN
NCBI GI
                   g4105602
BLAST score
                   261
E value
                   1.0e-145
                   273
Match length
                   99
% identity
NCBI Description Oryza sativa metallothionein (MTe) gene, complete cds
Seq. No.
                   412963
Seq. ID
                   uC-osflcyp117g10a1
Method
                   BLASTN
NCBI GI
                   g1815680
BLAST score
                   346
E value
                   0.0e + 00
Match length
                   426
                   95
% identity
NCBI Description Oryza sativa expansin (Os-EXP4) mRNA, complete cds
Seq. No.
                   412964
Seq. ID
                   uC-osflcyp117g11a1
Method
                   BLASTX
NCBI GI
                   g4557587
BLAST score
                   399
```

Match length 112 % identity fumarylacetoacetase >gi 119778 sp P16930 FAAA HUMAN NCBI Description FUMARYLACETOACETASE (FUMARYLACETOACETATE HYDROLASE) (BETA-DIKETONASE) (FAA) >gi_106043_pir__A37926 fumarylacetoacetase (EC 3.7.1.2) - human >gi 182393 (M55150) fumarylacetoacetate hydrolase [Homo sapiens] Seq. No. 412965 uC-osflcyp117h01a1 Seq. ID Method BLASTX NCBI GI g2662343 BLAST score 216 E value 2.0e-17 Match length 50 % identity 88 NCBI Description (D63581) EF-1 alpha [Oryza sativa] Seq. No. 412966 Seq. ID uC-osflcyp117h04a1 Method BLASTN NCBI GI g6016845 BLAST score 88 E value 1.0e-41 Match length 228 85 % identity NCBI Description Oryza sativa genomic DNA, chromosome 1, clone:P0711E10 412967 Seq. No. uC-osflcyp117h05a1 Seq. ID Method BLASTX NCBI GI q6015059 BLAST score 422 E value 2.0e-41 Match length 83 % identity 100 NCBI Description ELONGATION FACTOR 1-ALPHA (EF-1-ALPHA) >gi 2996096 (AF030517) translation elongation factor-1 alpha; EF-1 alpha [Oryza sativa] Seq. No. 412968 uC-osflcyp117h07a1 Seq. ID Method BLASTN NCBI GI g2662346 BLAST score 49 E value 7.0e-19 Match length 97 % identity 88 NCBI Description Oryza sativa mRNA for EF-1 alpha, complete cds

412969 Seq. No.

Seq. ID uC-osflcyp117h11a1

Method BLASTX NCBI GI g1362086 BLAST score 399 E value 1.0e-38 Match length 86

% identity 5-methyltetrahydropteroyltriglutamate--homocysteine NCBI Description S-methyltransferase (EC 2.1.1.14) - Madagascar periwinkle >gi_2129919_pir__S65957 $5-\texttt{methyltet} \\ \\ \overline{} \\ a \\ hy \\ \overline{dr} \\ opteroyltriglutamate--\\ homocysteine$ S-methyltransferase (EC 2.1.1.14) - Madagascar periwinkle >gi 886471 emb CAA58474 (X83499) methionine synthase [Catharanthus roseus] Seq. No. 412970 uC-osflcyp118a04a1 Seq. ID Method BLASTX g100293 NCBI GI BLAST score 142 E value 9.0e-09 Match length 46 65 % identity ribonucleoprotein A, 29K - wood tobacco NCBI Description >gi_19754_emb_CAA43427_ (X61113) 29kD A ribonucleoprotein [Nicotiana sylvestris] 412971 Seq. No. uC-osflcyp118a06a1 Seq. ID Method BLASTN g5922603 NCBI GI 179 BLAST score E value 4.0e-96 307 Match length 90 % identity NCBI Description Oryza sativa genomic DNA, chromosome 1, clone:P0705D01 412972 Seq. No. uC-osflcyp118a07a1 Seq. ID Method BLASTX q4006886 NCBI GI BLAST score 153 E value 5.0e-10 Match length 35 % identity NCBI Description (Z99708) putative protein [Arabidopsis thaliana] Seq. No. 412973 Seq. ID uC-osflcyp118a10a1 Method BLASTX NCBI GI g1350821 BLAST score 225 E value 3.0e-18 59 Match length 71 % identity 31 KD RIBONUCLEOPROTEIN, CHLOROPLAST PRECURSOR NCBI Description >gi 280403 pir S26204 RNA-binding protein 31 curled-leaved tobacco >gi 19710 emb CAA46233 (X65117) RNA binding protein 31 [Nicotiana plumbaginifolia]

Seq. No. 412974

Seq. ID uC-osflcyp118b03a1

Method BLASTN

E value

7.0e-15

```
q6063530
NCBI GI
BLAST score
                  196
E value
                  1.0e-106
Match length
                  196
                  100
% identity
NCBI Description Oryza sativa genomic DNA, chromosome 3, clone: P0043E01
                  412975
Seq. No.
Seq. ID
                  uC-osflcyp118b07a1
Method
                  BLASTX
NCBI GI
                  q4006886
BLAST score
                  164
E value
                  3.0e-11
Match length
                  43
% identity
                  70
NCBI Description (Z99708) putative protein [Arabidopsis thaliana]
                  412976
Seq. No.
Seq. ID
                  uC-osflcyp118b09a1
Method
                  BLASTX
NCBI GI
                  q600769
BLAST score
                  326
E value
                  4.0e-30
Match length
                  62
% identity
                  98
NCBI Description (L29470) cyclophilin 2 [Oryza sativa]
Seq. No.
                  412977
Seq. ID
                  uC-osflcyp118b10a1
Method
                  BLASTX
NCBI GI
                  g1658313
BLAST score
                  235
E value
                  1.0e-19
                  93
Match length
% identity
                  48
NCBI Description (Y08987) osr40g2 [Oryza sativa]
Seq. No.
                  412978
Seq. ID
                  uC-osflcyp118c02a1
Method
                  BLASTX
NCBI GI
                  g115800
BLAST score
                  263
E value
                  8.0e-23
Match length
                  61
% identity
                  82
NCBI Description CHLOROPHYLL A-B BINDING PROTEIN 3 PRECURSOR (LHCII TYPE I
                  CAB-3) (LHCP) >gi 81771 pir S01962 chlorophyll a/b-binding
                  protein 3 precursor - soybean >gi 18552 emb CAA31419
                  (X12981) chlorophyll a/b binding preprotein (AA - 32 to
                  231) [Glycine max]
                  412979
Seq. No.
Seq. ID
                  uC-osflcyp118c03a1
Method
                  BLASTX
NCBI GI
                  g169661
BLAST score
                  195
```

NCBI Description

```
39
Match length
% identity
                  (M62756) S-adenosylhomocysteine hydrolase [Petroselinum
NCBI Description
                  crispum]
                  412980
Seq. No.
                  uC-osflcyp118c08a1
Seq. ID
                  BLASTN
Method
NCBI GI
                  q6006355
BLAST score
                  94
                  3.0e-45
E value
Match length
                  260
                  87
% identity
NCBI Description Oryza sativa genomic DNA, chromosome 6, clone:P0493C11
                  412981
Seq. No.
                  uC-osflcyp118c12a1
Seq. ID
                  BLASTN
Method
                  g20342
NCBI GI
BLAST score
                  90
E value
                   5.0e-43
Match length
                  202
                  89
% identity
NCBI Description O.sativa Rcdc2-1 gene for p34-cdc2 protein kinase
                   412982
Seq. No.
Seq. ID
                  uC-osflcyp118d03a1
                  BLASTX
Method
NCBI GI
                  q4206195
                  193
BLAST score
E value
                   1.0e-14
                   53
Match length
% identity
                   64
                   (AF071527) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   >gi_4262169_gb_AAD14469_ (AC005275) hypothetical protein
                   [Arabidopsis thaliana]
                   412983
Seq. No.
Seq. ID
                  uC-osflcyp118d04a1
Method
                   BLASTX
NCBI GI
                   g1708424
BLAST score
                   259
E value
                   2.0e-22
Match length
                   59
                   75
% identity
NCBI Description ISOFLAVONE REDUCTASE HOMOLOG >gi 1230614 (U48590)
                   isoflavone reductase-like protein [Lupinus albus]
Seq. No.
                   412984
Seq. ID
                   uC-osflcyp118d05a1
Method
                   BLASTX
NCBI GI
                   q4107001
BLAST score
                   500
E value
                   1.0e-50
                  94
Match length
                   99
% identity
                  (D82035) OSK4 [Oryza sativa]
```

412985 Seq. No. uC-osflcyp118d08a1 Seq. ID Method BLASTN q6006355 NCBI GI 117 BLAST score 4.0e-59 E value 217 Match length 88 % identity NCBI Description Oryza sativa genomic DNA, chromosome 6, clone:P0493C11 412986 Seq. No. uC-osflcyp118d10a1 Seq. ID Method BLASTX g4107001 NCBI GI 377 BLAST score 3.0e-36 E value 77 Match length 95 % identity (D82035) OSK4 [Oryza sativa] NCBI Description 412987 Seq. No. uC-osflcyp118d11a1 Seq. ID Method BLASTX NCBI GI g4107001 BLAST score 348 7.0e-37 E value 103 Match length % identity 74 NCBI Description (D82035) OSK4 [Oryza sativa] 412988 Seq. No. uC-osflcyp118e07a1 Seq. ID Method BLASTN NCBI GI q1835728 BLAST score 154 E value 3.0e-81Match length 303 88 % identity NCBI Description Oryza sativa ribosomal protein mRNA, complete cds Seq. No. 412989 uC-osflcyp118e08a1 Seq. ID Method BLASTX NCBI GI g2739379 BLAST score 257 E value 4.0e-22 72 Match length % identity NCBI Description (AC002505) hypothetical protein [Arabidopsis thaliana]

Seq. No. 412990

Seq. ID uC-osflcyp118f11a1

Method BLASTX
NCBI GI g1777921
BLAST score 196
E value 5.0e-15

% identity

96

```
81
Match length
% identity
NCBI Description (U54774) glutamate decarboxylase [Nicotiana tabacum]
                   412991
Seq. No.
                   uC-osflcyp118f12a1
Seq. ID
Method
                   BLASTN
NCBI GI
                   g20181
BLAST score
                   113
E value
                   1.0e-56
Match length
                   217
                   88
% identity
                   Rice cab2R gene for light harvesting chlorophyll
NCBI Description
                   a/b-binding protein
                   412992
Seq. No.
Seq. ID
                   uC-osflcyp118g04a1
Method
                   BLASTX
NCBI GI
                   g729135
BLAST score
                   333
E value
                   5.0e-31
Match length
                   74
% identity
                   82
NCBI Description CAFFEIC ACID 3-O-METHYLTRANSFERASE
                    (S-ADENOSYSL-L-METHIONINE: CAFFEIC ACID
                   3-O-METHYLTRANSFERASE) (COMT) >gi_283034_pir__S28612 catechol O-methyltransferase (EC 2.1.1.6) - maize
                   >qi 168532 (M73235) O-methyltransferase [Zea mays]
Seq. No.
                   412993
                   uC-osflcyp118g08a1
Seq. ID
Method
                   BLASTN
                   q600766
NCBI GI
BLAST score
                   203
E value
                   1.0e-110
                   379
Match length
                   89
% identity
NCBI Description Oryza sativa cyclophilin 2 (Cyp2) gene, complete cds
                   412994
Seq. No.
                   uC-osflcyp118g09a1
Seq. ID
                   BLASTN
Method
                   g435648
NCBI GI
BLAST score
                   121
E value
                   1.0e-61
                   145
Match length
                   96
% identity
NCBI Description Rice mRNA for gamma-Tip, complete cds
                   412995
Seq. No.
Seq. ID
                   uC-osflcyp118h02a1
                   BLASTX
Method
NCBI GI
                   g3036951
BLAST score
                   269
E value
                   1.0e-23
Match length
                   53
```

```
NCBI Description
                   (AB012639) light harvesting chlorophyll a/b-binding protein
                   [Nicotiana sylvestris]
Seq. No.
                  412996
Seq. ID
                  uC-osflcyp118h03a1
Method
                  BLASTN
NCBI GI
                  q416266
BLAST score
                  71
E value
                  1.0e-31
                  93
Match length
% identity
                  94
NCBI Description Rice mRNA for oxygen-evolving protein, partial sequence
Seq. No.
                  412997
Seq. ID
                  uC-osflcyp118h07a1
Method
                  BLASTX
NCBI GI
                  g2494115
BLAST score
                  147
E value
                  4.0e-09
Match length
                  50
% identity
                  60
NCBI Description
                  (AC002376) Strong similarity to Arabidopsis ATHSAR1
                  (gb_M90418). ESTs gb_T44122,gb_N65276,gb_AA041135 come from
                  this gene. [Arabidopsis thaliana]
Seq. No.
                  412998
Seq. ID
                  uC-osflcyp118h08a1
Method
                  BLASTX
NCBI GI
                  q226263
BLAST score
                  217
E value
                  1.0e-17
Match length
                  50
                  84
% identity
NCBI Description chlorophyll a/b binding protein [Glycine max]
Seq. No.
                  412999
Seq. ID
                  uC-osflcyp120a01b1
Method
                  BLASTN
NCBI GI
                  q4158229
BLAST score
                  69
E value
                  3.0e-30
Match length
                  117
% identity
                  90
NCBI Description Triticum aestivum mRNA for amylogenin
Seq. No.
                  413000
Seq. ID
                  uC-osflcyp120a05b1
Method
                  BLASTN
NCBI GI
                  g596079
BLAST score
                  47
E value
                  2.0e-17
Match length
                  71
% identity
                  92
NCBI Description
                  Zea mays thiamine biosynthetic enzyme (thi1-2) mRNA,
                  complete cds
```

E value

7.0e-42

```
Seq. ID
                  uC-osflcyp120a06b1
Method
                  BLASTX
NCBI GI
                  q4914414
BLAST score
                  148
E value
                   3.0e-09
Match length
                  56
                   57
% identity
NCBI Description
                  (AL050352) Ca2+-transporting ATPase-like protein
                   [Arabidopsis thaliana]
Seq. No.
                   413002
Seq. ID
                  uC-osflcyp120a07b1
Method
                  BLASTX
NCBI GI
                  g6056418
BLAST score
                  325
E value
                  8.0e-37
Match length
                  110
                   69
% identity
NCBI Description
                  (AC009525) Similar to beta-glucosidases [Arabidopsis
                  thaliana]
                   413003
Seq. No.
                  uC-osflcyp120a08b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  a6041797
BLAST score
                  335
E value
                   3.0e - 31
Match length
                  127
% identity
                   50
NCBI Description (AC009755) unknown protein [Arabidopsis thaliana]
Seq. No.
                  413004
Seq. ID
                  uC-osflcyp120a09b1
Method
                  BLASTX
NCBI GI
                  g4027891
BLAST score
                  377
E value
                  3.0e-36
Match length
                  127
                  57
% identity
NCBI Description (AF049350) alpha-expansin precursor [Nicotiana tabacum]
Seq. No.
                   413005
Seq. ID
                  uC-osflcyp120a10b1
Method
                  BLASTX
NCBI GI
                  g6045135
BLAST score
                  450
                  9.0e-45
E value
Match length
                  142
                  56
% identity
NCBI Description (AB033335) oxidosqualene cyclase [Luffa cylindrica]
                  413006
Seq. No.
Seq. ID
                  uC-osflcyp120a11b1
                  BLASTX
Method
NCBI GI
                  g3913641
BLAST score
                  424
```

Match length 88 % identity FRUCTOSE-1, 6-BISPHOSPHATASE, CHLOROPLAST PRECURSOR NCBI Description (D-FRUCTOSE-1,6-BISPHOSPHATE 1-PHOSPHOHYDROLASE) (FBPASE) >gi 3041777 dbj BAA25423 (AB007194) fructose-1,6-bisphosphatase [Oryza sativa] 413007 Seq. No. Seq. ID uC-osflcyp120a12b1 Method BLASTX NCBI GI g118170 BLAST score 424 E value 9.0e-42 Match length 102 81 % identity NCBI Description CYSTEINE PROTEINASE INHIBITOR-I (ORYZACYSTATIN-I) >gi_82491_pir__A28464 oryzacystatin - rice >gi_169784 (J03469) oryzacystatin [Oryza sativa] >gi_169807 (M29259) oryzastatin [Oryza sativa] >gi_259137_bbs_120195 (S49967) oryzacystatin=cysteine protease inhibitor [Oryza=rice, Peptide, 102 aa] [Oryza] >gi_1280613 (U54702) oryzacystatin [Oryza sativa] 413008 Seq. No. Seq. ID uC-osflcyp120b03b1 Method BLASTX NCBI GI q4336436 BLAST score 411 E value 4.0e-40Match length 134 % identity NCBI Description (AF092432) protein phosphatase type 2C [Lotus japonicus] 413009 Seq. No. uC-osflcyp120b04b1 Seq. ID Method BLASTN NCBI GI q414704 BLAST score 115 E value 3.0e-58 Match length 151 % identity 94 NCBI Description O.sativa mRNA for cytochrome b5 Seq. No. 413010 Seq. ID uC-osflcyp120b05b1 Method BLASTX

Method BLASTX
NCBI GI g1168537
BLAST score 233
E value 2.0e-19
Match length 42
% identity 100

NCBI Description ASPARTIC PROTEINASE PRECURSOR >gi 82458 pir JS0732

aspartic proteinase (EC 3.4.23.-) - rice

>gi_218143_dbj_BAA02242 (D12777) aspartic proteinase

[Oryza sativa]

Seq. No. 413011

```
uC-osflcyp120b07b1
Seq. ID
Method
                  BLASTX
                  q3914422
NCBI GI
                  608
BLAST score
                  3.0e-63
E value
Match length
                  117
                  94
% identity
                  PROFILIN >gi 2154728 emb CAA69669 (Y08389) profilin 2
NCBI Description
                   [Cynodon dactylon] >gi 2154730 emb CAA69670_ (Y08390)
                  profilin 1 [Cynodon dactylon]
                  413012
Seq. No.
                  uC-osflcyp120b10b1
Seq. ID
                  BLASTX
Method
                  g1747296
NCBI GI
                  607
BLAST score
                  3.0e-63
E value
                  131
Match length
                  93
% identity
                  (D45384) vacuolar H+-pyrophosphatase [Oryza sativa]
NCBI Description
                  >gi_3298476_dbj_BAA31524_ (AB012766) ovp2 [Oryza sativa]
                   413013
Seq. No.
                  uC-osflcyp120b11b1
Seq. ID
                  BLASTN
Method
NCBI GI
                  g3618307
BLAST score
                  110
                  1.0e-54
E value
                   324
Match length
                   98
% identity
                  Oryza sativa mRNA for zinc finger protein, complete cds,
NCBI Description
                   clone:C60910
                   413014
Seq. No.
                  uC-osflcyp120b12b1
Seq. ID
Method
                  BLASTX
NCBI GI
                   q4567246
                   435
BLAST score
                   4.0e-43
E value
Match length
                   128
                   65
% identity
NCBI Description
                  (AC007070) unknown protein [Arabidopsis thaliana]
                   413015
Seq. No.
                   uC-osflcyp120c01b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2505874
BLAST score
                   714
E value
                   1.0e-75
Match length
                   161
% identity
                   83
NCBI Description
                  (Y12776) putative kinase [Arabidopsis thaliana]
Seq. No.
                   413016
                   uC-osflcyp120c02b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g224293
```

419 BLAST score 5.0e-41E value 86 Match length % identity 98 NCBI Description histone H4 [Triticum aestivum] 413017 Seq. No. uC-osflcyp120c05b1 Seq. ID Method BLASTX NCBI GI g5903036 BLAST score 373 E value 3.0e-38Match length 121 % identity 61 NCBI Description (AC008016) F6D8.5 [Arabidopsis thaliana] 413018 Seq. No. uC-osflcyp120c06b1 Seq. ID Method BLASTX NCBI GI g3107931 BLAST score 675 5.0e-71E value 162 Match length 83 % identity NCBI Description (AB013353) UDP-glucose pyrophosphorylase [Pyrus pyrifolia] Seq. No. 413019 uC-osflcyp120c07b1 Seq. ID Method BLASTX NCBI GI g1575595 BLAST score 826 E value 9.0e-89 Match length 175 % identity NCBI Description (U67717) fimbrin/plastin-like [Triticum aestivum] Seq. No. 413020 Seq. ID uC-osflcyp120c08b1 Method BLASTX NCBI GI g5360178 BLAST score 655 E value 8.0e-69 Match length 132 % identity 95 NCBI Description (AF159882) Cen-like protein FDR2 [Oryza sativa] Seq. No. 413021 Seq. ID uC-osflcyp120c12b1 Method BLASTX

Method BLASTX
NCBI GI g3695403
BLAST score 507
E value 2.0e-51
Match length 113
% identity 86

NCBI Description (AF096373) contains similarity to the pfkB family of

carbohydrate kinases (Pfam: PF00294, E=1.6e-75)
[Arabidopsis thaliana] >gi_4538955_emb_CAB39779.1_

(AL049488) fructokinase-like protein [Arabidopsis thaliana]

413022 Seq. No. uC-osflcyp120d01b1 Seq. ID Method BLASTX q542157 NCBI GI BLAST score 612 1.0e-63 E value 138 Match length 87 % identity NCBI Description ribosomal 5S RNA-binding protein - Rice 413023 Seq. No. uC-osflcyp120d04b1 Seq. ID Method BLASTX NCBI GI g3250676 468 BLAST score 9.0e-47 E value 177 Match length 53 % identity (AL024486) putative protein [Arabidopsis thaliana] NCBI Description

413024 Seq. No.

uC-osflcyp120d06b1 Seq. ID

Method BLASTX NCBI GI q4689034 BLAST score 179 7.0e-13 E value 69 Match length 55 % identity

NCBI Description (AJ133751) chloroplast ribosome recycling factor protein

[Spinacia oleracea]

413025 Seq. No.

uC-osflcyp120d08b1 Seq. ID

Method BLASTX NCBI GI q3914899 BLAST score 793 E value 7.0e-85 Match length 155 % identity 96

NCBI Description 40S RIBOSOMAL PROTEIN S4 >gi 2331301 (AF013487) ribosomal

protein S4 type I [Zea mays]

Seq. No. 413026

Seq. ID uC-osflcyp120d09b1

Method BLASTX NCBI GI g2493650 757 BLAST score E value 1.0e-80 Match length 169 % identity 89

NCBI Description RUBISCO SUBUNIT BINDING-PROTEIN BETA SUBUNIT (60 KD

CHAPERONIN BETA SUBUNIT) (CPN-60 BETA)

>gi_1167858_emb_CAA93139_ (Z68903) chaperonin [Secale

cereale]

BLAST score

243

```
413027
Seq. No.
                  uC-osflcyp120d10b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4803925
                  194
BLAST score
E value
                  1.0e-14
                  128
Match length
                  33
% identity
                  (AC006264) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  413028
                  uC-osflcyp120e01b1
Seq. ID
Method
                  BLASTX
                  g2980806
NCBI GI
BLAST score
                  211
                  1.0e-16
E value
                  83
Match length
                  49
% identity
                  (AL022197) putative protein [Arabidopsis thaliana]
NCBI Description
                  413029
Seq. No.
                  uC-osflcyp120e03b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2342682
BLAST score
                  530
E value
                  5.0e-54
Match length
                  136
% identity
                  72
                  (AC000106) Contains similarity to Rattus AMP-activated
NCBI Description
                  protein kinase (gb_X95577). [Arabidopsis thaliana]
Seq. No.
                  413030
                  uC-osflcyp120e04b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3123745
BLAST score
                  384
E value
                  5.0e-37
Match length
                  148
% identity
                  50
NCBI Description (AB013447) aluminum-induced [Brassica napus]
Seq. No.
                  413031
                  uC-osflcyp120e05b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2407281
BLAST score
                  807
E value
                  2.0e-86
Match length
                  154
% identity
NCBI Description
                  (AF017363) ribulose 1,5-bisphosphate carboxylase small
                  subunit [Oryza sativa]
Seq. No.
                  413032
                  uC-osflcyp120e06b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2829898
```

Match length

% identity

162

```
3.0e-35
E value
Match length
                   153
                   50
% identity
NCBI Description
                  (AC002311) Hypothetical protein [Arabidopsis thaliana]
                   413033
Seq. No.
                  uC-osflcyp120e07b1
Seq. ID
Method
                  BLASTX
NCBI GI
                   g3913018
BLAST score
                   748
E value
                   1.0e-79
Match length
                  151
                   100
% identity
                  FRUCTOSE-BISPHOSPHATE ALDOLASE, CHLOROPLAST PRECURSOR
NCBI Description
                   (ALDP) >gi 218155 dbj BAA02730 (D13513) chloroplastic
                   aldolase [Oryza sativa]
                   413034
Seq. No.
Seq. ID
                  uC-osflcyp120e08b1
Method
                  BLASTX
NCBI GI
                   g2739376
                   437
BLAST score
                   4.0e-43
E value
Match length
                   122
                   65
% identity
                  (AC002505) putative permease [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   413035
Seq. ID
                   uC-osflcyp120e10b1
Method
                   BLASTX
NCBI GI
                   g2073375
BLAST score
                   690
                   8.0e-73
E value
Match length
                   130
% identity
                   100
NCBI Description
                   (D85317) farnesyl pyrophosphate synthase [Oryza sativa]
                   >gi_4063829_dbj_BAA36276_ (AB021747) farnesyl diphosphate
                   synthase [Oryza sativa]
                   413036
Seq. No.
Seq. ID
                   uC-osflcyp120e11b1
Method
                   BLASTX
NCBI GI
                   q3885888
BLAST score
                   149
E value
                   1.0e-09
Match length
                   69
% identity
                   57
NCBI Description
                  (AF093632) high mobility group protein [Oryza sativa]
                   413037
Seq. No.
Seq. ID
                   uC-osflcyp120e12b1
Method
                   BLASTX
NCBI GI
                   q3914467
BLAST score
                   596
                   8.0e-62
E value
```

```
26S PROTEASOME REGULATORY SUBUNIT S3 (NUCLEAR ANTIGEN 21D7)
NCBI Description
                   >gi_1864003_dbj_BAA19252_ (AB001422) 21D7 [Nicotiana
                   tabacum]
                   413038
Seq. No.
                   uC-osflcyp120f01b1
Seq. ID
Method
                   BLASTX
                   g2827143
NCBI GI
                   338
BLAST score
                   2.0e-31
E value
                   168
Match length
% identity
                   46
                   (AF027174) cellulose synthase catalytic subunit
NCBI Description
                   [Arabidopsis thaliana]
                   413039
Seq. No.
                   uC-osflcyp120f03b1
Seq. ID
Method
                   BLASTX
                   g82734
NCBI GI
                   686
BLAST score
                   3.0e-72
E value
                   137
Match length
                   35
% identity
NCBI Description ubiquitin precursor - maize (fragment)
                   >gi_226763_prf__1604470A poly-ubiquitin [Zea mays]
                   413040
Seq. No.
                   uC-osflcyp120f04b1
Seq. ID
Method
                   BLASTX
                   g1174745
NCBI GI
                   611
BLAST score
                   2.0e-63
E value
                   133
Match length
                   88
% identity
                   TRIOSEPHOSPHATE ISOMERASE, CHLOROPLAST PRECURSOR (TIM)
NCBI Description
                   >gi_1363523_pir__S53761 triose-phosphate isomerase (EC
                   5.3.1.1) precursor, chloroplast - rye
                   >gi_609262_emb_CAA83533_ (Z32521) triosephosphate isomerase [Secale cereale] >gi_1095494_prf__2109226B triosephosphate
                   isomerase [Secale cereale]
Seq. No.
                   413041
                   uC-osflcyp120f05b1
Seq. ID
Method
                   BLASTX
                   q5830787
NCBI GI
BLAST score
                   214
E value
                   5.0e-17
Match length
                   87
% identity
NCBI Description (AL117188) ankyrin repeat-containing protein 2 [Arabidopsis
                   thaliana]
Seq. No.
                    413042
```

uC-osflcyp120f06b1 Seq. ID

Method BLASTX NCBI GI g2500353 BLAST score 645

E value 1.0e-67 124 Match length % identity 96 60S RIBOSOMAL PROTEIN L10-3 (QM/R22) >gi 1293784 (U55048) NCBI Description similar to human QM protein, a putative tumor supressor, and to maize ubiquinol-cytochrome C reductase complex subunit VI requiring protein SC34 [Oryza sativa] 413043 Seq. No. uC-osflcyp120f07b1 Seq. ID BLASTX Method NCBI GI g2262143 166 BLAST score 2.0e-15 E value Match length 118 % identity 45 (AC002330) putative serine/threonine protein kinase NCBI Description [Arabidopsis thaliana] 413044 Seq. No. uC-osflcyp120f08b1 Seq. ID Method BLASTX NCBI GI g2493131 BLAST score 509 1.0e-51 E value 106 Match length 97 % identity VACUOLAR ATP SYNTHASE SUBUNIT B ISOFORM 1 (V-ATPASE B NCBI Description SUBUNIT) >gi 167108 (L11862) vacuolar ATPase B subunit [Hordeum vulgare] 413045 Seq. No. uC-osflcyp120f10b1 Seq. ID BLASTX Method g4263509 NCBI GI BLAST score 244 E value 2.0e-20 77 Match length 60 % identity (AC004044) hypothetical protein [Arabidopsis thaliana] NCBI Description Seq. No. 413046 uC-osflcyp120f11b1 Seq. ID Method BLASTX NCBI GI q2833383 BLAST score 629 E value 6.0e-67 Match length 163 % identity 79 GRANULE-BOUND GLYCOGEN (STARCH) SYNTHASE PRECURSOR (GBSSI) NCBI Description >gi 2129897 pir S61504 UDPglucose--starch glucosyltransferase (EC 2.4.1.11) isoform I precursor garden pea >qi 385411 bbs 131618 granule-bound starch synthase isoform I, GBSSI [Pisum sativum=peas, BC1/9RR,

(starch) synthase [Pisum sativum]

Peptide, 603 aa] >gi 887571_emb_CAA61268_ (X88789) glycogen

Method

NCBI GI

BLASTX

g2286153

```
413047
Seq. No.
                  uC-osflcyp120f12b1
Seq. ID
                  {\tt BLASTX}
Method
NCBI GI
                  q4567245
                  232
BLAST score
                   3.0e-19
E value
                   99
Match length
                   54
% identity
                  (AC007070) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   413048
                  uC-osflcyp120g01b1
Seq. ID
                  BLASTX
Method
NCBI GI
                  g5596472
                   279
BLAST score
                   8.0e-25
E value
                   98
Match length
                   58
% identity
                  (AL096882) putative protein [Arabidopsis thaliana]
NCBI Description
                   413049
Seq. No.
                  uC-osflcyp120g02b1
Seq. ID
Method
                  BLASTX
                   g3881976
NCBI GI
                   285
BLAST score
                   2.0e-25
E value
Match length
                   65
                   80
% identity
                  (AJ012409) hypothetical protein [Homo sapiens]
NCBI Description
                   413050
Seq. No.
                   uC-osflcyp120g03b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3643082
                   153
BLAST score
E value
                   7.0e-10
Match length
                   92
                   45
% identity
                  (AF075579) protein phosphatase-2C; PP2C [Mesembryanthemum
NCBI Description
                   crystallinum]
Seq. No.
                   413051
                   uC-osflcyp120g04b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g6016729
BLAST score
                   641
E value
                   5.0e-67
Match length
                   175
% identity
                   47
                   (AC009325) unknown protein [Arabidopsis thaliana]
NCBI Description
                   >qi 6091716 gb AAF03428.1 AC010797 4 (AC010797) unknown
                   protein [Arabidopsis thaliana]
                   413052
Seq. No.
                   uC-osflcyp120g06b1
Seq. ID
```

```
626
BLAST score
                  3.0e-65
E value
Match length
                  133
                  93
% identity
                  (AF007581) cytoplasmic malate dehydrogenase [Zea mays]
NCBI Description
                  413053
Seq. No.
                  uC-osflcyp120g07b1
Seq. ID
                  BLASTX
Method
                  g1885310
NCBI GI
                  178
BLAST score
                  5.0e-13
E value
                  40
Match length
                  80
% identity
                  (X91659) Endoxyloglucan transferase (EXT) [Hordeum vulgare]
NCBI Description
                  413054
Seq. No.
                  uC-osflcyp120g08b1
Seq. ID
Method
                  BLASTX
                  g3023713
NCBI GI
                  738
BLAST score
                  2.0e-78
E value
Match length
                  149
                  97
% identity
                  ENOLASE (2-PHOSPHOGLYCERATE DEHYDRATASE)
NCBI Description
                   (2-PHOSPHO-D-GLYCERATE HYDRO-LYASE) (OSE1) >gi 780372
                   (U09450) enolase [Oryza sativa]
                  413055
Seq. No.
                  uC-osflcyp120g09b1
Seq. ID
                  BLASTX
Method
                  g1946329
NCBI GI
BLAST score
                  531
                  4.0e-54
E value
                  141
Match length
                   72
% identity
                  (U69154) prohibitin [Nicotiana tabacum]
NCBI Description
                   413056
Seq. No.
Seq. ID
                  uC-osflcyp120g11b1
Method
                  BLASTX
NCBI GI
                   g5295980
                   668
BLAST score
                   3.0e-70
E value
                   130
Match length
                   100
% identity
NCBI Description (AB003323) MADS box-like protein [Oryza sativa]
Seq. No.
                   413057
                   uC-osflcyp120g12b1
Seq. ID
Method
                  BLASTX
NCBI GI
                   q3075488
BLAST score
                   514
E value
                   3.0e-52
Match length
                   118
% identity
NCBI Description (AF058796) chlorophyll a/b-binding protein [Oryza sativa]
```

Seq. ID

413058 Seq. No. Seq. ID uC-osflcyp120h01b1 Method BLASTX NCBI GI q3513737 BLAST score 150 E value 1.0e-09 Match length 64 44 % identity NCBI Description (AF080118) contains similarity to C3HC4-type zinc fingers (Pfam:zf-C3HC4.hmm, score: 34.87) [Arabidopsis thaliana] 413059 Seq. No. uC-osflcyp120h03b1 Seq. ID Method BLASTX NCBI GI g5302770 BLAST score 476 8.0e-48 E value Match length 113 % identity 85 (Z97336) protein kinase [Arabidopsis thaliana] NCBI Description Seq. No. 413060 uC-osflcyp120h04b1 Seq. ID Method BLASTX NCBI GI g1707011 BLAST score 286 E value 2.0e-25 Match length 121 48 % identity (U78721) auxin-repressed protein isolog [Arabidopsis NCBI Description thaliana] Seq. No. 413061 uC-osflcyp120h06b1 Seq. ID Method BLASTX NCBI GI g3142290 BLAST score 644 E value 2.0e-67 Match length 163 78 % identity NCBI Description (AC002411) Contains similarity to gb Z69902 from C. elegans. [Arabidopsis thaliana] 413062 Seq. No. uC-osflcyp120h09b1 Seq. ID Method BLASTX NCBI GI g3882356 BLAST score 213 2.0e-17 E value Match length 78 % identity 53 NCBI Description (U92460) 12-oxophytodienoate reductase OPR2 [Arabidopsis thaliana] Seq. No. 413063

53773

uC-osflcyp121a05b1

```
BLASTX
Method
                  q6006848
NCBI GI
BLAST score
                  733
                  7.0e-78
E value
Match length
                  158
% identity
                  84
                  (AC009540) unknown protein, 5' partial [Arabidopsis
NCBI Description
                  thaliana]
                  413064
Seq. No.
Seq. ID
                  uC-osflcyp121a06b1
Method
                  BLASTX
NCBI GI
                  q4455246
BLAST score
                  255
E value
                  5.0e-23
Match length
                  122
                  54
% identity
NCBI Description
                 (AL035523) putative protein [Arabidopsis thaliana]
Seq. No.
                  413065
Seq. ID
                  uC-osflcyp121a08b1
Method
                  BLASTX
NCBI GI
                  q4115337
BLAST score
                  482
                  2.0e-48
E value
Match length
                  103
                  16
% identity
NCBI Description (L81141) ubiquitin [Pisum sativum]
                  413066
Seq. No.
Seq. ID
                  uC-osflcyp121a09b1
Method
                  BLASTX
NCBI GI
                  q4836912
BLAST score
                  550
E value
                  2.0e-56
Match length
                  141
% identity
                  74
NCBI Description (AC007153) 60811 [Arabidopsis thaliana]
Seq. No.
                   413067
Seq. ID
                  uC-osflcyp121a11b1
Method
                  BLASTX
NCBI GI
                   g4679028
BLAST score
                   216
E value
                   3.0e-17
Match length
                  100
% identity
                   43
                   (AF077207) HSPC021 [Homo sapiens]
NCBI Description
                   >gi 5106781 gb AAD39841.1 (AF083243) HSPC025 [Homo
                   sapiens]
```

Method BLASTX
NCBI GI g4006978
BLAST score 198
E value 2.0e-15

Match length 88 % identity 42 (AJ131335) pollen allergen (group II) [Cynodon dactylon] NCBI Description 413069 Seq. No. uC-osflcyp121b03b1 Seq. ID Method BLASTX g3183094 NCBI GI 730 BLAST score 2.0e-77 E value 162 Match length 86 % identity ORNITHINE CARBAMOYLTRANSFERASE PRECURSOR (OTCASE) NCBI Description (ORNITHINE TRANSCARBAMYLASE) >gi_971168 (U13684) ornithine carbamoyltransferase [Pisum sativum] Seq. No. 413070 uC-osflcyp121b06b1 Seq. ID Method BLASTX NCBI GI g3702314 BLAST score 290 6.0e-26 E value 97 Match length 58 % identity (AC002535) similar to SWI/SNF complex subunit BAF170 NCBI Description [Arabidopsis thaliana] 413071 Seq. No. uC-osflcyp121b07b1 Seq. ID BLASTX Method NCBI GI g4455159 BLAST score 533 2.0e-54 E value 133 Match length 77 % identity NCBI Description (AL021687) putative protein [Arabidopsis thaliana] Seq. No. 413072 uC-osflcyp121b09b1 Seq. ID BLASTX Method NCBI GI q4585871 BLAST score 645 E value 1.0e-67 Match length 163 75 % identity NCBI Description (AC005850) Unknown protein [Arabidopsis thaliana] Seq. No. 413073 Seq. ID uC-osflcyp121b10b1 Method BLASTX NCBI GI g2832660 BLAST score 350 6.0e-33 E value Match length 161 % identity 45

NCBI Description (AL021710) lipase-like protein [Arabidopsis thaliana]

NCBI GI

BLAST score

```
413074
Seq. No.
                  uC-osflcyp121b11b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4733973
BLAST score
                  168
                  1.0e-11
E value
Match length
                  132
                  33
% identity
                  (AC007264) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                  413075
Seq. No.
                  uC-osflcyp121b12b1
Seq. ID
Method
                  BLASTX
                  g1215812
NCBI GI
BLAST score
                  396
E value
                  2.0e-38
Match length
                  116
                  67
% identity
                  (D38170) probenazole-inducible protein PBZ1 [Oryza sativa]
NCBI Description
                  >gi 2780343 dbj BAA24277 (D82066) PBZ1 [Oryza sativa]
                  413076
Seq. No.
                  uC-osflcyp121c01b1
Seq. ID
Method
                  BLASTX
                  g6090879
NCBI GI
BLAST score
                  892
E value
                  2.0e-96
Match length
                  161
                   98
% identity
                  (AF169966) putative cycloartenol synthase [Oryza sativa]
NCBI Description
                  413077
Seq. No.
                  uC-osflcyp121c03b1
Seq. ID
Method
                  BLASTX
                   q5915855
NCBI GI
BLAST score
                   326
E value
                   3.0e - 30
Match length
                  142
                   49
% identity
                  CYTOCHROME P450 97B2 >gi 2738996 gb AAB94586 (AF022457)
NCBI Description
                  CYP97B2p [Glycine max]
                   413078
Seq. No.
                   uC-osflcyp121c05b1
Seq. ID
Method
                  BLASTX
NCBI GI
                   q3135263
BLAST score
                   168
E value
                   9.0e-12
Match length
                  56
% identity
                   54
NCBI Description
                  (AC003058) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   413079
                   uC-osflcyp121c06b1
Seq. ID
Method
                   BLASTX
```

53776

g3004565

```
1.0e-28
E value
                  94
Match length
                   63
% identity
                  (AC003673) putative protein kinase [Arabidopsis thaliana]
NCBI Description
                  413080
Seq. No.
                  uC-osflcyp121c07b1
Seq. ID
                  BLASTX
Method
                  g2407281
NCBI GI
BLAST score
                   480
                   3.0e-76
E value
                  149
Match length
                   93
% identity
                  (AF017363) ribulose 1,5-bisphosphate carboxylase small
NCBI Description
                  subunit [Oryza sativa]
Seq. No.
                   413081
                  uC-osflcyp121c08b1
Seq. ID
Method
                  BLASTX
                   g100638
NCBI GI
BLAST score
                   324
                   5.0e-31
E value
                   96
Match length
                   67
% identity
                  pollen allergen Lol p I precursor (clone 5A) - perennial
NCBI Description
                   ryegrass >gi 168316 (M57474) pollen allergen [Lolium
                   perenne]
                   413082
Seq. No.
                   uC-osflcyp121c09b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g5912299
BLAST score
                   618
                   2.0e-67
E value
                   144
Match length
                   95
% identity
NCBI Description
                  (AJ133787) gigantea homologue [Oryza sativa]
                   413083
Seq. No.
                   uC-osflcyp121c10b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   q1350680
                   348
BLAST score
E value
                   1.0e-32
                   131
Match length
% identity
                   52
NCBI Description 60S RIBOSOMAL PROTEIN L1
Seq. No.
                   413084
                   uC-osflcyp121c12b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   q3021508
BLAST score
                   305
                   1.0e-30
E value
Match length
                   106
% identity
                  (AJ001769) glucose-6-phosphate dehydrogenase [Nicotiana
NCBI Description
```



tabacum]

```
Seq. No.
                  413085
Seq. ID
                  uC-osflcyp121d01b1
Method
                  BLASTX
NCBI GI
                  g1514643
BLAST score
                  586
E value
                  1.0e-60
Match length
                  158
% identity
                  74
                  (Z70524) PDR5-like ABC transporter [Spirodela polyrrhiza]
NCBI Description
                  413086
Seq. No.
                  uC-osflcyp121d05b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3236249
                  390
BLAST score
E value
                  1.0e-37
Match length
                  150
                   52
% identity
NCBI Description
                  (AC004684) hypothetical protein [Arabidopsis thaliana]
                  413087
Seq. No.
                  uC-osflcyp121d07b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1168587
BLAST score
                  248
                  3.0e-21
E value
Match length
                  125
                  52
% identity
                  ATP SYNTHASE DELTA CHAIN, CHLOROPLAST PRECURSOR
NCBI Description
                  >gi 1084467 pir S43728 H+-transporting ATP synthase (EC
                   3.6.1.34) - sorghum >gi_311231_emb_CAA46803_ (X66004)
                  H(+)-transporting ATP synthase [Sorghum bicolor]
Seq. No.
                  413088
Seq. ID
                  uC-osflcyp121d10b1
Method
                  BLASTX
NCBI GI
                   q4455192
BLAST score
                  184
E value
                   2.0e-13
Match length
                  96
% identity
                   47
NCBI Description
                 (AL035440) putative protein [Arabidopsis thaliana]
Seq. No.
                   413089
Seq. ID
                  uC-osflcyp121d12b1
Method
                  BLASTX
NCBI GI
                   g3980378
BLAST score
                  699
E value
                   7.0e-74
Match length
                  143
% identity
                  85
                  (AC004561) putative RNA binding protein [Arabidopsis
NCBI Description
```

53778

thaliana]

413090

Seq. No.

```
uC-osflcyp121e03b1
Seq. ID
Method
                  BLASTX
                  g3914431
NCBI GI
BLAST score
                  777
E value
                  5.0e-83
Match length
                  164
                  88
% identity
                  PROTEASOME COMPONENT C8 (MACROPAIN SUBUNIT C8)
NCBI Description
                  (MULTICATALYTIC ENDOPEPTIDASE COMPLEX SUBUNIT C8)
                  >gi_2285802_dbj_BAA21651_ (D78173) 26S proteasome alpha
                  subunit [Spinacia oleracea]
Seq. No.
                  413091
                  uC-osflcyp121e04b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4038044
BLAST score
                  252
                  2.0e-21
E value
                  66
Match length
                  65
% identity
                  (AC005936) unknown protein [Arabidopsis thaliana]
NCBI Description
                  >gi_4406788_gb_AAD20098_ (AC006532) unknown protein
                  [Arabidopsis thaliana]
Seq. No.
                  413092
                  uC-osflcyp121e06b1
Seq. ID
Method
                  BLASTX
                  g3860323
NCBI GI
BLAST score
                  349
E value
                  7.0e-33
Match length
                  77
% identity
                  83
NCBI Description (AJ012688) hypothetical protein [Cicer arietinum]
                  413093
Seq. No.
Seq. ID
                  uC-osflcyp121e07b1
Method
                  BLASTN
NCBI GI
                  q5257255
BLAST score
                  50
E value
                  7.0e-19
Match length
                  227
% identity
NCBI Description Oryza sativa genomic DNA, chromosome 8, clone: P0026F07
Seq. No.
                  413094
Seq. ID
                  uC-osflcyp121e08b1
Method
                  BLASTX
NCBI GI
                  g399333
BLAST score
                  563
E value
                   4.0e-58
Match length
                  121
% identity
                  90
                  CYSTEINE SYNTHASE, CHLOROPLAST PRECURSOR (O-ACETYLSERINE
NCBI Description
                  SULFHYDRYLASE) (O-ACETYLSERINE (THIOL)-LYASE) (CSASE)
                  >gi_322740_pir__A43407 cysteine synthase (EC 4.2.99.8)
                  precursor - pepper >gi_17944 emb CAA46086_ (X64874)
                  O-acetylserine (thiol)-lyase [Capsicum annuum]
```

413095 Seq. No. uC-osflcyp121e09b1 Seq. ID BLASTX Method g4006978 NCBI GI 201 BLAST score 1.0e-15 E value 90 Match length 42 % identity (AJ131335) pollen allergen (group II) [Cynodon dactylon] NCBI Description 413096 Seq. No. uC-osflcyp121e10b1 Seq. ID BLASTX Method NCBI GI q3885882 BLAST score 279 1.0e-24 E value Match length 56 98 % identity (AF093629) inorganic pyrophosphatase [Oryza sativa] NCBI Description 413097 Seq. No. uC-osflcyp121e11b1 Seq. ID BLASTX Method g4734014 NCBI GI 395 BLAST score 3.0e-38 E value Match length 133 51 % identity (AC007112) unknown protein [Arabidopsis thaliana] NCBI Description 413098 Seq. No. uC-osflcyp121e12b1 Seq. ID BLASTX Method g3980400 NCBI GI 366 BLAST score E value 7.0e-35 Match length 155 % identity 51 (AC004561) putative tropinone reductase [Arabidopsis NCBI Description thaliana] 413099 Seq. No. uC-osflcyp121f01b1 Seq. ID Method BLASTX q3894157 NCBI GI BLAST score 511 E value 7.0e-52 Match length 162 % identity (ACO05312) putative protein kinase, 3' partial [Arabidopsis NCBI Description thaliana] 413100 Seq. No. Seq. ID uC-osflcyp121f02b1 Method BLASTN NCBI GI g4958936

```
BLAST score
                  195
E value
                  1.0e-105
                  199
Match length
% identity
                  99
NCBI Description Oryza sativa ICT mRNA, partial cds
                  413101
Seq. No.
                  uC-osflcyp121f03b1
Seq. ID
Method
                  BLASTX
                  g3548818
NCBI GI
                  653
BLAST score
                  1.0e-68
E value
                  146
Match length
                  84
% identity
                  (AC005313) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  413102
                  uC-osflcyp121f04b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3819164
BLAST score
                  348
                  1.0e-32
E value
                  129
Match length
                  54
% identity
NCBI Description
                  (AJ012318) cytosolic chaperonin, delta-subunit [Glycine
                  max]
                   413103
Seq. No.
                  uC-osflcyp121f05b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g131225
                   543
BLAST score
                   5.0e - 59
E value
                  142
Match length
                   85
% identity
NCBI Description
                  PHOTOSYSTEM I REACTION CENTRE SUBUNIT XI PRECURSOR (SUBUNIT
                  V) (PSI-L) >gi_100605_pir__A39759 photosystem I 18K protein
                  precursor - barley >gi 167087 (M61146) photosystem I
                  hydrophobic protein [Hordeum vulgare]
Seq. No.
                   413104
Seq. ID
                   uC-osflcyp121f06b1
Method
                  BLASTX
NCBI GI
                   g4371296
BLAST score
                   675
E value
                   4.0e-71
```

Match length 163

(AC006260) putative receptor protein kinase [Arabidopsis NCBI Description

thaliana]

Seq. No. 413105

% identity

Seq. ID uC-osflcyp121f07b1

Method BLASTX NCBI GI g283008 BLAST score 861 E value 7.0e-93

Seq. No.

Seq. ID

413110

uC-osflcyp121g02b1

```
163
Match length
                    99
% identity
                    sucrose synthase (EC 2.4.1.13) - rice
NCBI Description
                    >gi 20366 emb CAA46017_ (X64770) sucrose synthase [Oryza
                    sativa]
                    413106
Seq. No.
                    uC-osflcyp121f08b1
Seq. ID
Method
                    BLASTX
                    g4769004
NCBI GI
                    495
BLAST score
                    5.0e-50
E value
                    89
Match length
                    94
% identity
NCBI Description
                   (AF140598) ring-box protein 1 [Homo sapiens]
                    >gi 4769006_gb_AAD29716.1_AF140599_1 (AF140599) ring-box
                    protein 1 [Mus musculus]
                    >qi 4809216 qb AAD30146.1 AF142059 1 (AF142059) RING finger
                    protein [Homo sapiens]
Seq. No.
                    413107
                    uC-osflcyp121f09b1
Seq. ID
Method
                    BLASTX
NCBI GI
                    g3914005
                    519
BLAST score
E value
                    7.0e-53
Match length
                    126
% identity
                    84
NCBI Description MITOCHONDRIAL LON PROTEASE HOMOLOG 1 PRECURSOR >gi_1816586
                    (U85494) LON1 protease [Zea mays]
Seq. No.
                    413108
                    uC-osflcyp121f10b1
Seq. ID
Method
                    BLASTX
NCBI GI
                    q3281870
BLAST score
                    227
E value
                    1.0e-18
Match length
                    156
                    33
% identity
NCBI Description (AL031004) putative protein [Arabidopsis thaliana]
Seq. No.
                    413109
                    uC-osflcyp121f11b1
Seq. ID
Method
                    BLASTX
NCBI GI
                    g462195
BLAST score
                    531
E value
                    3.0e-54
Match length
                    113
% identity
                    90
                   PROTEIN TRANSLATION FACTOR SUI1 HOMOLOG (GOS2 PROTEIN)
NCBI Description
                    >gi_100682_pir___S21636 GOS2 protein - rice
>gi_20238_emb_CAA36190_ (X51910) GOS2 [Oryza sativa]
>gi_3789950 (AF094774) translation initiation factor [Oryza
                    sativa]
```



```
Method BLASTX
NCBI GI g2586082
BLAST score 232
E value 3.0e-19
Match length 140
% identity 40
```

NCBI Description (U72725) retrofit [Oryza longistaminata]

Seq. No. 413111

Seq. ID uC-osflcyp121g03b1

Method BLASTX
NCBI GI g2117937
BLAST score 700
E value 4.0e-74
Match length 137
% identity 96

NCBI Description UTP--glucose-1-phosphate uridylyltransferase (EC 2.7.7.9) -

barley >gi 1212996 emb CAA62689 (X91347) UDP-glucose

pyrophosphorylase [Hordeum vulgare]

Seq. No. 413112

Seq. ID uC-osflcyp121g04b1

Method BLASTX
NCBI GI g132105
BLAST score 592
E value 2.0e-61
Match length 132
% identity 85

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR

(RUBISCO SMALL SUBUNIT C) >gi_68094_pir__RKRZS9

ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_

(D00643) small subunit of ribulose-1,5-bisphosphate

carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364)
ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
sativa] >gi_226375_prf__1508256A ribulose bisphosphate

carboxylase S [Oryza sativa]

Seq. No. 413113

Seq. ID uC-osflcyp121g05b1

Method BLASTN
NCBI GI g218141
BLAST score 61
E value 1.0e-25
Match length 129
% identity 88

NCBI Description Rice mRNA abundantly expressed at microspore stage

Seq. No. 413114

Seq. ID uC-osflcyp121g06b1

Method BLASTX
NCBI GI g419760
BLAST score 536
E value 8.0e-55
Match length 156
% identity 36

NCBI Description P-glycoprotein atpgp1 - Arabidopsis thaliana

Method

NCBI GI

E value

BLAST score

BLASTX

681

g4584525

9.0e-72





```
(AC006922) putative P-glycoprotein pgp1 [Arabidopsis
                  thaliana
Seq. No.
                  413115
Seq. ID
                  uC-osflcyp121g07b1
Method
                  BLASTX
NCBI GI
                  g1169382
BLAST score
                  268
                  2.0e-23
E value
Match length
                  72
                  74
% identity
                  DNAJ PROTEIN HOMOLOG 2 >gi 542196 pir S42031 LDJ2 protein
NCBI Description
                  - leek >gi_454303_emb_CAA54720_ (X77632) LDJ2 [Allium
                  porrum]
                  413116
Seq. No.
Seq. ID
                  uC-osflcyp121g08b1
Method
                  BLASTX
                  g548492
NCBI GI
BLAST score
                  307
                  6.0e-28
E value
                  92
Match length
                  63
% identity
                 EXOPOLYGALACTURONASE PRECURSOR (EXOPG) (PECTINASE)
NCBI Description
                  (GALACTURAN 1,4-ALPHA-GALACTURONIDASE)
                  >gi 629853 pir S30066 polygalacturonase - maize
                  >gi 288379 emb CAA45751 (X64408) polygalacturonase [Zea
                  mays]
Seq. No.
                  413117
                  uC-osflcyp121g09b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4455302
BLAST score
                  502
E value
                  8.0e-51
Match length
                  141
% identity
NCBI Description (AL035528) putative protein [Arabidopsis thaliana]
Seq. No.
                  413118
Seq. ID
                  uC-osflcyp121g10b1
Method
                  BLASTX
NCBI GI
                  g5734754
BLAST score
                  295
E value
                  1.0e-26
Match length
                  71
% identity
NCBI Description (AC007651) Unknown protein [Arabidopsis thaliana]
Seq. No.
                   413119
Seq. ID
                  uC-osflcyp121g11b1
```

>gi_3849833_emb_CAA43646_ (X61370) P-glycoprotein

[Arabidopsis thaliana] >gi_4883607_gb_AAD31576.1_AC006922_8

Match length 162 75 % identity (AL049607) protein phosphatase 2C-like protein [Arabidopsis NCBI Description thaliana] 413120 Seq. No. uC-osflcyp121g12b1 Seq. ID BLASTX Method g5802606 NCBI GI 702 BLAST score 3.0e-74E value Match length 142 93 % identity (AF174486) methylenetetrahydrofolate reductase [Zea mays] NCBI Description Seq. No. 413121 uC-osflcyp121h01b1 Seq. ID Method BLASTX q3929333 NCBI GI BLAST score 192 1.0e-14E value Match length 63 60 % identity CYTOCHROME P450 76B1 (7-ETHOXYCOUMARIN O-DEETHYLASE) (ECOD) NCBI Description (PHENYLUREA DEALKYLASE) >gi_2370230_emb_CAA71054_ (Y09920) 7-ethoxycoumarin O-deethylase [Helianthus tuberosus] Seq. No. 413122 Seq. ID uC-osflcyp121h02b1 Method BLASTX q2130069 NCBI GI 507 BLAST score 1.0e-51 E value 96 Match length 98 % identity catalase (EC 1.11.1.6) catA - rice NCBI Description >gi_1261858_dbj_BAA06232_ (D29966) catalase [Oryza sativa] Seq. No. 413123 uC-osflcyp121h07b1 Seq. ID Method BLASTX g1136120 NCBI GI 517 BLAST score 1.0e-52 E value 109 Match length 90 % identity (X91806) alpha-tubulin [Oryza sativa] NCBI Description Seq. No. 413124 uC-osflcyp121h08b1 Seq. ID Method BLASTX NCBI GI q1709128 BLAST score 582 E value 3.0e-60 Match length 153 75 % identity NCBI Description GLYCOGEN SYNTHASE KINASE-3 HOMOLOG MSK-2

```
[Medicago sativa]
Seq. No.
                  413125
                  uC-osflcyp121h09b1
Seq. ID
Method
                  BLASTX
                  g2130069
NCBI GI
                  526
BLAST score
                  7.0e-54
E value
                  98
Match length
% identity
                  99
                  catalase (EC 1.11.1.6) catA - rice
NCBI Description
                  >gi 1261858 dbj BAA06232 (D29966) catalase [Oryza sativa]
Seq. No.
                  413126
                  uC-osflcyp121h10b1
Seq. ID
Method
                  BLASTX
                  q3063471
NCBI GI
                  294
BLAST score
                  2.0e-26
E value
Match length
                  87
% identity
                   62
                  (AC003981) F22013.33 [Arabidopsis thaliana]
NCBI Description
                   413127
Seq. No.
                  uC-osflcyp121h11b1
Seq. ID
Method
                  BLASTX
                  g2286153
NCBI GI
BLAST score
                  546
                  5.0e-56
E value
Match length
                  113
                   96
% identity
                  (AF007581) cytoplasmic malate dehydrogenase [Zea mays]
NCBI Description
                   413128
Seq. No.
                  uC-osflcyp122a03b1
Seq. ID
Method
                  BLASTX
NCBI GI
                   q3850588
                   402
BLAST score
                   6.0e-41
E value
                   144
Match length
                   60
% identity
                  (AC005278) Contains similarity to gb AB011110 KIAA0538
NCBI Description
                   protein from Homo sapiens brain and to phospholipid-binding
                   domain C2 PF_00168. ESTs gb_AA585988 and gb_T04384 come
                   from this gene. [Arabidopsis thaliana]
                   413129
Seq. No.
Seq. ID
                   uC-osflcyp122a04b1
Method
                   BLASTX
NCBI GI
                   q5734735
BLAST score
                   258
                   3.0e-22
E value
                   103
Match length
% identity
                   49
                  (AC007259) Similar to protein kinases [Arabidopsis
NCBI Description
```

>gi_481019_pir__S37643 protein kinase MSK-2 (EC 2.7.1.-) - alfalfa >gi_313146_emb_CAA48473_ (X68410) protein kinase



thaliana]

Seq. No. 413130

Seq. ID uC-osflcyp122a06b1

Method BLASTX
NCBI GI g3550436
BLAST score 313
E value 1.0e-29
Match length 111
% identity 65

NCBI Description (AJ001317) putative transcription repressor HOTR [Hordeum

vulgare]

Seq. No. 413131

Seq. ID uC-osflcyp122a08b1

Method BLASTX
NCBI GI 9730463
BLAST score 301
E value 3.0e-27
Match length 102
% identity 56

NCBI Description 60S RIBOSOMAL PROTEIN L33-B (L37B) (YL37) (RP47)

>gi_630323_pir__S44069 ribosomal protein L35a.e.c15 - yeast

(Saccharomyces cerevisiae) >gi_484241 (L23923) ribosomal

protein L37 [Saccharomyces cerevisiae]

>gi 1420537 emb CAA99454_ (Z75142) ORF YOR234c

[Saccharomyces cerevisiae]

Seq. No. 413132

Seq. ID uC-osflcyp122a09b1

Method BLASTX
NCBI GI g4126473
BLAST score 258
E value 3.0e-22
Match length 113
% identity 47

NCBI Description (AB014884) adenylyl cyclase associated protein [Gossypium

hirsutum]

Seq. No. 413133

Seq. ID uC-osflcyp122a10b1

Method BLASTX
NCBI GI g584825
BLAST score 155
E value 3.0e-10
Match length 45
% identity 67

NCBI Description B2 PROTEIN >gi_322726_pir__S32124 B2 protein - carrot

>gi_297889_emb_CAA51078_ (X72385) B2 protein [Daucus

carota]

Seq. No. 413134

Seq. ID uC-osflcyp122a11b1

Method BLASTX
NCBI GI g2117937
BLAST score 261
E value 3.0e-46

Seq. No. Seq. ID

```
Match length
                  124
% identity
                  82
                  UTP--glucose-1-phosphate uridylyltransferase (EC 2.7.7.9) -
NCBI Description
                  barley >gi 1212996 emb CAA62689 (X91347) UDP-glucose
                  pyrophosphorylase [Hordeum vulgare]
Seq. No.
                  413135
                  uC-osflcyp122b01b1
Seq. ID
Method
                  BLASTX
                  g1168587
NCBI GI
BLAST score
                  416
E value
                  1.0e-40
Match length
                  104
% identity
                  81
                  ATP SYNTHASE DELTA CHAIN, CHLOROPLAST PRECURSOR
NCBI Description
                  >gi 1084467 pir S43728 H+-transporting ATP synthase (EC
                  3.6.1.34) - sorghum >gi 311231 emb CAA46803 (X66004)
                  H(+)-transporting ATP synthase [Sorghum bicolor]
                  413136
Seq. No.
                  uC-osflcyp122b03b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g322854
BLAST score
                  696
                  4.0e-74
E value
Match length
                  146
% identity
                  95
NCBI Description
                  pollen-specific protein - rice >gi 20310 emb CAA78897
                  (Z16402) pollen specific gene [Oryza sativa]
                  413137
Seq. No.
                  uC-osflcyp122b04b1
Seq. ID
Method
                  BLASTX
                  g2497953
NCBI GI
BLAST score
                  215
                  9.0e-18
E value
Match length
                  51
% identity
                  80
                  MOLYBDOPTERIN BIOSYNTHESIS CNX1 PROTEIN (MOLYBDENUM
NCBI Description
                  COFACTOR BIOSYNTHESIS ENZYME CNX1) >gi_1263314 (L47323)
                  molybdenum cofactor biosynthesis enzyme [Arabidopsis
                  thaliana] >gi 4469123 emb CAB38312 (AJ236870) molybdenum
                  cofactor biosynthesis enzyme [Arabidopsis thaliana]
                  413138
Seq. No.
                  uC-osflcyp122b05b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4544436
BLAST score
                  235
E value
                  2.0e-19
Match length
                  116
% identity
NCBI Description
                  (AC006592) anthocyanidin-3-glucoside rhamnosyltransferase,
                  3' partial [Arabidopsis thaliana]
```

53788

uC-osflcyp122b06b1

Match length

135

```
Method
                  BLASTX
                  g3953471
NCBI GI
                  559
BLAST score
                  2.0e-57
E value
                  153
Match length
                  67
% identity
                  (AC002328) F2202.16 [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  413140
                  uC-osflcyp122b07b1
Seq. ID
                  BLASTX
Method
                  g4929751
NCBI GI
                  202
BLAST score
                  1.0e-15
E value
Match length
                  98
% identity
                  42
                  (AF151899) CGI-141 protein [Homo sapiens]
NCBI Description
                  413141
Seq. No.
                  uC-osflcyp122b08b1
Seq. ID
                  BLASTX
Method
NCBI GI
                  g1076668
                  398
BLAST score
                  2.0e-38
E value
                  137
Match length
                  64
% identity
NCBI Description
                  NADH dehydrogenase (EC 1.6.99.3) - potato
                  >gi_639834_emb_CAA58823_ (X83999) NADH dehydrogenase
                   [Solanum tuberosum]
                   413142
Seq. No.
Seq. ID
                  uC-osflcyp122b09b1
Method
                  BLASTX
NCBI GI
                  g4887756
BLAST score
                  202
                  1.0e-15
E value
Match length
                  61
% identity
                   57
NCBI Description (AC006533) putative protein kinase [Arabidopsis thaliana]
                   413143
Seq. No.
Seq. ID
                  uC-osflcyp122b10b1
Method
                  BLASTX
NCBI GI
                   q4741844
                   643
BLAST score
                   2.0e-67
E value
Match length
                  141
% identity
NCBI Description (AF112964) small GTP-binding protein [Triticum aestivum]
                   413144
Seq. No.
Seq. ID
                  uC-osflcyp122b11b1
Method
                  BLASTX
NCBI GI
                   g2801536
BLAST score
                   387
E value
                   2.0e-37
```

```
% identity
                  (AF039531) lysophospholipase homolog [Oryza sativa]
NCBI Description
Seq. No.
                  413145
                  uC-osflcyp122c01b1
Seq. ID
                  BLASTX
Method
                  q4530585
NCBI GI
                  315
BLAST score
                  7.0e-29
E value
                  85
Match length
                  68
% identity
                  (AF130978) B12D protein [Ipomoea batatas]
NCBI Description
                  413146
Seq. No.
                  uC-osflcyp122c03b1
Seq. ID
Method
                  BLASTX
                  q3288883
NCBI GI
BLAST score
                  588
                  4.0e-65
E value
                  142
Match length
                   96
% identity
                  (AB015431) SAR DNA binding protein [Oryza sativa]
NCBI Description
                   413147
Seq. No.
                  uC-osflcyp122c06b1
Seq. ID
Method
                  BLASTX
                  q1363504
NCBI GI
BLAST score
                   538
                   3.0e-55
E value
Match length
                  116
                   91
% identity
NCBI Description aspartic proteinase (EC 3.4.-.-) L5 - rice (fragment)
                   413148
Seq. No.
                   uC-osflcyp122c07b1
Seq. ID
                   BLASTX
Method
NCBI GI
                   q3560531
BLAST score
                   745
E value
                   2.0e-84
                   155
Match length
                   100
% identity
                  (AF042332) cycloartenol-C24-methyltransferase [Oryza sativa
NCBI Description
                   subsp. japonica]
                   413149
Seq. No.
                   uC-osflcyp122c08b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   q4314378
BLAST score
                   241
                   4.0e-20
E value
                   90
Match length
                   53
% identity
NCBI Description
                   (AC006232) putative lipase [Arabidopsis thaliana]
                   >gi 5306262 gb AAD41994.1 AC006233 5 (AC006233) putative
                   lipase [Arabidopsis thaliana]
```

413150

Seq. No.

```
uC-osflcyp122c10b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g115787
BLAST score
                   485
E value
                   6.0e-49
                  112
Match length
                  87
% identity
                  CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I
NCBI Description
                  CAB-2) (LHCP) >qi 82461 pir S03706 chlorophyll a/b-binding
                  protein 2R precursor - rice >gi 20182 emb CAA32109
                   (X13909) chlorophyll a/b-binding preprotein (AA -28 to 235)
                   [Oryza sativa]
                   413151
Seq. No.
                  uC-osflcyp122c11b1
Seq. ID
                  BLASTX
Method
NCBI GI
                   q4160402
                   265
BLAST score
E value
                   4.0e-23
                   137
Match length
                   45
% identity
                   (AJ132240) eukaryotic translation initiation factor 5 [Zea
NCBI Description
                  mays]
                   413152
Seq. No.
                  uC-osflcyp122c12b1
Seq. ID
Method
                   BLASTX
                   q4835766
NCBI GI
BLAST score
                   268
                   2.0e-23
E value
Match length
                   60
                   83
% identity
                  (AC007202) Contains similarity to gb_AB017693 transfactor
NCBI Description
                   (WERBP-1) from Nicotiana tabacum. ESTs gb H39299,
                   gb T41875, gb H38232 and gb N38325 come from this gene.
                   [Arabidopsis thaliana]
Seq. No.
                   413153
Seq. ID
                   uC-osflcyp122d01b1
Method
                   BLASTX
NCBI GI
                   q5777632
                   269
BLAST score
                   2.0e-23
E value
Match length
                   169
                   33
% identity
                  (AJ245900) CAA303720.1 protein [Oryza sativa]
NCBI Description
                   413154
Seq. No.
                   uC-osflcyp122d02b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3236242
                   412
BLAST score
E value
                   3.0e-40
Match length
                   104
                   79
% identity
                  (AC004684) putative ribosomal protein L36 [Arabidopsis
NCBI Description
                   thaliana]
```

```
Seq. No.
                  413155
                  uC-osflcyp122d03b1
Seq. ID
                  BLASTX
Method
NCBI GI
                  q3582339
                  184
BLAST score
                  1.0e-13
E value
Match length
                  39
                  74
% identity
                  (AC005496) unknown protein [Arabidopsis thaliana]
NCBI Description
                  413156
Seq. No.
Seq. ID
                  uC-osflcyp122d04b1
                  BLASTX
Method
                  q3935181
NCBI GI
BLAST score
                  434
                  6.0e-43
E value
                  98
Match length
                  79
% identity
NCBI Description (AC004557) F17L21.24 [Arabidopsis thaliana]
                  413157
Seq. No.
Seq. ID
                  uC-osflcyp122d05b1
                  BLASTX
Method
                  q1814403
NCBI GI
                  616
BLAST score
                  3.0e-64
E value
                  131
Match length
                  87
% identity
                  (U84889) methionine synthase [Mesembryanthemum
NCBI Description
                  crystallinum]
                   413158
Seq. No.
                  uC-osflcyp122d06b1
Seq. ID
Method
                  BLASTX
NCBI GI
                   g4105561
BLAST score
                   324
                   5.0e-30
E value
Match length
                  86
% identity
                   78
NCBI Description (AF047444) ribulose-5-phosphate-3-epimerase [Oryza sativa]
                   413159
Seq. No.
                   uC-osflcyp122d07b1
Seq. ID
Method
                   BLASTX
                   g466172
NCBI GI
                   566
BLAST score
                   2.0e-58
E value
                   113
Match length
% identity
                   97
NCBI Description GTP-BINDING PROTEIN YPTM2 >gi_283056_pir__B38202 ypt family
                   - maize >gi 287835 emb CAA44919 (X63278) yptm2 [Zea mays]
                   413160
Seq. No.
                   uC-osflcyp122d08b1
Seq. ID
Method
                   BLASTX
                   g1729971
NCBI GI
```

Seq. No.

Seq. ID Method

413165

BLASTX

uC-osflcyp122e04b1

BLAST score 468 E value 8.0e-47 Match length 124 % identity 77 NCBI Description TONOPLAST INTRINSIC PROTEIN, GAMMA (GAMMA TIP) (AQUAPORIN-TIP) >gi 1076745 pir S52004 gamma-Tip protein rice >gi_473997_dbj_BAA05017_ (D25534) gamma-Tip [Oryza sativa] 413161 Seq. No. Seq. ID uC-osflcyp122d09b1 Method BLASTX NCBI GI g4314378 BLAST score 332 E value 6.0e-31 Match length 149 % identity 45 (AC006232) putative lipase [Arabidopsis thaliana] NCBI Description >qi 5306262 gb AAD41994.1 AC006233 5 (AC006233) putative lipase [Arabidopsis thaliana] 413162 Seq. No. uC-osflcyp122d10b1 Seq. ID Method BLASTX NCBI GI g400879 BLAST score 496 4.0e-50 E value 149 Match length % identity 66 NCBI Description PHOTOSYSTEM I REACTION CENTRE SUBUNIT PSAN PRECURSOR (PSI-N) >qi 479690 pir S35159 photosystem I chain psaN barley >gi 19095 emb CAA47056 (X66428) photosystem I subunit N [Hordeum vulgare] Seq. No. 413163 uC-osflcyp122e01b1 Seq. ID Method BLASTX NCBI GI g4567305 BLAST score 501 1.0e-50 E value Match length 152 % identity 61 NCBI Description (AC005956) hypothetical protein [Arabidopsis thaliana] 413164 Seq. No. uC-osflcyp122e03b1 Seq. ID Method BLASTX NCBI GI g5689413 BLAST score 170 6.0e-12 E value 94 Match length % identity 39 (AB028961) KIAA1038 protein [Homo sapiens] NCBI Description

NCBI GI g2244973 BLAST score 152 9.0e-10 E value Match length 150 % identity 31 (Z97340) transcription factor like protein [Arabidopsis NCBI Description thaliana] Seq. No. 413166 Seq. ID uC-osflcyp122e05b1 Method BLASTX NCBI GI q1170937 BLAST score 360 4.0e-34 E value Match length 66 100 % identity NCBI Description S-ADENOSYLMETHIONINE SYNTHETASE 1 (METHIONINE ADENOSYLTRANSFERASE 1) (ADOMET SYNTHETASE 1) >gi_450549_emb_CAA81481_ (Z26867) S-adenosyl methionine synthetase [Oryza sativa] 413167 Seq. No. uC-osflcyp122e06b1 Seq. ID Method BLASTN g3746580 NCBI GI BLAST score 68 1.0e-29 E value Match length 259 % identity 82 NCBI Description Oryza sativa glutathione S-transferase II mRNA, complete Seq. No. 413168 uC-osflcyp122e08b1 Seq. ID Method BLASTN NCBI GI g857573 BLAST score 239 1.0e-132 E value Match length 246 % identity 100 NCBI Description Oryza sativa vacuolar H+-ATPase (vatp-P1) mRNA, complete cds Seq. No. 413169 Seq. ID uC-osflcyp122e09b1 Method BLASTX NCBI GI g2286109 BLAST score 374 E value 7.0e-36

Match length 81 % identity 91

NCBI Description (U78782) MADS box protein [Oryza sativa]

413170 Seq. No.

Seq. ID uC-osflcyp122e11b1

Method BLASTX NCBI GI g82734

```
BLAST score
                  521
                  3.0e-53
E value
Match length
                  110
% identity
                  28
                  ubiquitin precursor - maize (fragment)
NCBI Description
                  >gi 226763 prf 1604470A poly-ubiquitin [Zea mays]
Seq. No.
                  413171
Seq. ID
                  uC-osflcyp122f02b1
                  BLASTX
Method
NCBI GI
                  g4522012
BLAST score
                   433
E value
                   1.0e-42
Match length
                  115
                   69
% identity
                  (AC007069) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   413172
Seq. No.
Seq. ID
                  uC-osflcyp122f03b1
                   BLASTX
Method
NCBI GI
                   q115874
BLAST score
                   541
                   2.0e-68
E value
Match length
                   167
% identity
                   78
                  SERINE CARBOXYPEPTIDASE III PRECURSOR (CP-WIII) >gi_170704
NCBI Description
                   (J02817) gibberellin responsive protein [Triticum aestivum]
Seq. No.
                   413173
                   uC-osflcyp122f05b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g671740
BLAST score
                   409
E value
                   7.0e-40
Match length
                   75
                   99
% identity
                  (X84730) ribulose-bisphosphate carboxylase [synthetic
NCBI Description
                   construct]
                   413174
Seq. No.
                   uC-osflcyp122f09b1
Seq. ID
Method
                   BLASTX
                   q5295980
NCBI GI
BLAST score
                   328
E value
                   1.0e-57
                   117
Match length
                   97
% identity
                  (AB003323) MADS box-like protein [Oryza sativa]
NCBI Description
Seq. No.
                   413175
                   uC-osflcyp122f10b1
Seq. ID
                   BLASTX
Method
NCBI GI
                   g2407281
                   714
BLAST score
                   1.0e-75
E value
                   134
Match length
                   99
% identity
```

```
(AF017363) ribulose 1,5-bisphosphate carboxylase small
NCBI Description
                  subunit [Oryza sativa]
                  413176
Seq. No.
                  uC-osflcyp122g01b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3687224
                  317
BLAST score
                  4.0e-29
E value
Match length
                  84
% identity
                  73
                  (AC005169) putative N-acetyl-gamma-glutamyl-phosphate
NCBI Description
                  reductase [Arabidopsis thaliana]
Seq. No.
                  413177
Seq. ID
                  uC-osflcyp122g02b1
Method
                  BLASTX
NCBI GI
                  g5880464
BLAST score
                  452
E value
                   6.0e-45
Match length
                  140
                   59
% identity
                  (AF088901) actin bundling protein ABP135 [Lilium
NCBI Description
                  longiflorum]
                   413178
Seq. No.
                  uC-osflcyp122g03b1
Seq. ID
Method
                  BLASTX
                  g3063465
NCBI GI
                  150
BLAST score
                   2.0e-09
E value
                   99
Match length
                   40
% identity
                  (AC003981) F22013.27 [Arabidopsis thaliana]
NCBI Description
                   413179
Seq. No.
                   uC-osflcyp122g04b1
Seq. ID
                   BLASTX
Method
NCBI GI
                   g2773154
                   301
BLAST score
                   3.0e-27
E value
Match length
                   134
                   48
% identity
                  (AF039573) abscisic acid- and stress-inducible protein
NCBI Description
                   [Oryza sativa]
                   413180
Seq. No.
                   uC-osflcyp122g05b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2827143
                   767
BLAST score
                   8.0e-82
E value
                   168
Match length
                   87
% identity
                  (AF027174) cellulose synthase catalytic subunit
NCBI Description
                   [Arabidopsis thaliana]
```

```
413181
Seq. No.
Seq. ID
                  uC-osflcyp122g06b1
                  BLASTX
Method
                  g4263711
NCBI GI
BLAST score
                  492
                  1.0e-49
E value
                  147
Match length
                  63
% identity
                   (AC006223) putative CCR4-associated transcription factor
NCBI Description
                   [Arabidopsis thaliana]
                  413182
Seq. No.
Seq. ID
                  uC-osflcyp122g08b1
                  BLASTX
Method
                  q4455309
NCBI GI
BLAST score
                   354
                   2.0e-33
E value
                   124
Match length
                   60
% identity
                  (AL035528) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   413183
Seq. No.
                   uC-osflcyp122g10b1
Seq. ID
                   BLASTX
Method
                   q2130080
NCBI GI
BLAST score
                   375
                   5.0e-38
E value
                   103
Match length
                   79
% identity
                   Nramp1 protein - rice >gi_1470320_bbs 177441 (S81897)
NCBI Description
                   OsNramp1=Nramp1 homolog/Bcg product homolog [Oryza sativa,
                   indica, cv. IR 36, etiolated shoots, Peptide, 517 aa]
                   [Oryza sativa] >qi 2231132 (L41217) integral membrane
                   protein [Oryza sativa]
                   413184
Seq. No.
                   uC-osflcyp122g11b1
Seq. ID
                   BLASTX
Method
                   g3334276
NCBI GI
BLAST score
                   244
                   2.0e-20
E value
Match length
                   115
                   44
% identity
                   AUTOANTIGEN NGP-1 >qi 179285 gb AAC37588.1_ (L05425)
NCBI Description
                   nucleolar GTPase [Homo sapiens]
                   413185
Seq. No.
                   uC-osflcyp122g12b1
Seq. ID
                   BLASTX
Method
NCBI GI
                   g4321401
BLAST score
                   280
                   4.0e-25
E value
                   89
Match length
                   33
 % identity
                  (AF047353) LIM domain protein PLIM-2 [Helianthus annuus]
NCBI Description
                   413186
 Seq. No.
```

Seq. ID uC-osflcyp122h01b1 Method BLASTN NCBI GI q600766 BLAST score 59 E value 3.0e-24 Match length 74 96 % identity NCBI Description Oryza sativa cyclophilin 2 (Cyp2) gene, complete cds 413187 Seq. No. Seq. ID uC-osflcyp122h02b1 BLASTX Method NCBI GI g2160322 BLAST score 407 1.0e-39 E value Match length 86 % identity 91 NCBI Description (D16139) cytokinin binding protein CBP57 [Nicotiana sylvestris] 413188 Seq. No. uC-osflcyp122h04b1 Seq. ID BLASTX Method NCBI GI g4490316 BLAST score 233 3.0e-19 E value Match length 154 % identity NCBI Description (AL035678) nucellin-like protein [Arabidopsis thaliana] Seq. No. 413189 uC-osflcyp122h05b1 Seq. ID Method BLASTX NCBI GI q416583 BLAST score 177 1.0e-12 E value 137 Match length 36 % identity ACETYL-COENZYME A SYNTHETASE (ACETATE--COA LIGASE) NCBI Description (ACYL-ACTIVATING ENZYME) >gi_396404 (U00006) acetyl-CoA sythetase [Escherichia coli] >gi_1790505 (AE000480) acetyl-CoA synthetase [Escherichia coli] 413190 Seq. No. uC-osflcyp122h06b1 Seq. ID BLASTX Method g2995990 NCBI GI 289 BLAST score E value 9.0e-26 125 Match length 49 % identity

(AF053746) dormancy-associated protein [Arabidopsis NCBI Description thaliana] >gi_2995992 (AF053747) dormancy-associated

protein [Arabidopsis thaliana]

Seq. No. 413191

uC-osflcyp122h08b1 Seq. ID

```
Method
                   BLASTX
NCBI GI
                   g2130069
BLAST score
                   879
                   6.0e-95
E value
Match length
                   165
                   98
% identity
NCBI Description
                   catalase (EC 1.11.1.6) catA - rice
                   >qi 1261858 dbj BAA06232 (D29966) catalase [Oryza sativa]
Seq. No.
                   413192
                   uC-osflcyp122h10b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   q435942
BLAST score
                   425
E value
                   9.0e-42
Match length
                   77
% identity
                   99
NCBI Description (U04295) DNA-binding factor of bZIP class [Oryza sativa]
Seq. No.
                   413193
Seq. ID
                   uC-osflcyp122h11b1
Method
                   BLASTX
NCBI GI
                   q6016691
BLAST score
                   381
                   1.0e-36
E value
Match length
                   102
                   68
% identity
NCBI Description (AC009991) unknown protein [Arabidopsis thaliana]
Seq. No.
                   413194
                   uC-osflcyp123a01b1
Seq. ID
Method
                   BLASTX
                   q3075488
NCBI GI
BLAST score
                   592
                   2.0e-61
E value
Match length
                   133
                   84
% identity
NCBI Description (AF058796) chlorophyll a/b-binding protein [Oryza sativa]
                   413195
Seq. No.
                   uC-osflcyp123a03b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g1346396
BLAST score
                   168
E value
                   1.0e-11
Match length
                   80
                   45
% identity
NCBI Description PUTATIVE RECEPTOR PROTEIN KINASE ZMPK1 PRECURSOR
                   >gi_100913_pir__S10930 probable receptor protein kinase (EC
                   2.7.1.-) precursor - maize >gi_22432_emb_CAA36611_ (X52384)
                   precursor protein (AA -26 to 791) [Zea mays]
                   >gi_22436_emb_CAA47962 (X67733) receptor-like protein
kinase [Zea mays] >gi_226927_prf__1611404A receptor protein
                   kinase [Zea mays]
Seq. No.
                   413196
                   uC-osflcyp123a04b1
Seq. ID
```

```
BLASTX
Method
                  g1841894
NCBI GI
BLAST score
                  295
                  8.0e-27
E value
                  100
Match length
                  61
% identity
                  (D78136) Glutathione Reductase [Oryza sativa]
NCBI Description
                  413197
Seq. No.
Seq. ID
                  uC-osflcyp123a05b1
Method
                  BLASTX
                  q3894172
NCBI GI
                  151
BLAST score
                  5.0e-10
E value
                  93
Match length
% identity
                  33
                  (ACO05312) putative cinnamoyl-CoA reductase [Arabidopsis
NCBI Description
                  thaliana]
                  413198
Seq. No.
Seq. ID
                  uC-osflcyp123a07b1
Method
                  BLASTX
NCBI GI
                  q119150
                  619
BLAST score
                  1.0e-64
E value
                  134
Match length
                  90
% identity
                  ELONGATION FACTOR 1-ALPHA (EF-1-ALPHA)
NCBI Description
                  >gi_82081_pir__S10507 translation elongation factor eEF-1
                  alpha chain - tomato >gi 19273 emb CAA32618 (X14449) EF
                  1-alpha (AA 1-448) [Lycopersicon esculentum]
                  >gi 295810 emb CAA37212 (X53043) elongation factor 1-alpha
                  [Lycopersicon esculentum]
                  413199
Seq. No.
Seq. ID
                  uC-osflcyp123a10b1
                  BLASTX
Method
NCBI GI
                  q320618
BLAST score
                  490
                  1.0e-49
E value
                  123
Match length
% identity
                  chlorophyll a/b-binding protein I precursor - rice
NCBI Description
                  >gi_218172_dbj_BAA00536_ (D00641) type I light-harvesting
                  chlorophyll a/b-binding protein [Oryza sativa]
                  >gi 227611 prf 1707316A chlorophyll a/b binding protein 1
                  [Oryza sativa]
                  413200
Seq. No.
                  uC-osflcyp123a12b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4587556
BLAST score
                  588
E value
                  6.0e-61
Match length
                  153
% identity
                  (AC006577) Similar to gi 1653162 (p)ppGpp
NCBI Description
```

3-pyrophosphohydrolase from Synechocystis sp genome gb_D90911. EST gb_W43807 comes from this gene. [Arabidopsis thaliana]

Seq. No. 413201

Seq. ID uC-osflcyp123b02b1

Method BLASTX
NCBI GI g1077569
BLAST score 173 \
E value 2.0e-12
Match length 87
% identity 41

NCBI Description probable membrane protein YDR109c - yeast (Saccharomyces

cerevisiae) >gi_747884_emb_CAA88663_ (Z48758) unknown

[Saccharomyces cerevisiae]

Seq. No. 413202

Seq. ID uC-osflcyp123b03b1

Method BLASTX
NCBI GI g6093778
BLAST score 602
E value 2.0e-62
Match length 131
% identity 93

NCBI Description PROTEASOME COMPONENT C3 (MACROPAIN SUBUNIT C3)

(MULTICATALYTIC ENDOPEPTIDASE COMPLEX SUBUNIT C3) >gi_2511574_emb_CAA73619.1_ (Y13176) multicatalytic

endopeptidase [Arabidopsis thaliana] >gi_3421075 (AF043520)

20S proteasome subunit PAB1 [Arabidopsis thaliana]

>gi_4966368_gb_AAD34699.1_AC006341_27 (AC006341) Identical

to gb Y13176 Arabidopsis thaliana mRNA for proteasome

subunit prc3. ESTs gb_H36972, gb_T22551 and gb_T13800 come

from this gene

Seq. No. 413203

Seq. ID uC-osflcyp123b08b1

Method BLASTX
NCBI GI g2570505
BLAST score 227
E value 8.0e-19
Match length 74
% identity 72

NCBI Description (AF022735) proteasome component [Oryza sativa]

Seq. No. 413204

Seq. ID uC-osflcyp123b09b1

Method BLASTX
NCBI GI g1173347
BLAST score 385
E value 2.0e-37
Match length 101
% identity 77

NCBI Description SEDOHEPTULOSE-1,7-BISPHOSPHATASE, CHLOROPLAST PRECURSOR

(SEDOHEPTULOSE-BISPHOSPHATASE) (SBPASE) (SED(1,7)P2ASE) >gi_100803_pir__S23452 sedoheptulose-bisphosphatase (EC 3.1.3.37) precursor - wheat >gi_14265_emb_CAA46507_(X65540) sedoheptulose-1,7-bisphosphatase [Triticum

Seq. ID

Method

aestivum]

Seq. No. 413205 Seq. ID uC-osflcyp123b10b1 Method BLASTX NCBI GI g3023713 647 BLAST score E value 5.0e-68Match length 125 % identity 99 NCBI Description ENOLASE (2-PHOSPHOGLYCERATE DEHYDRATASE) (2-PHOSPHO-D-GLYCERATE HYDRO-LYASE) (OSE1) >gi_780372 (U09450) enolase [Oryza sativa] 413206 Seq. No. Seq. ID uC-osflcyp123b11b1 Method BLASTX g2104681 NCBI GI BLAST score 159 E value 9.0e-11 Match length 60 60 % identity NCBI Description (X97907) transcription factor [Vicia faba] Seq. No. 413207 Seq. ID uC-osflcyp123c01b1 BLASTX Method NCBI GI g2293332 BLAST score 307 5.0e-28 E value Match length 95 63 % identity NCBI Description (AF011338) unknown [Dictyostelium discoideum] 413208 Seq. No. Seq. ID uC-osflcyp123c02b1 Method BLASTX NCBI GI g2208988 BLAST score 176 E value 1.0e-12 Match length 66 % identity 56 NCBI Description (Y10117) signal recognition particle subunit 9 [Zea mays] Seq. No. 413209 Seq. ID uC-osflcyp123c03b1 Method BLASTN NCBI GI g2208987 71 BLAST score 2.0e-31 E value Match length 203 % identity 83 NCBI Description Z.mays mRNA for signal recognition particle subunit 413210 Seq. No.

53802

uC-osflcyp123c05b1

BLASTN

Match length

44

```
NCBI GI
                  q5410347
                  95
BLAST score
                  1.0e-45
E value
Match length
                  409
% identity
                  87
NCBI Description Sorghum bicolor BAC clone 110K5, partial sequence
                  413211
Seq. No.
                  uC-osflcyp123c06b1
Seq. ID
Method
                  BLASTN
                  g218209
NCBI GI
BLAST score
                  176
E value
                  3.0e-94
                  240
Match length
                  94
% identity
NCBI Description
                  Oryza sativa mRNA for the small subunit of
                  ribulose-1,5-bisphosphate carboxylase, complete cds, clone
                  pOSSS2106
                  413212
Seq. No.
Seq. ID
                  uC-osflcyp123c08b1
                  BLASTX
Method
                  g2208988
NCBI GI
                  399
BLAST score
E value
                  1.0e-38
                  91
Match length
% identity
                  81
                 (Y10117) signal recognition particle subunit 9 [Zea mays]
NCBI Description
                  413213
Seq. No.
                  uC-osflcyp123c09b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2829923
BLAST score
                  140
                  5.0e-09
E value
Match length
                  45
% identity
                  56
NCBI Description
                  (AC002291) Similar to uridylyl transferases [Arabidopsis
                  thaliana]
Seq. No.
                   413214
Seq. ID
                  uC-osflcyp123c10b1
Method
                  BLASTX
NCBI GI
                  q5912299
BLAST score
                  490
                  2.0e-49
E value
Match length
                  113
% identity
NCBI Description
                  (AJ133787) gigantea homologue [Oryza sativa]
Seq. No.
                   413215
Seq. ID
                  uC-osflcyp123d05b1
Method
                  BLASTX
NCBI GI
                  g4874286
BLAST score
                  202
                   4.0e-16
E value
```

BLAST score

E value

645

2.0e-67

% identity (AC007212) putative MAP kinase 7 [Arabidopsis thaliana] NCBI Description 413216 Seq. No. uC-osflcyp123d10b1 Seq. ID BLASTX Method q417154 NCBI GI 364 BLAST score E value 4.0e-35 84 Match length 87 % identity HEAT SHOCK PROTEIN 82 >gi_100685_pir__S25541 heat shock NCBI Description protein 82 - rice (strain Taichung Native One) >gi_20256_emb_CAA77978_ (Z11920) heat shock protein 82 (HSP82) [Oryza sativa] 413217 Seq. No. uC-osflcyp123e01b1 Seq. ID Method BLASTN NCBI GI g2894376 49 BLAST score 2.0e-18 E value 81 Match length % identity NCBI Description Hordeum vulgare DNA for chromosome 4H Seq. No. 413218 uC-osflcyp123e02b1 Seq. ID Method BLASTX NCBI GI g5922612 BLAST score 300 5.0e-27 E value Match length 164 42 % identity NCBI Description (AP000492) EST AU078118(E3904) corresponds to a region of the predicted gene.; similar to Arabidopsis thaliana BAC IG002P16; No definition line found. (AF007270) [Oryza sativa] 413219 Seq. No. Seq. ID uC-osflcyp123e03b1 Method BLASTX NCBI GI g5702186 BLAST score 390 E value 1.0e-37 Match length 101 77 % identity (AF106085) 4-coumarate:CoA ligase 2 [Arabidopsis thaliana] NCBI Description >gi_5702188_gb_AAD47193.1_AF106086_1 (AF106086) 4-coumarate:CoA ligase 2 [Arabidopsis thaliana] Seq. No. 413220 uC-osflcyp123e04b1 Seq. ID BLASTX Method NCBI GI g2943792

162 Match length 72 % identity (AB006809) PV72 [Cucurbita sp.] NCBI Description Seq. No. 413221 uC-osflcyp123e05b1 Seq. ID Method BLASTX NCBI GI q730526 BLAST score 550 E value 2.0e-56 137 Match length 80 % identity 60S RIBOSOMAL PROTEIN L13 (BBC1 PROTEIN HOMOLOG) NCBI Description >gi_480787_pir__S37271 ribosomal protein L13 - Arabidopsis thaliana >gi 404166 emb CAA53005 (X75162) BBC1 protein [Arabidopsis thaliana] 413222 Seq. No. uC-osflcyp123e10b1 Seq. ID Method BLASTX g4337210 NCBI GI BLAST score 442 9.0e-44E value 170 Match length % identity 50 NCBI Description (AC006403) hypothetical protein [Arabidopsis thaliana] 413223 Seq. No. uC-osflcyp123f08b1 Seq. ID Method BLASTN NCBI GI q5360220 40 BLAST score 4.0e-13 E value 60 Match length 92 % identity NCBI Description Oryza sativa mRNA for nuclear transport factor 2 (NTF2), complete cds Seq. No. 413224 uC-osflcyp123q06b1 Seq. ID Method BLASTN NCBI GI g607894 BLAST score 34 7.0e-10 E value Match length 42 % identity 95 NCBI Description Oryza sativa IR54 anther specific (RTS2) gene, complete cds Seq. No. 413225 Seq. ID uC-osflcyp123h02b1 Method BLASTN NCBI GI g20365 BLAST score 50 2.0e-19 E value Match length 102

53805

88

NCBI Description O.sativa RSsl gene for sucrose synthase

% identity

```
Seq. No.
                  413226
                  uC-osflcyp123h10b1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g20177
                  33
BLAST score
                  7.0e-10
E value
                  49
Match length
                  92
% identity
                  Rice cab1R gene for light harvesting chlorophyll
NCBI Description
                  a/b-binding protein
Seq. No.
                  413227
                  uC-osflcyp124a05b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g419757
BLAST score
                  535
                   9.0e-55
E value
                   140
Match length
                   74
% identity
                  ketol-acid reductoisomerase (EC 1.1.1.86) precursor -
NCBI Description
                  Arabidopsis thaliana
                   413228
Seq. No.
                  uC-osflcyp124a06b1
Seq. ID
Method
                  BLASTX
NCBI GI
                   g1617213
BLAST score
                   185
                   1.0e-13
E value
                   71
Match length
                   54
% identity
                  (Z72487) CP12 [Spinacia oleracea]
NCBI Description
                   413229
Seq. No.
                   uC-osflcyp124a08b1
Seq. ID
Method
                  BLASTX
NCBI GI
                   g2194132
BLAST score
                   332
E value
                   6.0e-31
Match length
                   105
                   66
% identity
NCBI Description
                  (AC002062) No definition line found [Arabidopsis thaliana]
                   413230
Seq. No.
Seq. ID
                   uC-osflcyp124a09b1
Method
                   BLASTX
NCBI GI
                   g2245125
BLAST score
                   168
E value
                   1.0e-11
                   74
Match length
% identity
                  (Z97343) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   413231
                   uC-osflcyp124a10b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3023816
```

BLAST score 506 E value 2.0e-51 Match length 112 % identity 88

NCBI Description GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC

>gi 968996 (U31676) glyceraldehyde-3-phosphate

dehydrogenase [Oryza sativa]

Seq. No. 413232

Seq. ID uC-osflcyp124a11b1

Method BLASTX
NCBI GI g6056388
BLAST score 159
E value 4.0e-23
Match length 97
% identity 65

NCBI Description (AC009324) 26S proteasome ATPase subunit [Arabidopsis

thaliana]

Seq. No. 413233

Seq. ID uC-osflcyp124b01b1

Method BLASTX
NCBI GI g548770
BLAST score 590
E value 4.0e-61
Match length 117
% identity 95

NCBI Description 60S RIBOSOMAL PROTEIN L3 >gi_481228_pir__S38359 ribosomal

protein L3 - rice >gi_303853_dbj_BAA02155_ (D12630)

ribosomal protein L3 [Oryza sativa]

Seq. No. 413234

Seq. ID uC-osflcyp124b03b1

Method BLASTX
NCBI GI g1323748
BLAST score 233
E value 3.0e-19
Match length 103
% identity 50

NCBI Description (U32430) thiol protease [Triticum aestivum]

Seq. No. 413235

Seq. ID uC-osflcyp124b08b1

Method BLASTX
NCBI GI g3914557
BLAST score 584
E value 1.0e-60
Match length 112
% identity 97

NCBI Description RAS-RELATED PROTEIN RAB7 (POSSIBLE APOSPORY-ASSOCIATED

PROTEIN) >gi_1155265 (U40219) possible apospory-associated

protein [Pennisetum ciliare]

Seq. No. 413236

Seq. ID uC-osflcyp124b10b1

Method BLASTX NCBI GI q5823020

BLAST score

E value

276

3.0e-41

```
BLAST score
                   287
E value
                   1.0e-25
Match length
                  118
% identity
                   50
NCBI Description
                  (AF089849) senescence-specific cysteine protease [Brassica
                  napus]
Seq. No.
                   413237
Seq. ID
                  uC-osflcyp124b12b1
Method
                  BLASTX
NCBI GI
                  q4204294
BLAST score
                  294
E value
                   1.0e-26
Match length
                  109
% identity
                   61
NCBI Description
                  (AC003027) lcl prt seq No definition line found
                   [Arabidopsis thaliana]
Seq. No.
                  413238
Seq. ID
                  uC-osflcyp124c03b1
Method
                  BLASTN
NCBI GI
                  g1532047
BLAST score
                  232
E value
                  1.0e-127
Match length
                  408
% identity
                  89
NCBI Description O.sativa mRNA for S-adenosylmethionine decarboxylase
Seq. No.
                  413239
Seq. ID
                  uC-osflcyp124c04b1
Method
                  BLASTX
NCBI GI
                  g544242
BLAST score
                  389
E value
                  9.0e-52
Match length
                  145
                  78
% identity
NCBI Description
                  ENDOPLASMIN HOMOLOG PRECURSOR (GRP94 HOMOLOG)
                  >gi 485498 pir S33533 heat shock protein 90 homolog
                  precursor - barley >gi_22652_emb_CAA48143_ (X67960) GRP94
                  homologue [Hordeum vulgare]
Seq. No.
                  413240
Seq. ID
                  uC-osflcyp124c05b1
Method
                  BLASTX
NCBI GI
                  g4753658
BLAST score
                  203
E value
                  3.0e-16
                  53
Match length
% identity
NCBI Description (AL049751) putative protein [Arabidopsis thaliana]
Seq. No.
                  413241
Seq. ID
                  uC-osflcyp124c07b1
Method
                  BLASTX
NCBI GI
                  g2565305
```

```
Match length
                   117
% identity
                   77
NCBI Description
                   (AF024589) glycine decarboxylase P subunit [Hordeum sp. x
                   Triticum sp.]
Seq. No.
                   413242
Seq. ID
                   uC-osflcyp124c08b1
Method
                   BLASTX
NCBI GI
                   g1724114
BLAST score
                   413
E value
                   1.0e-49
Match length
                   164
                   70
% identity
NCBI Description (U80041) Af10-protein [Avena fatua]
Seq. No.
                   413243
Seq. ID
                   uC-osflcyp124c11b1
Method
                  BLASTX
NCBI GI
                   g1617197
BLAST score
                   180
E value
                   1.0e-21
Match length
                  73
% identity
                   77
NCBI Description (Z72488) CP12 [Nicotiana tabacum]
Seq. No.
                   413244
Seq. ID
                  uC-osflcyp124d01b1
Method
                  BLASTX
NCBI GI
                  g5441893
BLAST score
                   486
E value
                   6.0e-49
Match length
                  139
% identity
                  73
                  (AP000367) ESTs C99174(E10437), D22295(C10709) correspond to
NCBI Description
                  a region of the predicted gene.; Similar to Arabidopsis
                  thaliana BAC genomic sequence. (AC005314) [Oryza sativa]
Seq. No.
                   413245
Seq. ID
                  uC-osflcyp124d03b1
Method
                  BLASTX
NCBI GI
                  g4455208
BLAST score
                  274
E value
                  1.0e-24
Match length
                  91
% identity
NCBI Description (AL035440) putative protein [Arabidopsis thaliana]
Seq. No.
                  413246
Seq. ID
                  uC-osflcyp124d06b1
Method
                  BLASTX
NCBI GI
                  g2498586
BLAST score
                  429
E value
                  9.0e-43
Match length
                  121
% identity
                  81
NCBI Description MAJOR POLLEN ALLERGEN ORY S 1 PRECURSOR (ORY S I)
```

>gi_1173557 (U31771) Ory s 1 [Oryza sativa] 53809

```
Seq. No.
                  413247
Seq. ID
                  uC-osflcyp124d09b1
Method
                  BLASTX
                  q4539347
NCBI GI
BLAST score
                  228
E value
                  2.0e-19
Match length
                  62
                  73
% identity
NCBI Description (AL035539) putative growth regulator protein [Arabidopsis
                  thaliana]
Seq. No.
                  413248
Seq. ID
                  uC-osflcyp124d10b1
Method
                  BLASTX
NCBI GI
                  g3386621
BLAST score
                  287
E value
                  8.0e-26
                  77
Match length
                  74
% identity
NCBI Description (AC004665) unknown protein [Arabidopsis thaliana]
                  413249
Seq. No.
                  uC-osflcyp124d11b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1076511
BLAST score
                  303
E value
                  9.0e-28
Match length
                  78
                  82
% identity
NCBI Description
                  H+-transporting ATPase (EC 3.6.1.35) - kidney bean
                  >gi 758250 emb CAA59799 (X85804) H(+)-transporting ATPase
                  [Phaseolus vulgaris]
                  413250
Seq. No.
Seq. ID
                  uC-osflcyp124d12b1
Method
                  BLASTX
NCBI GI
                  q544242
BLAST score
                  236
E value
                  9.0e-20
Match length
                  79
% identity
                  63
NCBI Description
                  ENDOPLASMIN HOMOLOG PRECURSOR (GRP94 HOMOLOG)
                  >gi_485498_pir__S33533 heat shock protein 90 homolog
                  precursor - barley >gi_22652_emb_CAA48143_ (X67960) GRP94
                  homologue [Hordeum vulgare]
Seq. No.
                  413251
Seq. ID
                  uC-osflcyp124e01b1
Method
                  BLASTX
NCBI GI
                  q3367732
BLAST score
                  347
E value
                  1.0e-32
Match length
                  74
                  92
% identity
```

NCBI Description (Y17835) p7 protein [Phleum pratense]

Seq. No. 413252 Seq. ID

uC-osflcyp124e02b1 Method BLASTX

NCBI GI q4314378 BLAST score 274 E value 4.0e-24 Match length 130 % identity 42

NCBI Description (AC006232) putative lipase [Arabidopsis thaliana]

>gi_5306262_gb_AAD41994.1_AC006233_5 (AC006233) putative

lipase [Arabidopsis thaliana]

Seq. No. 413253

Seq. ID uC-osflcyp124e03b1

Method BLASTX NCBI GI g283008 774 BLAST score 1.0e-82 E value Match length 176 % identity 85

NCBI Description sucrose synthase (EC 2.4.1.13) - rice

>gi_20366_emb_CAA46017_ (X64770) sucrose synthase [Oryza

sativa]

Seq. No. 413254

Seq. ID uC-osflcyp124e07b1

Method BLASTX NCBI GI q3128186 BLAST score 251 E value 2.0e-21 Match length 74 % identity 68

NCBI Description (AC004521) hypothetical protein [Arabidopsis thaliana]

Seq. No. 413255

Seq. ID uC-osflcyp124e08b1

Method BLASTX NCBI GI g132105 BLAST score 715 E value 9.0e-76 Match length 153 89 % identity

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR

(RUBISCO SMALL SUBUNIT C) >gi_68094_pir_RKRZS9 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538

(D00643) small subunit of ribulose-1,5-bisphosphate

carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa] >gi 226375 prf 1508256A ribulose bisphosphate

carboxylase S [Oryza sativa]

Seq. No. 413256

Seq. ID uC-osflcyp124e09b1

Method BLASTX NCBI GI g5441893 BLAST score 459

9.0e-48 E value 150 Match length 73 % identity

NCBI Description (AP000367) ESTs C99174(E10437), D22295(C10709) correspond to a region of the predicted gene.; Similar to Arabidopsis

thaliana BAC genomic sequence. (AC005314) [Oryza sativa]

413257 Seq. No.

uC-osflcyp124e11b1 Seq. ID

Method BLASTX NCBI GI g4325371 BLAST score 308 E value 4.0e-28 Match length 142 48 % identity

NCBI Description (AF128396) contains similarity to Medicago truncatula N7

protein (GB:Y17613) [Arabidopsis thaliana]

413258 Seq. No.

Seq. ID uC-osflcyp124e12b1

Method BLASTN NCBI GI g4097337 BLAST score 254 E value 1.0e-140 Match length 340 99 % identity

NCBI Description Oryza sativa metallothionein-like protein mRNA, complete

413259 Seq. No.

Seq. ID uC-osflcyp124f05b1

Method BLASTX NCBI GI q2244996 BLAST score 386 E value 4.0e-37 Match length 168

% identity 42

NCBI Description (Z97341) salt-inducible protein homolog [Arabidopsis

thaliana]

Seq. No. 413260

Seq. ID uC-osflcyp124f06b1

Method BLASTX NCBI GI g4455208 BLAST score 289 E value 6.0e-26Match length 117 57 % identity

NCBI Description (AL035440) putative protein [Arabidopsis thaliana]

Seq. No. 413261

Seq. ID uC-osflcyp124f07b1

Method BLASTX NCBI GI g3023816 BLAST score 519 E value 8.0e-53 Match length 109

```
% identity
                  92
NCBI Description
                  GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC
                  >gi_968996 (U31676) glyceraldehyde-3-phosphate
                  dehydrogenase [Oryza sativa]
Seq. No.
                  413262
Seq. ID
                  uC-osflcyp124f08b1
Method
                  BLASTX
NCBI GI
                  q3860262
BLAST score
                  175
E value
                  7.0e-13
Match length
                  48
% identity
                  69
NCBI Description (AC005824) unknown protein [Arabidopsis thaliana]
                  413263
Seq. No.
Seq. ID
                  uC-osflcyp124f11b1
Method
                  BLASTX
NCBI GI
                  g170031
BLAST score
                  407
E value
                  9.0e-40
                  133
Match length
% identity
                  60
NCBI Description (M10594) nodulin 35 [Glycine max]
Seq. No.
                  413264
Seq. ID
                  uC-osflcyp124g01b1
                  BLASTX
Method
NCBI GI
                  g1321661
BLAST score
                  259
E value
                  8.0e-23
Match length
                  58
% identity
                  90
NCBI Description (D45423) ascorbate peroxidase [Oryza sativa]
Seq. No.
                  413265
Seq. ID
                  uC-osflcyp124g09b1
Method
                  BLASTX
NCBI GI
                  q115813
BLAST score
                  143
E value
                  2.0e-09
Match length
                  61
% identity
                  54
NCBI Description CHLOROPHYLL A-B BINDING PROTEIN 8 PRECURSOR (LHCI TYPE III
                  CAB-8) >gi_19182_emb_CAA33330_ (X15258) Type III
                  chlorophyll a/b-binding protein [Lycopersicon esculentum]
Seq. No.
                  413266
Seq. ID
                  uC-osflcyp124g10b1
Method
                  BLASTX
NCBI GI
                  g2894378
BLAST score
                  199
E value
                  1.0e-15
Match length
                  56
% identity
                  75
```

NCBI Description (Y14573) putative ribophorin I homologue [Hordeum vulgare]

NCBI GI

BLAST score

q129916

442

```
Seq. No.
                   413267
Seq. ID
                  uC-osflcyp124g11b1
Method
                  BLASTN
NCBI GI
                  g2641618
BLAST score
                  58
E value
                  4.0e-24
Match length
                  66
% identity
                  97
NCBI Description Zea mays ubiquitin-conjugating enzyme protein E2 (ubc7)
                  mRNA, complete cds
                  413268
Seq. No.
Seq. ID
                  uC-osflcyp124g12b1
Method
                  BLASTX
NCBI GI
                  g4733891
BLAST score
                  467
E value
                  8.0e-47
Match length
                  132
% identity
                  76
NCBI Description (AF104924) unconventional myosin heavy chain [Zea mays]
Seq. No.
                  413269
Seq. ID
                  uC-osflcyp124h01b1
Method
                  BLASTX
NCBI GI
                  q4490332
BLAST score
                  272
E value
                  5.0e-24
                  91
Match length
% identity
                  58
NCBI Description (AL035656) putative protein [Arabidopsis thaliana]
                  413270
Seq. No.
Seq. ID
                  uC-osflcyp125a02b1
Method
                  BLASTX
NCBI GI
                  q3298540
BLAST score
                  505
E value
                  4.0e-51
Match length
                  144
% identity
                  69
NCBI Description (AC004681) unknown protein [Arabidopsis thaliana]
                  413271
Seq. No.
Seq. ID
                  uC-osflcyp125a03b1
Method
                  BLASTX
                  q3850621
NCBI GI
BLAST score
                  476
E value
                  9.0e-48
Match length
                  138
% identity
                  67
NCBI Description
                  (Y15382) putative RNA binding protein [Arabidopsis
                  thaliana]
                  413272
Seq. No.
Seq. ID
                  uC-osflcyp125a05b1
Method
                  BLASTX
```

E value

6.0e-55

```
3.0e-68
E value
Match length
                   154
                   87
% identity
                   PHOSPHOGLYCERATE KINASE, CYTOSOLIC >gi_66911_pir__TVWTGY
NCBI Description
                   phosphoglycerate kinase (EC 2.7.2.3), cytosolic - wheat
                   >gi_21835_emb_CAA33302_ (X15232) phosphoglycerate kinase
                   (AA 1 - 401) [Triticum aestivum]
Seq. No.
                   413273
Seq. ID
                   uC-osflcyp125a06b1
Method
                   BLASTX
NCBI GI
                   q543711
BLAST score
                   266
E value
                   3.0e-23
                   54
Match length
                   96
% identity
NCBI Description 14-3-3-LIKE PROTEIN S94 >gi_419796_pir__S30927 14-3-3 protein homolog - rice >gi_303859_dbj_BAA03711_ (D16140)
                   brain specific protein [Oryza sativa]
Seq. No.
                   413274
Seq. ID
                   uC-osflcyp125a07b1
Method
                   BLASTX
NCBI GI
                   g1084455
BLAST score
                   418
E value
                   5.0e-41
Match length
                   109
% identity
                   77
NCBI Description peptidylprolyl isomerase (EC 5.2.1.8) Cyp2 - rice
                   >gi_600767 (L29469) cyclophilin 2 [Oryza sativa]
                   413275
Seq. No.
Seq. ID
                   uC-osflcyp125a08b1
Method
                   BLASTX
NCBI GI
                   q485517
BLAST score
                   163
E value
                   4.0e-11
Match length
                   34
                   94
% identity
NCBI Description ADP, ATP carrier protein - rice
                   413276
Seq. No.
Seq. ID
                   uC-osflcyp125a09b1
Method
                   BLASTX
NCBI GI
                   g4678349
BLAST score
                   494
E value
                   6.0e-50
Match length
                   149
                   33
% identity
NCBI Description (AL049659) putative protein [Arabidopsis thaliana]
                   413277
Seq. No.
Seq. ID
                   uC-osflcyp125a11b1
Method
                   BLASTX
NCBI GI
                   q3789948
BLAST score
                   537
```

```
124
                  84
                 (AF094773) translation initiation factor 5A [Oryza sativa]
NCBI Description
                  413278
```

Seq. ID uC-osflcyp125b02b1 Method BLASTX NCBI GI q1321661 BLAST score 673 E value 7.0e-71 Match length 136 96 % identity

Match length % identity

Seq. No.

NCBI Description (D45423) ascorbate peroxidase [Oryza sativa]

Seq. No. 413279 Seq. ID

uC-osflcyp125b03b1

Method BLASTX NCBI GI g3386614 BLAST score 513 E value 4.0e-52 Match length 139 % identity

(AC004665) putative transcription factor SF3 [Arabidopsis NCBI Description

thaliana]

Seq. No. 413280

uC-osflcyp125b04b1 Seq. ID

Method BLASTX NCBI GI g3122858 BLAST score 149 2.0e-09 E value Match length 48

% identity 67

D-3-PHOSPHOGLYCERATE DEHYDROGENASE PRECURSOR (PGDH) NCBI Description

>gi 2189964 dbj BAA20405 (AB003280) Phosphoglycerate

dehydrogenase [Arabidopsis thaliana]

>qi 2804258 dbj BAA24440 (AB010407) phosphoglycerate

dehydrogenase [Arabidopsis thaliana]

Seq. No. 413281

Seq. ID uC-osflcyp125b07b1

Method BLASTX NCBI GI g2072555 BLAST score 237 E value 9.0e-20 Match length 44 % identity 100

(AF001396) metallothionein-like protein [Oryza sativa] NCBI Description

>gi_6103441_gb_AAF03603.1_ (AF147786) metallothionein-like

protein [Oryza sativa]

413282 Seq. No.

Seq. ID uC-osflcyp125b12b1

BLASTX Method NCBI GI g3096910 BLAST score 672 1.0e-70 E value

Seq. No.

Seq. ID

413288

uC-osflcyp125d06b1

```
164
Match length
% identity
                  77
NCBI Description (AJ005813) neoxanthin cleavage enzyme [Arabidopsis
                  thaliana]
Seq. No.
                  413283
Seq. ID
                  uC-osflcyp125c03b1
                  BLASTX
Method
                  g3688398
NCBI GI
BLAST score
                  187
                  1.0e-16
E value
Match length
                  89
% identity
                  64
NCBI Description (AJ006358) ascorbate peroxidase [Hordeum vulgare]
                  413284
Seq. No.
Seq. ID
                  uC-osflcyp125c08b1
Method
                  BLASTX
NCBI GI
                  g1362009
                  506
BLAST score
                  3.0e-51
E value
Match length
                  122
                  53
% identity
NCBI Description ubiquitin-like protein 7 - Arabidopsis thaliana
                  413285
Seq. No.
Seq. ID
                  uC-osflcyp125c09b1
Method
                  BLASTX
NCBI GI
                  g2431771
BLAST score
                  268
E value
                  2.0e-23
Match length
                  113
% identity
                  51
NCBI Description (U62753) acidic ribosomal protein P2b [Zea mays]
                  413286
Seq. No.
                  uC-osflcyp125c12b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1871186
BLAST score
                  465
E value
                  1.0e-46
Match length
                  121
% identity
NCBI Description (U90439) protein kinase isolog [Arabidopsis thaliana]
                  413287
Seq. No.
Seq. ID
                  uC-osflcyp125d02b1
Method
                  BLASTX
NCBI GI
                  g3668069
BLAST score
                  629
E value
                  1.0e-68
Match length
                  147
% identity
NCBI Description (U28007) Pto kinase interactor 1 [Lycopersicon esculentum]
```



Method BLASTX NCBI GI g548770 BLAST score 749 E value 5.0e-85 Match length 158 99 % identity

NCBI Description 60S RIBOSOMAL PROTEIN L3 >gi_481228_pir__ S38359 ribosomal protein L3 - rice >gi_303853_dbj_BAA02155_ (D12630) ribosomal protein L3 [Oryza sativa]

Seq. No. 413289

Seq. ID uC-osflcyp125d07b1

Method BLASTX NCBI GI q4835778 BLAST score 229 E value 8.0e-19 71 Match length % identity 62

NCBI Description (AC007296) F25C20.6 [Arabidopsis thaliana]

Seq. No. 413290

Seq. ID uC-osflcyp125d08b1

Method BLASTX NCBI GI q3881976 BLAST score 579 E value 8.0e-60 162 Match length % identity 68

NCBI Description (AJ012409) hypothetical protein [Homo sapiens]

Seq. No. 413291

Seq. ID uC-osflcyp125d09b1

Method BLASTX NCBI GI g3258570 BLAST score 197 9.0e-17 E value Match length 62 % identity 74

NCBI Description (U89959) Unknown protein [Arabidopsis thaliana]

Seq. No. 413292

Seq. ID uC-osflcyp125d10b1

Method BLASTX NCBI GI g129591 BLAST score 409 E value 2.0e-73 Match length 164 % identity 96

NCBI Description PHENYLALANINE AMMONIA-LYASE >gi 295824 emb CAA34226

(X16099) phenylalanine ammonia-lyase [Oryza sativa]

Seq. No. 413293

Seq. ID uC-osflcyp125d11b1

Method BLASTX q1706956 NCBI GI BLAST score 465 E value 2.0e-61

% identity

37

```
162
Match length
% identity
                  75
NCBI Description (U58283) cellulose synthase [Gossypium hirsutum]
                  413294
Seq. No.
Seq. ID
                  uC-osflcyp125d12b1
Method
                  BLASTX
NCBI GI
                  g3738315
BLAST score
                  303
E value
                  2.0e-27
Match length
                  118
% identity
                  58
NCBI Description (AC005170) unknown protein [Arabidopsis thaliana]
Seq. No.
                  413295
Seq. ID
                  uC-osflcyp125e01b1
Method
                  BLASTX
NCBI GI
                  g4220474
BLAST score
                  375
E value
                  7.0e-36
Match length
                  126
% identity
NCBI Description (AC006069) putative myosin heavy chain [Arabidopsis
                  thaliana]
                  413296
Seq. No.
Seq. ID
                  uC-osflcyp125e03b1
Method
                  BLASTX
NCBI GI
                  g2696231
BLAST score
                  626
E value
                  2.0e-65
Match length
                  136
% identity
                  89
NCBI Description
                 (D55713) chitinase [Oryza sativa]
                  >gi_4826582_dbj_BAA21743.2_ (AB006188) acidic class III
                  chitinase OsChib3a [Oryza sativa]
                  >gi_4827249_dbj_BAA77605.1_ (AB026998) acidic class III
                  chitinase OsChib3a [Oryza sativa]
Seq. No.
                  413297
Seq. ID
                  uC-osflcyp125e04b1
Method
                  BLASTX
NCBI GI
                  g5360230
BLAST score
                  822
E value
                  3.0e-88
Match length
                  149
                  100
% identity
NCBI Description (AB015287) Ran [Oryza sativa]
                  413298
Seq. No.
Seq. ID
                  uC-osflcyp125e06b1
                  BLASTX
Method
NCBI GI
                  g1928886
BLAST score
                  152
E value
                  9.0e-10
                  79
Match length
```

% identity

75

```
NCBI Description (U92010) lin-10 protein homolog [Rattus norvegicus]
Seq. No.
                   413299
Seq. ID
                   uC-osflcyp125e07b1
Method
                   BLASTX
NCBI GI
                  g1171008
BLAST score
                   467
E value
                   1.0e-46
Match length
                   129
% identity
                   64
NCBI Description POLLEN ALLERGEN PHL P 1 PRECURSOR (PHL P I)
                   >gi_629812_pir__S44182 allergen Phl p I - common timothy
                  >gi 473360_emb CAA55390_ (X78813) Phl p I allergen [Phleum
                  pratense]
                   413300
Seq. No.
Seq. ID
                  uC-osflcyp125e08b1
Method
                  BLASTX
NCBI GI
                   g4585991
BLAST score
                  229
E value
                  9.0e-19
Match length
                  107
% identity
                   47
                  (ACO05287) very similar to mouse Dhm1 and Dhm2 [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                   413301
Seq. ID
                  uC-osflcyp125e10b1
Method
                  BLASTX
NCBI GI
                  g633110
BLAST score
                  660
E value
                  2.0e-69
                  153
Match length
% identity
                  90
NCBI Description (D31843) plasma membrane H+-ATPase [Oryza sativa]
Seq. No.
                  413302
Seq. ID
                  uC-osflcyp125e11b1
Method
                  BLASTX
NCBI GI
                  g1076800
BLAST score
                  578
E value
                  1.0e-59
Match length
                  131
% identity
                  83
                  L-ascorbate peroxidase (EC 1.11.1.11), cytosolic isozyme -
NCBI Description
                  maize >gi 600116_emb_CAA84406_ (Z34934) cytosolic ascorbate
                  peroxidase [Zea mays] >gi 1096503 prf 2111423A ascorbate
                  peroxidase [Zea mays]
Seq. No.
                  413303
Seq. ID
                  uC-osflcyp125f01b1
Method
                  BLASTX
NCBI GI
                  q2497746
BLAST score
                  434
E value
                  8.0e-43
Match length
                  118
```

```
NCBI Description NONSPECIFIC LIPID-TRANSFER PROTEIN 2 PRECURSOR (LTP 2)
                   >gi 951334 (U31766) lipid transfer protein precursor [Oryza
                  sativa]
Seq. No.
                   413304
Seq. ID
                   uC-osflcyp125f07b1
Method
                  BLASTX
NCBI GI
                   q3337361
BLAST score
                  758
E value
                   8.0e-81
Match length
                  166
% identity
                   80
NCBI Description (AC004481) ankyrin-like protein [Arabidopsis thaliana]
Seq. No.
                   413305
Seq. ID
                  uC-osflcyp125f08b1
Method
                  BLASTX
NCBI GI
                   g2580499
BLAST score
                  208
E value
                   2.0e-21
Match length
                  165
% identity
                   39
NCBI Description (U67186) NADPH: ferrihemoprotein oxidoreductase
                   [Eschscholzia californica]
                   413306
Seq. No.
Seq. ID
                  uC-osflcyp125f10b1
Method
                  BLASTX
NCBI GI
                  g2511541
BLAST score
                  390
E value
                  7.0e-38
Match length
                  109
% identity
                  83
NCBI Description (AF020787) DNA-binding protein GBP16 [Oryza sativa]
                   413307
Seq. No.
Seq. ID
                  uC-osflcyp125g01b1
                  {\tt BLASTX}
Method
NCBI GI
                  g401140
BLAST score
                  870
E value
                   6.0e-94
Match length
                  167
% identity
                   99
NCBI Description
                  SUCROSE SYNTHASE 2 (SUCROSE-UDP GLUCOSYLTRANSFERASE 2)
                  >gi_20095_emb_CAA41774 (X59046) sucrose-UDP
                  glucosyltransferase (isoenzyme 2) [Oryza sativa]
                  >gi 1587662_prf__2207194A sucrose synthase:ISOTYPE=2 [Oryza
                  sativa]
Seq. No.
                   413308
Seq. ID
                  uC-osflcyp125g02b1
Method
                  BLASTX
NCBI GI
                  g4335763
BLAST score
                  244
E value
                  1.0e-20
                  98
Match length
% identity
                  46
```

```
NCBI Description (AC006284) unknown protein [Arabidopsis thaliana]
  Seq. No.
                     413309
  Seq. ID
                     uC-osflcyp125g03b1
  Method
                     BLASTX
  NCBI GI
                     g2633727
  BLAST score
                     179
  E value
                     6.0e-13
  Match length
                    109
  % identity
                     40
  NCBI Description (Z99111) ykrT [Bacillus subtilis]
  Seq. No.
                     413310
  Seq. ID
                     uC-osflcyp125g04b1
  Method
                    BLASTX
  NCBI GI
                     g2500194
  BLAST score
                     282
  E value
                     5.0e-25
  Match length
                     56
% identity
                     96
  NCBI Description RAC-LIKE GTP BINDING PROTEIN ARAC5 >gi_1293668 (U52350)
                    GTP-binding protein [Arabidopsis thaliana]
  Seq. No.
                     413311
  Seq. ID
                     uC-osflcyp125g06b1
  Method
                    BLASTX
  NCBI GI
                     q66298
  BLAST score
                     619
  E value
                     1.0e-81
  Match length
                    164
                     92
  % identity
  NCBI Description catalase (EC 1.11.1.6) - rice >gi_20192_emb_CAA43814_
                     (X61626) catalase [Oryza sativa]
  Seq. No.
                     413312
  Seq. ID
                    uC-osflcyp125g08b1
  Method
                    BLASTX
  NCBI GI
                    g3935147
  BLAST score
                    541
  E value
                    2.0e-55
                    151
  Match length
  % identity
                     68
  NCBI Description (AC005106) T25N20.11 [Arabidopsis thaliana]
  Seq. No.
                    413313
  Seq. ID
                    uC-osflcyp125g09b1
  Method
                    BLASTX
  NCBI GI
                    q1710780
  BLAST score
                    343
  E value
                    4.0e-49
  Match length
                    154
  % identity
                    62
  NCBI Description 40S RIBOSOMAL PROTEIN S9 (S7) >gi 1321917 emb CAA65433
                     (X96613) cytoplasmic ribosomal protein S7 [Podospora
                    anserina]
  Seq. No.
                    413314
```

E value

2.0e-82

```
Seq. ID
                  uC-osflcyp125h01b1
Method
                  BLASTX
NCBI GI
                  g2293480
BLAST score
                  151
E value
                  1.0e-09
Match length
                  32
% identity
                  91
NCBI Description (AF011331) glycine-rich protein [Oryza sativa]
Seq. No.
                  413315
Seq. ID
                  uC-osflcyp125h02b1
Method
                  BLASTX
NCBI GI
                  g82426
BLAST score
                  644
E value
                  2.0e-67
Match length
                  151
                  41
% identity
NCBI Description ubiquitin precursor - barley (fragment)
                  >gi_755763 emb CAA27751 (X04133) ubiquitin polyprecursor
                  (171 aa) [Hordeum vulgare]
                  413316
Seq. No.
Seq. ID
                  uC-osflcyp125h03b1
Method
                  BLASTX
NCBI GI
                  g2827631
BLAST score
                  369
E value
                  3.0e - 35
                  148
Match length
% identity
                  48
NCBI Description (AL021636) putative protein [Arabidopsis thaliana]
Seq. No.
                  413317
Seq. ID
                  uC-osflcyp125h04b1
Method
                  BLASTX
NCBI GI
                  q4769012
BLAST score
                  726
E value
                  4.0e-77
Match length
                  159
% identity
                  88
NCBI Description (AF143746) CER1 [Oryza sativa]
Seq. No.
                  413318
Seq. ID
                  uC-osflcyp125h06b1
Method
                  BLASTX
                  g4996646
NCBI GI
BLAST score
                  452
E value
                  6.0e-45
Match length
                  106
% identity
                  78
NCBI Description (AB028132) Dof zinc finger protein [Oryza sativa]
Seq. No.
                  413319
Seq. ID
                  uC-osflcyp125h11b1
Method
                  BLASTX
NCBI GI
                  g2696804
BLAST score
                  772
```

```
Match length
                  164
% identity
                   91
NCBI Description
                  (AB009665) water channel protein [Oryza sativa]
Seq. No.
                  413320
Seq. ID
                  uC-osflcyp125h12b1
Method
                  BLASTX
NCBI GI
                  q4467099
BLAST score
                  526
E value
                  1.0e-53
Match length
                  131
                  85
% identity
NCBI Description
                  (AL035538) glycine hydroxymethyltransferase like protein
                   [Arabidopsis thaliana]
Seq. No.
                  413321
Seq. ID
                  uC-osflcyp126a02b1
Method
                  BLASTX
NCBI GI
                  q730290
BLAST score
                  150
E value
                  1.0e-09
Match length
                  61
% identity
                  51
NCBI Description
                  PECTATE LYASE PRECURSOR >gi_322883 pir S29612 pectate
                  lyase - trumpet lily >gi_19451_emb_CAA78976_ (Z17328)
                  pectate lyase [Lilium longiflorum] >gi 308902 (L18911)
                  pectate lyase [Lilium longiflorum]
Seq. No.
                  413322
Seq. ID
                  uC-osflcyp126a04b1
Method
                  BLASTX
NCBI GI
                  g5262204
BLAST score
                  194
E value
                  9.0e-15
Match length
                  164
% identity
                  19
NCBI Description (AL080252) putative protein [Arabidopsis thaliana]
                  413323
Seq. No.
Seq. ID
                  uC-osflcyp126a05b1
Method
                  BLASTN
NCBI GI
                  g6016845
BLAST score
                  127
E value
                  7.0e-65
Match length
                  170
% identity
                  94
NCBI Description Oryza sativa genomic DNA, chromosome 1, clone:P0711E10
Seq. No.
                  413324
Seq. ID
                  uC-osflcyp126a06b1
Method
                  BLASTX
NCBI GI
                  g1086886
BLAST score
                  154
E value
                  5.0e-10
Match length
                  107
% identity
                  36
NCBI Description
                 (U41276) Similar to potassium channel protein.
```

[Caenorhabditis elegans] Seq. No. 413325 Seq. ID uC-osflcyp126a10b1

Method BLASTX
NCBI GI g5031275
BLAST score 549
E value 2.0e-56
Match length 141
% identity 72

NCBI Description (AF139496) unknown [Prunus armeniaca]

Seq. No. 413326

Seq. ID uC-osflcyp126a11b1

Method BLASTX
NCBI GI g3859659
BLAST score 428
E value 4.0e-42
Match length 168
% identity 55

NCBI Description (AL031394) putative potassium transporter AtKT5p (AtKT5)

[Arabidopsis thaliana]

Seq. No. 413327

Seq. ID uC-osflcyp126a12b1

Method BLASTX
NCBI GI g1841464
BLAST score 370
E value 3.0e-35
Match length 106
% identity 42

NCBI Description (Y11002) LIM-domain SF3 protein [Nicotiana tabacum]

>gi_5932420_gb_AAD56951.1_AF184886_1 (AF184886) LIM domain

protein WLIM2 [Nicotiana tabacum]

Seq. No. 413328

Seq. ID uC-osflcyp126b01b1

Method BLASTX
NCBI GI g3288821
BLAST score 482
E value 1.0e-48
Match length 117
% identity 78

NCBI Description (AF063901) alanine:glyoxylate aminotransferase;

transaminase [Arabidopsis thaliana]

>gi_4733989_gb_AAD28669.1_AC007209 5 (AC007209)

alanine-glyoxylate aminotransferase [Arabidopsis thaliana]

Seq. No. 413329

Seq. ID uC-osflcyp126b02b1

Method BLASTX
NCBI GI g5731756
BLAST score 373
E value 1.0e-35
Match length 118
% identity 58

NCBI Description (AL109819) putative protein [Arabidopsis thaliana]

Seq. No.

413335

```
413330
Seq. No.
Seq. ID
                  uC-osflcyp126b05b1
Method
                  BLASTX
NCBI GI
                  g3024363
BLAST score
                  485
E value
                  6.0e-49
Match length
                  133
% identity
                  71
NCBI Description PHENYLALANINE AMMONIA-LYASE >gi 1483610 emb CAA68036
                  (X99705) phenylalanine ammonia-lyase [Triticum aestivum]
                  413331
Seq. No.
Seq. ID
                  uC-osflcyp126b06b1
Method
                  BLASTX
NCBI GI
                  g2286111
                  518
BLAST score
E value
                  9.0e-53
Match length
                  102
                  99
% identity
NCBI Description (U78891) MADS box protein [Oryza sativa]
Seq. No.
                  413332
Seq. ID
                  uC-osflcyp126b07b1
Method
                  BLASTX
                  g5478807
NCBI GI
BLAST score
                  646
E value
                  1.0e-67
                  179
Match length
% identity
                  69
NCBI Description (AB021316) chlorophyll b synthase [Arabidopsis thaliana]
Seq. No.
                  413333
Seq. ID
                  uC-osflcyp126b12b1
Method
                  BLASTX
NCBI GI
                  g131225
BLAST score
                  588
E value
                  6.0e-61
Match length
                  141
% identity
                  83
NCBI Description PHOTOSYSTEM I REACTION CENTRE SUBUNIT XI PRECURSOR (SUBUNIT
                  V) (PSI-L) >gi_100605_pir__A39759 photosystem I 18K protein
                  precursor - barley >gi 167087 (M61146) photosystem I
                  hydrophobic protein [Hordeum vulgare]
                  413334
Seq. No.
Seq. ID
                  uC-osflcyp126c01b1
Method
                  BLASTX
NCBI GI
                  g5007084
BLAST score
                  894
E value
                  1.0e-96
                  172
Match length
% identity
NCBI Description (AF155333) NADP-specific isocitrate dehydrogenase [Oryza
                  satival
```

NCBI GI

BLAST score

```
uC-osflcyp126c03b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2224663
BLAST score
                  311
E value
                  3.0e-28
Match length
                  180
                  39
% identity
NCBI Description (AB002359) KIAA0361 [Homo sapiens]
                  413336
Seq. No.
Seq. ID
                  uC-osflcyp126c07b1
Method
                  BLASTX
NCBI GI
                  q4455158
BLAST score
                  665
E value
                  6.0e-70
Match length
                  163
                  73
% identity
NCBI Description (AL021687) kinase-like protein [Arabidopsis thaliana]
Seq. No.
                  413337
                  uC-osflcyp126c08b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3935181
BLAST score
                  812
                  4.0e-87
E value
Match length
                  164
                  87
% identity
NCBI Description (AC004557) F17L21.24 [Arabidopsis thaliana]
                  413338
Seq. No.
Seq. ID
                  uC-osflcyp126c11b1
Method
                  BLASTX
NCBI GI
                  g2995370
BLAST score
                  279
E value
                  1.0e-24
Match length
                  138
                  37
% identity
NCBI Description (AL022245) hypothetical protein [Schizosaccharomyces pombe]
Seq. No.
                  413339
Seq. ID
                  uC-osflcyp126c12b1
Method
                  BLASTX
NCBI GI
                  g135399
BLAST score
                  719
E value
                  3.0e-76
Match length
                  165
% identity
                  85
                  TUBULIN ALPHA-1 CHAIN >gi 100716 pir S20758 tubulin
NCBI Description
                  alpha-1 chain - rice >gi 20379 emb CAA77988 (Z11931) alpha
                  1 tubulin [Oryza sativa] > gi 1136124 emb CAA62918 (X91808)
                  alfa-tubulin [Oryza sativa]
Seq. No.
                  413340
Seq. ID
                  uC-osflcyp126d02b1
Method
                  BLASTX
```

53827

g3193303

Match length

88

```
4.0e-31
E value
                  98
Match length
                  64
% identity
                  (AF069298) similar to several proteins containing a tandem
NCBI Description
                  repeat region such as Plasmodium falciparum GGM tandem
                  repeat protein (GB:U27807); partial CDS [Arabidopsis
                  thaliana]
                  413341
Seq. No.
                  uC-osflcyp126d03b1
Seq. ID
                  BLASTX
Method
NCBI GI
                  g4033424
BLAST score
                  285
                  3.0e-25
E value
Match length
                  70
                  74
% identity
                  SOLUBLE INORGANIC PYROPHOSPHATASE (PYROPHOSPHATE
NCBI Description
                  PHOSPHO-HYDROLASE) (PPASE) >gi_2668746 (AF034947) inorganic
                  pyrophosphatase [Zea mays]
                  413342
Seq. No.
                  uC-osflcyp126d04b1
Seq. ID
                  BLASTX
Method
                  g1654144
NCBI GI
                   360
BLAST score
                   4.0e-34
E value
Match length
                  105
% identity
                   71
NCBI Description (U38471) small GTP-binding protein rab [Brassica rapa]
                   413343
Seq. No.
                   uC-osflcyp126d05b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   q4006978
                   196
BLAST score
                   7.0e-15
E value
Match length
                   87
% identity
                   43
NCBI Description (AJ131335) pollen allergen (group II) [Cynodon dactylon]
                   413344
Seq. No.
Seq. ID
                   uC-osflcyp126d06b1
                   BLASTX
Method
                   q4406808
NCBI GI
                   197
BLAST score
E value
                   5.0e-15
Match length
                   144
% identity
NCBI Description (AC006201) unknown protein [Arabidopsis thaliana]
                   413345
Seq. No.
Seq. ID
                   uC-osflcyp126d08b1
Method
                   BLASTX
NCBI GI
                   g2984709
                   464
BLAST score
                   2.0e-46
E value
```

Match length

% identity

96

% identity (AF053468) DnaJ-related protein ZMDJ1 [Zea mays] NCBI Description 413346 Seq. No. uC-osflcyp126d09b1 Seq. ID BLASTX Method NCBI GI g1350742 BLAST score 310 E value 3.0e-28 102 Match length % identity 58 PROBABLE 60S RIBOSOMAL PROTEIN L35A >gi 1086831 (U41264) NCBI Description coded for by C. elegans cDNA yk64g10.5; coded for by C. elegans cDNA yk51f3.5; coded for by C. elegans cDNA yk115e7.3; coded for by C. elegans cDNA yk99d1.3; coded for by C. elegans cDNA yk99d1.5; coded for by C. elegans cDNA yk64q1 413347 Seq. No. Seq. ID uC-osflcyp126d10b1 Method BLASTX NCBI GI q6006894 BLAST score 203 9.0e-16 E value Match length 149 % identity 40 NCBI Description (AC008153) unknown protein [Arabidopsis thaliana] 413348 Seq. No. uC-osflcyp126d11b1 Seq. ID Method BLASTX NCBI GI g2462763 BLAST score 356 E value 1.0e-33 Match length 94 % identity 74 (AC002292) Highly similar to auxin-induced protein NCBI Description (aldo/keto reductase family) [Arabidopsis thaliana] Seq. No. 413349 Seq. ID uC-osflcyp126d12b1 Method BLASTX NCBI GI g4220527 BLAST score 564 E value 5.0e-58Match length 167 % identity 62 NCBI Description (AL035356) putative protein [Arabidopsis thaliana] 413350 Seq. No. Seq. ID uC-osflcyp126e04b1 Method BLASTX NCBI GI g2642648 820 BLAST score 5.0e-88 E value 165

```
NCBI Description
                  (AF033852) cytosolic heat shock 70 protein; HSC70-3
                  [Spinacia oleracea] >gi_2660768 (AF034616) cytosolic heat
                  shock 70 protein [Spinacia oleracea] >gi 2660770 (AF034617)
                  cytosolic heat shock 70 protein [Spinacia oleracea]
Seq. No.
                  413351
Seq. ID
                  uC-osflcyp126e06b1
Method
                  BLASTX
NCBI GI
                  g3122703
BLAST score
                  475
E value
                  1.0e-47
Match length
                  142
                  71
% identity
NCBI Description 60S RIBOSOMAL PROTEIN L23A >gi 2641201 (AF031542) ribosomal
                  protein L23a [Fritillaria agrestis]
Seq. No.
                  413352
Seq. ID
                  uC-osflcyp126e07b1
Method
                  BLASTX
NCBI GI
                  g2668744
BLAST score
                  678
                  2.0e-71
E value
Match length
                  128
                  97
% identity
NCBI Description (AF034946) ubiquitin conjugating enzyme [Zea mays]
Seq. No.
                  413353
Seq. ID
                  uC-osflcyp126e10b1
Method
                  BLASTX
NCBI GI
                  g231587
BLAST score
                  481
E value
                  2.0e-48
Match length
                  153
% identity
                  68
NCBI Description ATP SYNTHASE BETA CHAIN, MITOCHONDRIAL PRECURSOR
                  >gi 283001 pir S25304 H+-transporting ATP synthase (EC
                  3.6.1.34) beta chain precursor, mitochondrial - rice
                  >gi 218147 dbj BAA01372 (D10491) mitochondrial F1-ATPase
                  [Oryza satīva]
Seq. No.
                  413354
Seq. ID
                  uC-osflcyp126e11b1
Method
                  BLASTX
NCBI GI
                  g3128228
BLAST score
                  615
                  4.0e-64
E value
Match length
                  122
% identity
NCBI Description
                  (AC004077) putative ribosomal protein L18A [Arabidopsis
                  thaliana] >gi 3337376 (AC004481) putative ribosomal protein
                  L18A [Arabidopsis thaliana]
```

Seq. No. 413355

Seq. ID uC-osflcyp126e12b1

Method BLASTX NCBI GI g4469023 BLAST score 630

```
E value
                   8.0e-66
Match length
                   132
% identity
                   87
NCBI Description
                  (AL035602) putative protein [Arabidopsis thaliana]
Seq. No.
                   413356
Seq. ID
                   uC-osflcyp126f01b1
Method
                   BLASTX
NCBI GI
                   g3193304
BLAST score
                   236
E value
                   8.0e-35
Match length
                   97
% identity
                   80
NCBI Description
                   (AF069298) contains similarity to RNA recognition motifs
                   (Pfam: rrm.hmm, score; 82.09 and 30.80); similar to
                   alternative splicing factor ASF [Arabidopsis thaliana]
Seq. No.
                   413357
Seq. ID
                   uC-osflcyp126f03b1
Method
                   BLASTX
NCBI GI
                   q3193292
BLAST score
                   510
E value
                   1.0e-51
Match length
                   163
                   58
% identity
NCBI Description
                  (AF069298) similar to ATPases associated with various
                   cellular activites (Pfam: AAA.hmm, score: 230.91)
                   [Arabidopsis thaliana]
Seq. No.
                   413358
Seq. ID
                   uC-osflcyp126f04b1
Method
                   BLASTX
NCBI GI
                   g2117700
BLAST score
                   746
E value
                   2.0e-79
Match length
                   170
                   84
% identity
NCBI Description transketolase (EC 2.2.1.1) precursor - potato (fragment)
Seq. No.
                   413359
Seq. ID
                   uC-osflcyp126f05b1
Method
                   BLASTX
NCBI GI
                   g3126967
BLAST score
                   804
E value
                   3.0e-86
Match length
                   163
% identity
                   18
NCBI Description (AF061807) polyubiquitin [Elaeagnus umbellata]
Seq. No.
                   413360
Seq. ID
                   uC-osflcyp126f06b1
Method
                   BLASTX
NCBI GI
                   g6002955
BLAST score
                  195
E value
                   5.0e-15
Match length
                  105
% identity
                   43
```

```
(AF171877) cleavage and polyadenylation specificity factor
NCBI Description
                  73 kDa subunit [Homo sapiens]
Seq. No.
                  413361
                  uC-osflcyp126f07b1
Seq. ID
Method
                  BLASTX
                  q1890575
NCBI GI
                  746
BLAST score
E value
                  2.0e-79
                  150
Match length
                  89
% identity
NCBI Description
                  (X93174) xyloglucan endotransglycosylase (XET) [Hordeum
                  vulgare]
                   413362
Seq. No.
                  uC-osflcyp126f08b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1170937
                   873
BLAST score
E value
                   3.0e - 94
                  165
Match length
                   100
% identity
NCBI Description
                  S-ADENOSYLMETHIONINE SYNTHETASE 1 (METHIONINE
                   ADENOSYLTRANSFERASE 1) (ADOMET SYNTHETASE 1)
                   >gi_450549_emb_CAA81481_ (Z26867) S-adenosyl methionine
                   synthetase [Oryza sativa]
                   413363
Seq. No.
                  uC-osflcyp126f09b1
Seq. ID
Method
                  BLASTX
NCBI GI
                   q2286111
BLAST score
                   741
E value
                   8.0e-79
Match length
                   153
                   97
% identity
NCBI Description (U78891) MADS box protein [Oryza sativa]
                   413364
Seq. No.
                   uC-osflcyp126f12b1
Seq. ID
Method
                   BLASTN
NCBI GI
                   g2773153
BLAST score
                   478
E value
                   0.0e + 00
                   490
Match length
                   99
% identity
                  Oryza sativa abscisic acid- and stress-inducible protein
NCBI Description
                   (Asr1) mRNA, complete cds
                   413365
Seq. No.
Seq. ID
                   uC-osflcyp126g02b1
                   BLASTX
Method
NCBI GI
                   g4262140
                   284
BLAST score
                   2.0e-25
E value
Match length
                   98
% identity
NCBI Description (AC005275) putative C-type U1 snRNP [Arabidopsis thaliana]
```

```
Seq. No.
                  413366
                  uC-osflcyp126g03b1
Seq. ID
Method
                  BLASTX
                  q1698670
NCBI GI
                  279
BLAST score
                  1.0e-24
E value
                  124
Match length
                  41
% identity
                 (U66241) S-like RNase [Zea mays]
NCBI Description
                  413367
Seq. No.
                  uC-osflcyp126g04b1
Seq. ID
Method
                  BLASTX
NCBI GI
                   a2245004
                   375
BLAST score
                   5.0e - 36
E value
                  135
Match length
                   56
% identity
                  (Z97341) membrane transporter like protein [Arabidopsis
NCBI Description
                  thaliana]
                   413368
Seq. No.
                   uC-osflcyp126g06b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   q6006862
                   446
BLAST score
                   3.0e-44
E value
Match length
                   169
                   55
% identity
NCBI Description (AC009540) unknown protein [Arabidopsis thaliana]
                   413369
Seq. No.
Seq. ID
                   uC-osflcyp126g08b1
Method
                   BLASTX
NCBI GI
                   g543711
                   256
BLAST score
                   6.0e-22
E value
                   49
Match length
                   100
% identity
NCBI Description 14-3-3-LIKE PROTEIN S94 >gi_419796 pir S30927 14-3-3
                   protein homolog - rice >gi_303859_dbj_BAA03711_ (D16140)
                   brain specific protein [Oryza satīva]
                   413370
Seq. No.
Seq. ID
                   uC-osflcyp126g09b1
Method
                   BLASTX
NCBI GI
                   q974782
                   683
BLAST score
                   5.0e-72
E value
Match length
                   157
                   83
% identity
                  (Z49150) cobalamine-independent methionine synthase
NCBI Description
                   [Solenostemon scutellarioides]
Seq. No.
                   413371
Seq. ID
                   uC-osflcyp126g10b1
```

```
Method
                   BLASTN
NCBI GI
                   q498737
BLAST score
                   43
E value
                   1.0e-14
Match length
                   171
                   81
% identity
                  H.vulgare (pMaW21) pseudo mRNA for beta-ketoacyl-ACP
NCBI Description
                   synthase (partial)
                   413372
Seq. No.
Seq. ID
                   uC-osflcyp126g11b1
                   BLASTX
Method
NCBI GI
                   q1353516
BLAST score
                   338
E value
                   1.0e-31
Match length
                   120
                   57
% identity
NCBI Description (U38651) sugar transporter [Medicago truncatula]
Seq. No.
                   413373
                   uC-osflcyp126h01b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   q1170937
BLAST score
                   745
                   2.0e-79
E value
Match length
                   143
                   99
% identity
NCBI Description S-ADENOSYLMETHIONINE SYNTHETASE 1 (METHIONINE
                   ADENOSYLTRANSFERASE 1) (ADOMET SYNTHETASE 1)
                   >gi 450549 emb CAA81481_ (Z26867) S-adenosyl methionine
                   synthetase [Oryza sativa]
                   413374
Seq. No.
Seq. ID
                   uC-osflcyp126h02b1
Method
                   BLASTX
NCBI GI
                   g1707998
BLAST score
                   607
E value
                   3.0e-63
Match length
                   132
% identity
                   89
NCBI Description SERINE HYDROXYMETHYLTRANSFERASE, MITOCHONDRIAL PRECURSOR
                   (SERINE METHYLASE) (GLYCINE HYDROXYMETHYLTRANSFERASE)
                   (SHMT) >gi 481944 pir S40218 glycine
                   hydroxymethyltransferase (EC 2.1.2.1) - potato
                   >gi_438247_emb_CAA81082_ (Z25863) glycine
hydroxymethyltransferase [Solanum tuberosum]
                   413375
Seq. No.
Seq. ID
                   uC-osflcyp126h03b1
                   BLASTX
Method
                   g2688824
NCBI GI
BLAST score
                   148
                   2.0e-09
E value
Match length
                   68
```

(U93273) putative auxin-repressed protein [Prunus

49

armeniaca]

% identity

NCBI Description

413376 Seq. No. uC-osflcyp126h04b1 Seq. ID Method BLASTX q1777312 NCBI GI 213 BLAST score E value 6.0e-17 61 Match length 66 % identity (D30622) novel serine/threonine protein kinase [Arabidopsis NCBI Description thaliana] 413377 Seq. No. uC-osflcyp126h06b1 Seq. ID Method BLASTX g2852449 NCBI GI 678 BLAST score 2.0e-71 E value 159 Match length 79 % identity (D88207) protein kinase [Arabidopsis thaliana] >gi_2947061 NCBI Description (AC002521) putative protein kinase [Arabidopsis thaliana] 413378 Seq. No. uC-osflcyp126h07b1 Seq. ID Method BLASTX q123549 NCBI GI 424 BLAST score 1.0e-41 E value 133 Match length % identity 66 17.5 KD CLASS II HEAT SHOCK PROTEIN >gi_100885_pir__S14998 NCBI Description heat shock protein, 18K - maize >gi_22339_emb_CAA38013_ (X54076) 18kDa heat shock protein [Zea mays] Seq. No. 413379 uC-osflcyp126h10b1 Seq. ID Method BLASTX q4895198 NCBI GI 533 BLAST score E value 2.0e-54 Match length 176 % identity 61 NCBI Description (AC007661) unknown protein [Arabidopsis thaliana] Seq. No. 413380 uC-osflcyp126h11b1 Seq. ID BLASTN Method q5670155 NCBI GI 56 BLAST score

E value 2.0e-22 Match length 116 88 % identity

NCBI Description Oryza sativa subsp. japonica BAC clone 34K24, complete

sequence

Seq. No. 413381

```
uC-osflcyp126h12b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1351014
BLAST score
                  554
E value
                  8.0e-57
Match length
                  123
                  90
% identity
NCBI Description 40S RIBOSOMAL PROTEIN S8 >gi 968902 dbj BAA07207 (D38010)
                  ribosomal protein S8 [Oryza sativa]
Seq. No.
                  413382
Seq. ID
                  uC-osflcyp127a01a1
Method
                  BLASTX
NCBI GI
                  q2055376
BLAST score
                  470
E value
                  6.0e-47
Match length
                  86
                  99
% identity
NCBI Description (U32109) MADS box protein [Oryza sativa]
                  413383
Seq. No.
                  uC-osflcyp127a02a1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2342494
BLAST score
                  253
E value
                  9.0e-22
Match length
                  68
                  62
% identity
NCBI Description
                  (D14058) bromelain [Ananas comosus]
                  >gi_2463582_dbj_BAA22543_ (D38531) FB31 precursor (FB13
                  precursor) [Ananas comosus]
Seq. No.
                  413384
Seq. ID
                  uC-osflcyp127a04a1
Method
                  BLASTN
NCBI GI
                  g340697
BLAST score
                  72
E value
                  5.0e-32
Match length
                  80
                  97
% identity
NCBI Description Soybean chloroplast 16S/23S ribosomal intergenic spacer DNA
Seq. No.
                  413385
Seq. ID
                  uC-osflcyp127b05a1
Method
                  BLASTX
NCBI GI
                  g1362009
BLAST score
                  310
E value
                  2.0e-28
                  81
Match length
                  43
% identity
NCBI Description ubiquitin-like protein 7 - Arabidopsis thaliana
Seq. No.
                  413386
Seq. ID
                  uC-osflcyp127b07a1
Method
                  BLASTX
NCBI GI
                  g4678364
BLAST score
                  218
```

Match length

67

```
2.0e-17
E value
Match length
                  91
% identity
                  54
                  (AL049659) putative protein [Arabidopsis thaliana]
NCBI Description
                  413387
Seq. No.
Seq. ID
                  uC-osflcyp127b11a1
Method
                  BLASTX
NCBI GI
                  g1170937
BLAST score
                  255
E value
                   6.0e-22
Match length
                  46
                   100
% identity
                  S-ADENOSYLMETHIONINE SYNTHETASE 1 (METHIONINE
NCBI Description
                   ADENOSYLTRANSFERASE 1) (ADOMET SYNTHETASE 1)
                   >gi_450549_emb_CAA81481_ (Z26867) S-adenosyl methionine
                   synthetase [Oryza sativa]
                   413388
Seq. No.
Seq. ID
                   uC-osflcyp127c04a1
                   BLASTX
Method
NCBI GI
                   g3913426
BLAST score
                   386
E value
                   3.0e-37
Match length
                   73
% identity
                   99
                  S-ADENOSYLMETHIONINE DECARBOXYLASE PROENZYME (ADOMETDC)
NCBI Description
                   (SAMDC) >gi 1532048 emb CAA69074 (Y07766)
                   S-adenosylmethionine decarboxylase [Oryza sativa]
                   413389
Seq. No.
                   uC-osflcyp127c05a1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3790441
BLAST score
                   354
E value
                   2.0e-33
                   77
Match length
                   88
% identity
NCBI Description (AF030515) chaperonin 60 alpha subunit [Canavalia lineata]
Seq. No.
                   413390
                   uC-osflcyp127c06a1
Seq. ID
                   BLASTX
Method
NCBI GI
                   g1136122
BLAST score
                   274
                   4.0e-24
E value
                   55
Match length
% identity
NCBI Description (X91807) alfa-tubulin [Oryza sativa]
Seq. No.
                   413391
                   uC-osflcyp127c07a1
Seq. ID
                   BLASTX
Method
                   g548605
NCBI GI
BLAST score
                   152
E value
                   8.0e-10
```

```
% identity
                 PHOTOSYSTEM I REACTION CENTRE SUBUNIT X PRECURSOR
NCBI Description
                  (LIGHT-HARVESTING COMPLEX I 7 KD PROTEIN) (PSI-K)
                  >gi_539055_pir__A48527 photosystem I protein psaK precursor
                  - barley >gi_304220 (L12707) photosystem I PSI-K subunit
                  [Hordeum vulgare]
                  413392
Seq. No.
                  uC-osflcyp127c11a1
Seq. ID
                  BLASTX
Method
                  g3746568
NCBI GI
BLAST score
                  309
                  3.0e-28
E value
Match length
                  80
                  74
% identity
                  (AF061638) branched-chain alpha-keto acid decarboxylase E1
NCBI Description
                  beta subunit [Arabidopsis thaliana]
                  413393
Seq. No.
                  uC-osflcyp127d01a1
Seq. ID
                  BLASTX
Method
                  g2130125
NCBI GI
                  362
BLAST score
                  2.0e-34
E value
                  76
Match length
                   82
% identity
                  DNA-binding protein Dof3 - maize (fragment)
NCBI Description
                  >gi 1061308 emb CAA56288 (X79935) Dof3 gene [Zea mays]
                   413394
Seq. No.
                  uC-osflcyp127d03a1
Seq. ID
Method
                  BLASTX
                   q488571
NCBI GI
                   297
BLAST score
E value
                   1.0e-26
Match length
                   62
% identity
                   97
NCBI Description (U09462) histone H3.2 [Medicago sativa]
                   413395
Seq. No.
Seq. ID
                   uC-osflcyp127d04a1
Method
                   BLASTX
NCBI GI
                   g4835765
BLAST score
                   254
E value
                   9.0e-22
Match length
                   54
% identity
                   83
                  (AC007202) Is a member of the PF 00171 aldehyde
NCBI Description
                   dehydrogenase family. ESTs gb_T21534, gb_N65241 and
                   gb AA395614 come from this gene. [Arabidopsis thaliana]
Seq. No.
                   413396
                   uC-osflcyp127d05a1
Seq. ID
                   BLASTX
Method
                   g166410
NCBI GI
BLAST score
                   222
```

53838

5.0e-18

E value

Match length 41 85 % identity (L07291) Alfin-1 [Medicago sativa] NCBI Description 413397 Seq. No. uC-osflcyp127d06a1 Seq. ID Method BLASTX g671740 NCBI GI 301 BLAST score 3.0e-27 E value 57 Match length 100 % identity (X84730) ribulose-bisphosphate carboxylase [synthetic NCBI Description construct] 413398 Seq. No. uC-osflcyp127d11a1 Seq. ID Method BLASTX g120668 NCBI GI 505 BLAST score 4.0e-51 E value 107 Match length 91 % identity GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC NCBI Description >gi_82399_pir__A24159 glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1.12), cytosolic - barley (fragment) >gi_167044 (M36650) glyceraldehyde-3-phosphate dehydrogenase [Hordeum vulgare] >gi_225347_prf_ dehydrogenase, glyceraldehydephosphate [Hordeum vulgare var. distichum] 413399 Seq. No. uC-osflcyp127d12a1 Seq. ID BLASTN Method q4996645 NCBI GI 459 BLAST score 0.0e + 00E value Match length 459 100 % identity NCBI Description Oryza sativa mRNA for Dof zinc finger protein, complete cds 413400 Seq. No. uC-osflcyp127e04a1 Seq. ID BLASTX Method NCBI GI q3885886 537 BLAST score E value 7.0e-55 Match length 96 99 % identity NCBI Description (AF093631) Rieske Fe-S precursor protein [Oryza sativa] 413401 Seq. No. uC-osflcyp127e10a1 Seq. ID BLASTX Method g1421730 NCBI GI 182 BLAST score

53839

2.0e-13

E value

Seq. ID

```
Match length
                    39
% identity
NCBI Description
                   (U43082) RF2 [Zea mays]
                    413402
Seq. No.
                    uC-osflcyp127e11a1
Seq. ID
Method
                    BLASTX
NCBI GI
                    q100934
BLAST score
                    520
                    6.0e-53
E value
Match length
                    104
% identity
                    15
                    ubiquitin precursor Ubi-1 - maize >gi_422037_pir__ S20926 ubiquitin precursor Ubi-2 - maize >gi_248337_bbs_94465
NCBI Description
                    (S94464) polyubiquitin(ubiquitin) [maize, Peptide, 533 aa]
                    [Zea mays] >gi_248339_bbs_94467 (S94466)
                    polyubiquitin(ubiquitin) [maize, Peptide, 533 aa] [Zea
                    mays]
Seq. No.
                    413403
                    uC-osflcyp127f06a1
Seq. ID
Method
                    BLASTX
NCBI GI
                    g115813
BLAST score
                    257
                    4.0e-22
E value
Match length
                    61
% identity
                    82
                    CHLOROPHYLL A-B BINDING PROTEIN 8 PRECURSOR (LHCI TYPE III
NCBI Description
                    CAB-8) >gi 19182 emb CAA33330 (X15258) Type III
                    chlorophyll a/b-binding protein [Lycopersicon esculentum]
                    413404
Seq. No.
Seq. ID
                    uC-osflcyp127f08a1
Method
                    BLASTN
NCBI GI
                    q3550984
BLAST score
                    113
E value
                    1.0e-56
Match length
                    120
% identity
                    98
NCBI Description Oryza sativa mRNA for OsS5a, complete cds
Seq. No.
                    413405
                    uC-osflcyp127f12a1
Seq. ID
Method
                    BLASTX
NCBI GI
                    g115787
BLAST score
                    445
E value
                    3.0e-44
                    84
Match length
% identity
                    100
NCBI Description CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I
                    CAB-2) (LHCP) >gi_82461_pir__S03706 chlorophyll a/b-binding protein 2R precursor - rice >gi_20182_emb_CAA32109_
                    (X13909) chlorophyll a/b-binding preprotein (AA -28 to 235)
                    [Oryza sativa]
Seq. No.
                    413406
```

uC-osflcyp127g03a1

```
Method
                  BLASTN
NCBI GI
                  g2613142
BLAST score
                  283
E value
                  1.0e-158
                  334
Match length
                  97
% identity
NCBI Description Oryza sativa tubulin (RiP3) mRNA, complete cds
                  413407
Seq. No.
Seq. ID
                  uC-osflcyp127g04a1
Method
                  BLASTX
NCBI GI
                  g3717987
BLAST score
                  147
E value
                  3.0e-09
Match length
                  71
                  52
% identity
NCBI Description (AJ005899) G subunit of Vacuolar-type H+-ATPase [Nicotiana
                  tabacum]
Seq. No.
                  413408
Seq. ID
                  uC-osflcyp127g06a1
Method
                  BLASTX
NCBI GI
                  g399333
BLAST score
                  188
E value
                  4.0e-14
                  44
Match length
% identity
                  82
NCBI Description CYSTEINE SYNTHASE, CHLOROPLAST PRECURSOR (O-ACETYLSERINE
                  SULFHYDRYLASE) (O-ACETYLSERINE (THIOL)-LYASE) (CSASE)
                  >gi_322740_pir__A43407 cysteine synthase (EC 4.2.99.8)
                  precursor - pepper >gi_17944_emb_CAA46086 (X64874)
                  O-acetylserine (thiol)-lyase [Capsicum annuum]
Seq. No.
                  413409
Seq. ID
                  uC-osflcyp127h03a1
Method
                  BLASTX
NCBI GI
                  g1890575
BLAST score
                  205
E value
                  3.0e-16
Match length
                  45
% identity
NCBI Description (X93174) xyloglucan endotransglycosylase (XET) [Hordeum
                  vulgare]
Seq. No.
                  413410
Seq. ID
                  uC-osflcyp127h10a1
Method
                  BLASTX
NCBI GI
                  q5051780
BLAST score
                  267
E value
                  3.0e-23
Match length
                  83
% identity
NCBI Description (AL078637) putative protein [Arabidopsis thaliana]
```

Seq. No. 413411

Seq. ID uC-osflcyp128a03a1

Method BLASTX

Seq. ID

```
q4586056
NCBI GI
                  189
BLAST score
E value
                  4.0e-14
Match length
                  149
                  33
% identity
                  (AC007020) unknown protein [Arabidopsis thaliana]
NCBI Description
                  413412
Seq. No.
                  uC-osflcyp128a04a1
Seq. ID
Method
                  BLASTN
                  q2586084
NCBI GI
                  33
BLAST score
                  4.0e-09
E value
                  77
Match length
                  86
% identity
                  Oryza longistaminata receptor kinase-like protein (Xa21)
NCBI Description
                  gene, complete cds and family member C, pseudogene
                  413413
Seq. No.
                  uC-osflcyp128a05a1
Seq. ID
                  BLASTX
Method
                  g2499417
NCBI GI
                  208
BLAST score
                  1.0e-17
E value
                  56
Match length
                  86
% identity
                  GLYCINE CLEAVAGE SYSTEM H PROTEIN PRECURSOR
NCBI Description
                   >gi_1085826_pir__S49248 H-protein - Flaveria anomala
                   >gi 547558 emb CAA85761 (Z37524) H-protein [Flaveria
                   anomala]
Seq. No.
                   413414
                   uC-osflcyp128a07a1
Seq. ID
                   BLASTX
Method
NCBI GI
                   q548493
                   214
BLAST score
E value
                   4.0e-17
Match length
                   51
                   71
% identity
NCBI Description EXOPOLYGALACTURONASE PRECURSOR (EXOPG) (PECTINASE)
                   (GALACTURAN 1,4-ALPHA-GALACTURONIDASE)
                   >gi_629854_pir__S30067 polygalacturonase - maize
                   >gi_288612_emb_CAA47052_ (X66422) polygalacturonase [Zea
                   mays]
                   413415
Seq. No.
Seq. ID
                   uC-osflcyp128a09a1
Method
                   BLASTX
NCBI GI
                   q5262202
                   175
BLAST score
                   2.0e-12
E value
Match length
                   78
% identity
NCBI Description (AL080252) nodulin-like protein [Arabidopsis thaliana]
                   413416
Seq. No.
```

53842

uC-osflcyp128a10a1

Method BLASTN NCBI GI g20191 BLAST score 356 0.0e + 00E value Match length 391 98 % identity

NCBI Description O.sativa mRNA for catalase

Seq. No. 413417

Seq. ID uC-osflcyp128b02a1

Method BLASTX NCBI GI q3874563 BLAST score 150 E value 1.0e-09 Match length 48 % identity 56

(Z81042) similar to Yeast hypothetical protein YEY6 like; NCBI Description

cDNA EST yk206h5.3 comes from this gene; cDNA EST yk206h5.5 comes from this gene; cDNA EST yk303h1.3 comes from this gene; cDNA EST yk303h1.5 comes from this gene; cDN... >gi 3924825 emb CAB05549.1 (Z83113) similar to Yeast hypothetical protein YEY6 like; cDNA EST yk206h5.3 comes from this gene; cDNA EST yk206h5.5 comes from this gene; cDNA EST yk303h1.3 comes from this gene; cDNA EST yk303h1.5

comes from this gene; cDN

Seq. No. 413418

uC-osflcyp128b04a1 Seq. ID

Method BLASTN NCBI GI g1777454 BLAST score 50 4.0e-19 E value Match length 209 % identity 81

NCBI Description Oryza sativa pyruvate decarboxylase 2 (pdc2) gene, complete

cds

413419 Seq. No.

Seq. ID uC-osflcyp128b07a1

Method BLASTX NCBI GI g5263319 BLAST score 231 E value 4.0e-19 Match length 59 % identity 63

(AC007727) ESTs gb_N96028, gb_F14286, gb_T20680, gb_F14443, NCBI Description

gb AA657300 and gb N65244 come from this gene. [Arabidopsis

thaliana]

Seq. No. 413420

Seq. ID uC-osflcyp128b10a1

Method BLASTX NCBI GI g2088643 BLAST score 300 E value 4.0e-27 Match length 59 % identity 50

```
(AF002109) transcription factor SF3 isolog [Arabidopsis
NCBI Description
                   thaliana]
                   413421
Seq. No.
                   uC-osflcyp128b12a1
Seq. ID
Method
                   BLASTN
NCBI GI
                   g2586084
BLAST score
                   33
E value
                   4.0e-09
                   77
Match length
% identity
                   86
NCBI Description Oryza longistaminata receptor kinase-like protein (Xa21)
                   gene, complete cds and family member C, pseudogene
Seq. No.
                   413422
                   uC-osflcyp128c03a1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g729135
BLAST score
                   266
                   3.0e-23
E value
                   53
Match length
% identity
                   92
NCBI Description CAFFEIC ACID 3-O-METHYLTRANSFERASE
                   (S-ADENOSYSL-L-METHIONINE: CAFFEIC ACID
                   3-O-METHYLTRANSFERASE) (COMT) >gi_283034_pir__S28612 catechol O-methyltransferase (EC \overline{2.1.1.6}) - maize
                   >qi 168532 (M73235) O-methyltransferase [Zea mays]
                   413423
Seq. No.
Seq. ID
                   uC-osflcyp128c07a1
                   BLASTX
Method
NCBI GI
                   g1136122
BLAST score
                   310
E value
                   2.0e-28
Match length
                   67
                   87
% identity
NCBI Description (X91807) alfa-tubulin [Oryza sativa]
                   413424
Seq. No.
Seq. ID
                   uC-osflcyp128d01a1
Method
                   BLASTX
NCBI GI
                   g5869965
BLAST score
                   420
E value
                   3.0e-41
Match length
                   89
% identity
NCBI Description (AJ010945) Isovaleryl-CoA Dehydrogenase [Pisum sativum]
Seq. No.
                   413425
Seq. ID
                   uC-osflcyp128d05a1
Method
                   BLASTX
NCBI GI
                   q4314378
BLAST score
                   194
E value
                   1.0e-14
Match length
                   58
% identity
NCBI Description (AC006232) putative lipase [Arabidopsis thaliana]
```

Seq. No.

Seq. ID

413431

uC-osflcyp128e07a1

```
lipase [Arabidopsis thaliana]
Seq. No.
                  413426
                  uC-osflcyp128d09a1
Seq. ID
                  BLASTX
Method
NCBI GI
                  g1946300
BLAST score
                  226
E value
                  2.0e-18
Match length
                  76
% identity
                  62
                  (Y12529) hypothetical protein [Silene latifolia]
NCBI Description
                  413427
Seq. No.
Seq. ID
                  uC-osflcyp128d10a1
                  BLASTN
Method
NCBI GI
                  g20367
BLAST score
                  228
                  1.0e-125
E value
Match length
                  370
                  95
% identity
NCBI Description Oryza sativa shoot GS1 mRNA for cytosolic glutamine
                  synthetase (EC 6.3.1.2) (clone lambda-GS28)
                  413428
Seq. No.
Seq. ID
                  uC-osflcyp128e02a1
                  BLASTX
Method
NCBI GI
                  q4538920
BLAST score
                  206
                   3.0e-16
E value
Match length
                   63
                   67
% identity
                  (AL049483) nitrogen fixation like protein [Arabidopsis
NCBI Description
                   thaliana]
                   413429
Seq. No.
                   uC-osflcyp128e03a1
Seq. ID
                  BLASTN
Method
NCBI GI
                   g2723470
BLAST score
                  65
E value
                   5.0e-28
                   227
Match length
                   81
% identity
NCBI Description Oryza sativa mRNA for sucrose transporter, complete cds
Seq. No.
                   413430
Seq. ID
                   uC-osflcyp128e06a1
                  BLASTX
Method
NCBI GI
                   g485517
BLAST score
                   165
                   2.0e-11
E value
                   33
Match length
                   100
% identity
NCBI Description ADP, ATP carrier protein - rice
```

>gi 5306262 gb AAD41994.1 AC006233 5 (AC006233) putative

Method BLASTX NCBI GI g3915847 BLAST score 350 5.0e-33 E value 91 Match length 76 % identity 40S RIBOSOMAL PROTEIN S2 >gi 2335095 (AC002339) putative NCBI Description 40S ribosomal protein S2 [Arabidopsis thaliana] Seq. No. 413432 uC-osflcyp128e10a1 Seq. ID BLASTN Method NCBI GI g4097337 BLAST score 418 E value 0.0e+00445 Match length 98 % identity NCBI Description Oryza sativa metallothionein-like protein mRNA, complete cds 413433 Seq. No. Seq. ID uC-osflcyp128f02a1 Method BLASTX NCBI GI q5902382 BLAST score 241 3.0e-20 E value 75 Match length 60 % identity NCBI Description (AC009322) Unknown protein [Arabidopsis thaliana] Seq. No. 413434 Seq. ID uC-osflcyp128f03a1 Method BLASTX NCBI GI g2072555 BLAST score 196 E value 4.0e-15 37 Match length 100 % identity (AF001396) metallothionein-like protein [Oryza sativa] NCBI Description >gi 6103441 gb AAF03603.1_ (AF147786) metallothionein-like protein [Oryza sativa] 413435 Seq. No. uC-osflcyp128f07a1 Seq. ID Method BLASTN NCBI GI g2196541 231 BLAST score 1.0e-127 E value Match length 276 99 % identity

NCBI Description Oryza sativa glycine-rich protein mRNA, complete cds

Seq. No. 413436

Seq. ID uC-osflcyp128f09a1

Method BLASTX
NCBI GI g2651310
BLAST score 241

E value 3.0e-20 Match length 92 49 % identity (ACO02336) putative PTR2-B peptide transporter [Arabidopsis NCBI Description thaliana] Seq. No. 413437 Seq. ID uC-osflcyp128f10a1 BLASTX Method g1170937 NCBI GI 325 BLAST score E value 4.0e-30 Match length 59 100 % identity S-ADENOSYLMETHIONINE SYNTHETASE 1 (METHIONINE NCBI Description ADENOSYLTRANSFERASE 1) (ADOMET SYNTHETASE 1) >gi_450549_emb_CAA81481_ (Z26867) S-adenosyl methionine synthetase [Oryza sativa] 413438 Seq. No. Seq. ID uC-osflcyp128g03a1 Method BLASTN NCBI GI q5852170 424 BLAST score E value 0.0e + 00428 Match length 100 % identity NCBI Description Oryza sativa indica(GLA4) genomic DNA, chromosome 4, BAC clone:t17804 413439 Seq. No. Seq. ID uC-osflcyp128g06a1 Method BLASTX NCBI GI q4678293 BLAST score 189 3.0e-14E value 54 Match length 32 % identity NCBI Description (AL049655) hypothetical protein [Arabidopsis thaliana] 413440 Seq. No. Seq. ID uC-osflcyp128g07a1 Method BLASTN NCBI GI q3885887 BLAST score 262 1.0e-145 E value 310 Match length % identity 96 NCBI Description Oryza sativa high mobility group protein (HMG) mRNA, complete cds Seq. No. 413441 Seq. ID uC-osflcyp128g10a1 Method BLASTN NCBI GI g2274987 BLAST score 42 E value 3.0e-14

```
82
Match length
                  88
% identity
NCBI Description Hordeum vulgare mRNA for expressed sequence tag
                  413442
Seq. No.
                  uC-osflcyp128h01a1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g20280
BLAST score
                  217
                  1.0e-118
E value
Match length
                  346
                  90
% identity
NCBI Description Rice gene for phenylalanine ammonia-lyase (EC 4.3.1.5)
                  413443
Seq. No.
                  uC-osflcyp128h03a1
Seq. ID
Method
                  BLASTN
                  g2331130
NCBI GI
                  209
BLAST score
E value
                  1.0e-114
                  269
Match length
                  94
% identity
                  Oryza sativa glycine-rich protein (OSGRP1) mRNA, complete
NCBI Description
                  cds
                  413444
Seq. No.
                  uC-osflcyp128h04a1
Seq. ID
Method
                  BLASTX
                  q1653142
NCBI GI
BLAST score
                   148
E value
                   2.0e-09
Match length
                  76
                   46
% identity
NCBI Description (D90911) hypothetical protein [Synechocystis sp.]
Seq. No.
                   413445
                   uC-osflcyp128h06a1
Seq. ID
Method
                   BLASTX
NCBI GI
                   q1076746
BLAST score
                   262
E value
                   9.0e-23
Match length
                   81
% identity
                   69
                  heat shock protein 70 - rice (fragment)
NCBI Description
                   >gi 763160 emb CAA47948 (X67711) heat shock protein 70
                   [Oryza sativa]
                   413446
Seq. No.
                   uC-osflcyp128h09a1
Seq. ID
Method
                   BLASTX
                   q3341511
NCBI GI
                   293
BLAST score
E value
                   2.0e-26
Match length
                   69
                   80
% identity
NCBI Description (AJ231134) cinnamoyl-CoA reductase [Saccharum officinarum]
```

```
413447
Seq. No.
                  uC-osflcyp129a03a1
Seq. ID
                  BLASTX
Method
NCBI GI
                  q2130069
                  230
BLAST score
                  6.0e-19
E value
                  54
Match length
% identity
                  catalase (EC 1.11.1.6) catA - rice
NCBI Description
                  >gi_1261858_dbj_BAA06232_ (D29966) catalase [Oryza sativa]
Seq. No.
                  uC-osflcyp129a04a1
Seq. ID
                  BLASTX
Method
NCBI GI
                  q3378652
                   302
BLAST score
                   2.0e-27
E value
                   60
Match length
                   98
% identity
                  (AJ005039) CaM-1 [Nicotiana plumbaginifolia]
NCBI Description
                   >gi_3378654_emb_CAA06307_ (AJ005040) CaM-2 [Nicotiana
                  plumbaginifolia]
                   413449
Seq. No.
                   uC-osflcyp129a08a1
Seq. ID
                   BLASTX
Method
                   q4584255
NCBI GI
                   838
BLAST score
                   4.0e-90
E value
                   158
Match length
% identity
                   91
NCBI Description (Y18471) SINA1p [Vitis vinifera]
                   413450
Seq. No.
                   uC-osflcyp129a09a1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g132105
BLAST score
                   707
                   8.0e-75
E value
Match length
                   129
                   100
% identity
NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
                   (RUBISCO SMALL SUBUNIT C) >gi_68094_pir__RKRZS9
                   ribulose-bisphosphate carboxylase (\overline{EC} 4.1.1.39) small chain
                   precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_
                   (D00643) small subunit of ribulose-1,5-bisphosphate
                   carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364)
                   ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
                   sativa] >gi_226375_prf__1508256A ribulose bisphosphate
                   carboxylase S [Oryza sativa]
 Seq. No.
                   413451
                   uC-osflcyp129a12a1
 Seq. ID
                   BLASTX
 Method
                   g6006879
 NCBI GI
                   203
 BLAST score
```

53849

4.0e-16

E value

E value

Match length

% identity

2.0e-27

56 98

```
Match length
% identity
                   (AC008153) putative eukaryotic translation initiation
NCBI Description
                  factor 3 subunit [Arabidopsis thaliana]
                  413452
Seq. No.
                  uC-osflcyp129b03a1
Seq. ID
                  BLASTN
Method
NCBI GI
                  q5295936
                  35
BLAST score
E value
                  5.0e-10
Match length
                  63
                  89
% identity
                  Oryza sativa genomic DNA, chromosome 6, clone:P0681F10,
NCBI Description
                  complete sequence
                   413453
Seq. No.
                  uC-osflcyp129b04a1
Seq. ID
Method
                  BLASTX
NCBI GI
                   g1946361
                   281
BLAST score
                   7.0e-25
E value
Match length
                   103
                   54
% identity
                  (U93215) C3HC4 zinc finger protein isolog [Arabidopsis
NCBI Description
                   thaliana]
                   413454
Seq. No.
                   uC-osflcyp129b06a1
Seq. ID
                   BLASTX
Method
NCBI GI
                   g1890575
BLAST score
                   224
E value
                   3.0e-18
Match length
                   47
% identity
                   85
                  (X93174) xyloglucan endotransglycosylase (XET) [Hordeum
NCBI Description
                   vulgare]
                   413455
Seq. No.
Seq. ID
                   uC-osflcyp129c02a1
Method
                   BLASTX
NCBI GI
                   g3608412
BLAST score
                   427
                   4.0e-42
E value
                   114
Match length
% identity
                   71
                  (AF079355) protein phosphatase-2c [Mesembryanthemum
NCBI Description
                   crystallinum]
                   413456
Seq. No.
                   uC-osflcyp129c03a1
Seq. ID
                   BLASTX
Method
                   g129591
NCBI GI
                   302
BLAST score
```

NCBI GI

```
NCBI Description PHENYLALANINE AMMONIA-LYASE >qi 295824 emb CAA34226
                   (X16099) phenylalanine ammonia-lyase [Oryza sativa]
Seq. No.
                   413457
Seq. ID
                  uC-osflcyp129c04a1
Method
                  BLASTX
NCBI GI
                  g2832633
BLAST score
                  321
E value
                  1.0e-29
Match length
                  67
% identity
                  97
NCBI Description (AL021711) putative protein [Arabidopsis thaliana]
Seq. No.
                  413458
Seq. ID
                  uC-osflcyp129c09a1
Method
                  BLASTX
NCBI GI
                  g481477
BLAST score
                  448
E value
                  2.0e-44
Match length
                  90
% identity
                  17
NCBI Description ubiquitin precursor - rice >gi_416038_emb_CAA53665
                   (X76064) polyubiquitin [Oryza sativa] >gi 1574944 (U37687)
                  polyubiquitin [Oryza sativa]
                  >gi_6013289_gb_AAF01315.1_AF184279_1 (AF184279)
                  polyubiquitin [Oryza sativa]
                  >gi_6013291_gb_AAF01316.1_AF184280_1 (AF184280)
                  polyubiquitin [Oryza sativa]
Seq. No.
                  413459
Seq. ID
                  uC-osflcyp129d01a1
Method
                  BLASTX
NCBI GI
                  q548605
BLAST score
                  442
E value
                  7.0e-44
                  98
Match length
% identity
                  88
NCBI Description PHOTOSYSTEM I REACTION CENTRE SUBUNIT X PRECURSOR
                  (LIGHT-HARVESTING COMPLEX I 7 KD PROTEIN) (PSI-K)
                  >gi 539055 pir A48527 photosystem I protein psaK precursor
                   - barley >gi 304220 (L12707) photosystem I PSI-K subunit
                  [Hordeum vulgare]
                  413460
Seq. No.
Seq. ID
                  uC-osflcyp129e01a1
                  BLASTN
Method
NCBI GI
                  g4105602
BLAST score
                  378
E value
                  0.0e + 00
Match length
                  378
% identity
                  100
NCBI Description Oryza sativa metallothionein (MTe) gene, complete cds
Seq. No.
                  413461
Seq. ID
                  uC-osflcyp129e04a1
Method
                  BLASTX
```

53851

g5091552

```
BLAST score
                   215
 E value
                   3.0e-17
 Match length
                   55
 % identity
                   65
 NCBI Description (AC007067) T10024.21 [Arabidopsis thaliana]
 Seq. No.
                   413462
 Seq. ID
                   uC-osflcyp129e05a1
 Method
                   BLASTX
 NCBI GI
                   q3763918
 BLAST score
                   218
 E value
                   2.0e-17
 Match length
                   58
 % identity
                   74
 NCBI Description (AC004450) putative isopropylmalate dehydratase
                   [Arabidopsis thaliana]
 Seq. No.
                   413463
 Seq. ID
                   uC-osflcyp129e06a1
 Method
                   BLASTX
NCBI GI
                   g5081779
BLAST score
                  272
E value
                   5.0e-24
Match length
                  57
% identity
NCBI Description (AF150630) cellulose synthase [Gossypium hirsutum]
Seq. No.
                  413464
Seq. ID
                   uC-osflcyp129e07a1
Method
                  BLASTX
NCBI GI
                  g3915847
BLAST score
                  273
E value
                  5.0e-24
Match length
                  74
% identity
                  72
NCBI Description 40S RIBOSOMAL PROTEIN S2 >gi_2335095 (AC002339) putative
                  40S ribosomal protein S2 [Arabidopsis thaliana]
Seq. No.
                  413465
Seq. ID
                  uC-osflcyp129e08a1
Method
                  BLASTX
NCBI GI
                  g3913426
BLAST score
                  521
E value
                  6.0e-53
Match length
                  98
% identity
                  96
NCBI Description S-ADENOSYLMETHIONINE DECARBOXYLASE PROENZYME (ADOMETDC)
                  (SAMDC) >gi_1532048_emb_CAA69074_ (Y07766)
                  S-adenosylmethionine decarboxylase [Oryza sativa]
Seq. No.
                  413466
Seq. ID
                  uC-osflcyp129e11a1
Method
                  BLASTX
NCBI GI
                  g100598
BLAST score
                  618
E value
                  2.0e-64
Match length
                  155
```



% identity 79

NCBI Description ubiquitin / ribosomal protein S27a-1 - barley >gi 167073

(M60175) ubiquitin [Hordeum vulgare]

Seq. No. 413467

Seq. ID uC-osflcyp129f04a1

Method BLASTX
NCBI GI g3183079
BLAST score 216
E value 2.0e-17
Match length 76
% identity 58

NCBI Description MALATE DEHYDROGENASE, GLYOXYSOMAL PRECURSOR

>gi_1375075_dbj_BAA12870.1_ (D85763) glyoxysomal malate

dehydrogenase [Oryza sativa]

Seq. No. 413468

Seq. ID uC-osflcyp129f12a1

Method BLASTX
NCBI GI g5733874
BLAST score 227
E value 2.0e-18
Match length 92
% identity 42

NCBI Description (AC007932) F11A17.8 [Arabidopsis thaliana]

Seq. No. 413469

Seq. ID uC-osflcyp129g01a1

Method BLASTN
NCBI GI g2286112
BLAST score 229
E value 1.0e-126
Match length 371
% identity 90

NCBI Description Oryza sativa MADS box protein (OsMADS8) mRNA, complete cds

Seq. No. 413470

Seq. ID uC-osflcyp129g02a1

Method BLASTN
NCBI GI g2286108
BLAST score 369
E value 0.0e+00
Match length 369
% identity 100

NCBI Description Oryza sativa MADS box protein (OsMADS6) mRNA, complete cds

Seq. No. 413471

Seq. ID uC-osflcyp129q07a1

Method BLASTX
NCBI GI g3421123
BLAST score 258
E value 3.0e-22
Match length 84
% identity 58

NCBI Description (AF043538) 20S proteasome beta subunit PBG1 [Arabidopsis

thaliana]

NCBI GI

```
413472
Seq. No.
Seq. ID
                  uC-osflcyp129g08a1
Method
                  BLASTX
NCBI GI
                  g829283
BLAST score
                  364
E value
                  1.0e-34
Match length
                  85
% identity
                  88
NCBI Description (Z15018) heat shock protein hsp82 [Oryza sativa]
Seq. No.
                  413473
Seq. ID
                  uC-osflcyp129g10a1
Method
                  BLASTX
NCBI GI
                  q267056
BLAST score
                  240
E value
                  3.0e-20
Match length
                  61
% identity
                  80
NCBI Description
                  SUCROSE SYNTHASE 1 (SUCROSE-UDP GLUCOSYLTRANSFERASE 1)
                  >gi_100710_pir__S25526 sucrose synthase (EC 2.4.1.13) -
                  rice >gi_20374_emb_CAA78747_ (Z15028) sucrose synthase
                   [Oryza sativa]
Seq. No.
                  413474
Seq. ID
                  uC-osflcyp129g11a1
Method
                  BLASTX
NCBI GI
                  g4098272
BLAST score
                  295
E value
                  1.0e-26
Match length
                  62
% identity
                  89
NCBI Description (U76558) alpha-tubulin [Triticum aestivum]
Seq. No.
                  413475
Seq. ID
                  uC-osflcyp129h02a1
Method
                  BLASTX
NCBI GI
                  q1762935
BLAST score
                  176
E value
                  1.0e-12
Match length
                  51
% identity
                  73
NCBI Description (U66264) ubiquitin [Nicotiana tabacum]
Seq. No.
                  413476
Seq. ID
                  uC-osflcyp129h03a1
Method
                  BLASTX
NCBI GI
                  q2586127
BLAST score
                  253
E value
                  1.0e-21
Match length
                  66
% identity
NCBI Description (U89510) b-keto acyl reductase [Hordeum vulgare]
Seq. No.
                  413477
Seq. ID
                  uC-osflcyp129h04a1
Method
                  BLASTX
```

53854

q5381253



BLAST score 409 E value 6.0e-40 Match length 98 77 % identity

NCBI Description (AB027752) peroxidase [Nicotiana tabacum]

Seq. No. 413478

Seq. ID uC-osflcyp129h09a1

Method BLASTX NCBI GI g2129825 BLAST score 322 E value 1.0e-29 Match length 74 86 % identity

NCBI Description dynamin-like protein phragmoplastin 12 - soybean

>gi_1217994 (U25547) SDL [Glycine max]

Seq. No. 413479

Seq. ID uC-osflcyp130a04a1

Method BLASTX NCBI GI g6094014 BLAST score 296 E value 9.0e-2775 Match length % identity 75

NCBI Description 60S RIBOSOMAL PROTEIN L15 >gi_3608479 (AF088912) ribosomal

protein L15 [Petunia x hybrida]

Seq. No. 413480

Seq. ID uC-osflcyp130b03a1

Method BLASTN NCBI GI q3885887 BLAST score 63 E value 9.0e-27 Match length 215 % identity 82

NCBI Description Oryza sativa high mobility group protein (HMG) mRNA,

complete cds

Seq. No. 413481

Seq. ID uC-osflcyp130b06a1

Method BLASTX NCBI GI g1170937 BLAST score 245 E value 1.0e-20 Match length 50 % identity 90

NCBI Description S-ADENOSYLMETHIONINE SYNTHETASE 1 (METHIONINE

ADENOSYLTRANSFERASE 1) (ADOMET SYNTHETASE 1)

>gi_450549_emb_CAA81481_ (Z26867) S-adenosyl methionine

synthetase [Oryza sativa]

Seq. No. 413482

Seq. ID uC-osflcyp130b07a1

Method BLASTX NCBI GI g1785856 BLAST score 172



4.0e-12 E value Match length 32 % identity 97

NCBI Description (D78505) w-3 fatty acid desaturase [Oryza sativa]

Seq. No. 413483

Seq. ID uC-osflcyp130b08a1

Method BLASTX NCBI GI g132105 BLAST score 326 E value 3.0e - 30Match length 61 % identity 100

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR

(RUBISCO SMALL SUBUNIT C) >gi_68094_pir_RKRZS9 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor (clone pOSSS1139) - rice >gi 218208 dbj BAA00538

(D00643) small subunit of ribulose-1,5-bisphosphate

carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa] >gi_226375_prf__1508256A ribulose bisphosphate

carboxylase S [Oryza sativa]

Seq. No. 413484

Seq. ID uC-osflcyp130c01a1

Method BLASTN NCBI GI q2407276 BLAST score 61 E value 1.0e-25 132

Match length % identity 87

Oryza sativa lipid transfer protein LPT IV mRNA, complete NCBI Description

Seq. No. 413485

Seq. ID uC-osflcyp130c02a1

Method BLASTX NCBI GI g2117620 BLAST score 212 E value 8.0e-17 Match length 84 55 % identity

NCBI Description peroxidase (EC 1.11.1.7) 1A - alfalfa

>gi_971558_emb_CAA62225_ (X90692) peroxidase1A [Medicago

sativa]

Seq. No. 413486

Seq. ID uC-osflcyp130c03a1

Method BLASTN NCBI GI g5902929 BLAST score 37 E value 3.0e-11 Match length 200 80 % identity

NCBI Description Oryza sativa mRNA for small GTP-binding protein OsRac3,

complete cds

Seq. ID

Method

```
413487
Seq. No.
Seq. ID
                  uC-osflcyp130c07a1
Method
                  BLASTX
NCBI GI
                  g5932555
BLAST score
                  382
E value
                  9.0e-37
Match length
                  102
% identity
                  72
NCBI Description (AC009465) putative ribose 5-phosphate isomerase
                  [Arabidopsis thaliana]
                  413488
Seq. No.
Seq. ID
                  uC-osflcyp130d01a1
Method
                  BLASTX
NCBI GI
                  g5306263
BLAST score
                  182
E value
                  3.0e-13
Match length
                  60
% identity
                  60
NCBI Description (AC006233) unknown protein [Arabidopsis thaliana]
Seq. No.
                  413489
Seq. ID
                  uC-osflcyp130d02a1
                  BLASTX
Method
NCBI GI
                  q4768911
                  408
BLAST score
                  9.0e-40
E value
Match length
                  79
% identity
                  96
NCBI Description (AF131201) plasma membrane MIP protein [Zea mays]
                  413490
Seq. No.
Seq. ID
                  uC-osflcyp130d03a1
Method
                  BLASTX
NCBI GI
                  q6015059
BLAST score
                  398
E value
                  1.0e-38
Match length
                  78
% identity
                  100
NCBI Description ELONGATION FACTOR 1-ALPHA (EF-1-ALPHA) >gi 2996096
                  (AF030517) translation elongation factor-1 alpha; EF-1
                  alpha [Oryza sativa]
Seq. No.
                  413491
Seq. ID
                  uC-osflcyp130d06a1
Method
                  BLASTX
NCBI GI
                  q2281085
BLAST score
                  201
E value
                  1.0e-15
Match length
                  64
% identity
NCBI Description (AC002333) CTR1 protein kinase isolog [Arabidopsis
                  thaliana]
Seq. No.
                  413492
```

53857

uC-osflcyp130d11a1

BLASTX

```
NCBI GI
                  q4586249
BLAST score
                  220
                  9.0e-18
E value
Match length
                  86
% identity
                  (AL049640) putative pollen surface protein [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  413493
                  uC-osflcyp130e04a1
Seq. ID
Method
                  BLASTN
                  g5670155
NCBI GI
BLAST score
                  62
                  4.0e-26
E value
Match length
                  126
                  87
% identity
NCBI Description Oryza sativa subsp. japonica BAC clone 34K24, complete
                  sequence
                  413494
Seq. No.
                  uC-osflcyp130e05a1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q464470
BLAST score
                  159
E value
                   1.0e-10
Match length
                  30
                   97
% identity
NCBI Description PROFILIN 3 >gi_422033_pir__S35798 profilin 3 - maize
                  >gi_313142_emb_CAA51720_ (X73281) profilin 3 [Zea mays]
Seq. No.
                   413495
                  uC-osflcyp130e06a1
Seq. ID
                  BLASTX
Method
NCBI GI
                   q2829892
BLAST score
                   174
E value
                   2.0e-12
Match length
                   60
% identity
NCBI Description (AC002311) putative pectinesterase [Arabidopsis thaliana]
Seq. No.
                   413496
                   uC-osflcyp130e09a1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g1170937
                   329
BLAST score
E value
                   2.0e-30
Match length
                   62
                   98
% identity
                   S-ADENOSYLMETHIONINE SYNTHETASE 1 (METHIONINE
NCBI Description
                   ADENOSYLTRANSFERASE 1) (ADOMET SYNTHETASE 1)
                   >gi_450549_emb_CAA81481_ (Z26867) S-adenosyl methionine
                   synthetase [Oryza sativa]
                   413497
Seq. No.
Seq. ID
                   uC-osflcyp130e11a1
Method
                   BLASTN
NCBI GI
                   g606418
```

E value

5.0e-12

```
BLAST score
                  93
E value
                  1.0e-44
Match length
                  212
% identity
                  86
NCBI Description Oryza Sativa (clone RGAE8) G protein alpha subunit (RGA1)
                  gene, complete cds
Seq. No.
                  413498
Seq. ID
                  uC-osflcyp130f02a1
Method
                  BLASTX
NCBI GI
                  g2642213
BLAST score
                  352
E value
                  3.0e - 33
Match length
                  73
% identity
                  88
                  (AF030385) nitrate-induced NOI protein [Zea mays]
NCBI Description
                  >gi 2895781 (AF045033) nitrate-induced NOI protein [Zea
                  mays]
                  413499
Seq. No.
Seq. ID
                  uC-osflcyp130f07a1
Method
                  BLASTN
NCBI GI
                  q4730883
BLAST score
                  283
E value
                  1.0e-158
Match length
                  356
                  94
% identity
NCBI Description Oryza sativa gene for alanine aminotransferase, complete
Seq. No.
                  413500
Seq. ID
                  uC-osflcyp130f11a1
Method
                  BLASTN
NCBI GI
                  g606418
BLAST score
                  272
E value
                  1.0e-151
Match length
                  287
                  99
% identity
NCBI Description Oryza Sativa (clone RGAE8) G protein alpha subunit (RGA1)
                  gene, complete cds
Seq. No.
                  413501
Seq. ID
                  uC-osflcyp130g01a1
Method
                  BLASTX
NCBI GI
                  g4539417
                  199
BLAST score
E value
                  2.0e-15
                  52
Match length
% identity
NCBI Description (AL049171) putative protein [Arabidopsis thaliana]
Seq. No.
                  413502
Seq. ID
                  uC-osflcyp130g12a1
                  BLASTX
Method
NCBI GI
                  g259138
BLAST score
                  170
```

```
Match length
                   41
% identity
NCBI Description
                  oryzacystatin=cysteine protease inhibitor [Oryza=rice,
                   Peptide Recombinant, 90 aa]
                   413503
Seq. No.
Seq. ID
                  uC-osflcyp130h01a1
Method
                  BLASTX
NCBI GI
                  g226263
BLAST score
                  272
E value
                   5.0e-24
Match length
                  68
% identity
                  75
NCBI Description chlorophyll a/b binding protein [Glycine max]
                   413504
Seq. No.
Seq. ID
                  uC-osflcyp130h04a1
Method
                  BLASTX
NCBI GI
                  g3885334
BLAST score
                  289
E value
                   7.0e-26
Match length
                  90
% identity
                   64
NCBI Description
                  (AC005623) putative argonaute protein [Arabidopsis
                  thaliana]
Seq. No.
                   413505
Seq. ID
                  uC-osflcyp130h08a1
Method
                  BLASTX
NCBI GI
                  g4139264
BLAST score
                  184
                  1.0e-13
E value
                  38
Match length
% identity
                  89
NCBI Description (AF111812) actin [Brassica napus]
Seq. No.
                   413506
Seq. ID
                  uC-osflcyp130h09a1
Method
                  BLASTX
NCBI GI
                  g1835731
BLAST score
                  173
E value
                  2.0e-12
Match length
                  49
% identity
NCBI Description (U86018) photosystem II 10 kDa polypeptide [Oryza sativa]
Seq. No.
                   413507
Seq. ID
                  uC-osflcyp130h10a1
Method
                  BLASTX
```

Method BLASTX
NCBI GI g5081779
BLAST score 235
E value 1.0e-19
Match length 53
% identity 83

NCBI Description (AF150630) cellulose synthase [Gossypium hirsutum]

Seq. No. 413508



Seq. ID uC-osflcyp131a01a1 Method BLASTN NCBI GI g5852170 BLAST score 180 E value 1.0e-96 Match length 252 % identity 96 NCBI Description Oryza sativa indica(GLA4) genomic DNA, chromosome 4, BAC clone:t17804 413509 Seq. No. Seq. ID uC-osflcyp131a02a1 Method BLASTX NCBI GI q710308 157 BLAST score E value 2.0e-10 33 Match length % identity 85 NCBI Description (U11693) victorin binding protein [Avena sativa] Seq. No. 413510 Seq. ID uC-osflcyp131a08a1 Method BLASTX NCBI GI q2073375 BLAST score 234 E value 2.0e-35 79 Match length 100 % identity NCBI Description (D85317) farnesyl pyrophosphate synthase [Oryza sativa] >gi_4063829_dbj_BAA36276_ (AB021747) farnesyl diphosphate synthase [Oryza sativa] Seq. No. 413511 Seq. ID uC-osflcyp131b01a1 BLASTN Method NCBI GI q2913890 BLAST score 346 E value 0.0e + 00Match length 366 % identity 99 NCBI Description Oryza sativa mRNA for LIP9, partial cds Seq. No. 413512 Seq. ID uC-osflcyp131b02a1 BLASTX q1617197 152 6.0e-10

Method NCBI GI BLAST score E value Match length 31 % identity

NCBI Description (Z72488) CP12 [Nicotiana tabacum]

Seq. No. 413513

Seq. ID uC-osflcyp131b04a1

Method BLASTX NCBI GI q1076820 BLAST score 328

```
E value
                   2.0e-30
Match length
                  71
                  90
% identity
NCBI Description phosphoglycerate mutase (EC 5.4.2.1) - maize
                  413514
Seq. No.
Seq. ID
                  uC-osflcyp131b08a1
Method
                  BLASTX
NCBI GI
                  g5305667
BLAST score
                  242
E value
                  2.0e-20
Match length
                  106
% identity
                   46
NCBI Description
                   (AF111842) isopentenyl pyrophosphate isomerase [Hevea
                  brasiliensis] >gi 5305669 gb AAD41766.1 AF111843 1
                   (AF111843) isopentenyl pyrophosphate isomerase [Hevea
                  brasiliensis]
Seq. No.
                   413515
Seq. ID
                  uC-osflcyp131c08a1
Method
                  BLASTN
NCBI GI
                  g2864607
BLAST score
                  36
E value
                  1.0e-10
Match length
                  68
% identity
                  88
NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F10M6
                   (ESSAII project)
Seq. No.
                  413516
Seq. ID
                  uC-osflcyp131c10a1
Method
                  BLASTN
NCBI GI
                  g2331130
BLAST score
                  205
E value
                  1.0e-111
                  205
Match length
                  100
% identity
NCBI Description Oryza sativa glycine-rich protein (OSGRP1) mRNA, complete
                  cds
Seq. No.
                  413517
Seq. ID
                  uC-osflcyp131d04a1
Method
                  BLASTX
NCBI GI
                  g4115377
BLAST score
                  236
E value
                  1.0e-19
                  54
Match length
% identity
NCBI Description (AC005967) unknown protein [Arabidopsis thaliana]
Seq. No.
                  413518
```

Seq. ID uC-osflcyp131d06a1

Method BLASTX NCBI GI g548774 BLAST score 337 E value 1.0e-31 85 Match length

% identity 80 60S RIBOSOMAL PROTEIN L7A >gi 542158_pir__ S38360 ribosomal NCBI Description protein L7a - rice >gi_303855_dbj_BAA02156_ (D12631) ribosomal protein L7A [Oryza sativa] 413519 Seq. No. Seq. ID uC-osflcyp131d09a1 Method BLASTX NCBI GI q871931 BLAST score 179 E value 5.0e-13Match length 62 % identity NCBI Description (D30763) ferredoxin [Oryza sativa] 413520 Seq. No. uC-osflcyp131d11a1 Seq. ID Method BLASTX . g1351017 NCBI GI BLAST score 186 5.0e-14E value 43 Match length % identity 79 NCBI Description 40S RIBOSOMAL PROTEIN S9 (S4) >gi 629697 pir S45375 ribosomal protein S4 - common tobacco (fragment) >gi_443960_emb_CAA78463_ (Z14085) RIBOSOMAL PROTEIN S4 [Nicotiana tabacum] 413521 Seq. No. Seq. ID uC-osflcyp131f11a1 Method BLASTX NCBI GI g3036951 BLAST score 467 E value 9.0e-47Match length 89 % identity 99 NCBI Description (AB012639) light harvesting chlorophyll a/b-binding protein [Nicotiana sylvestris] 413522 Seq. No. Seq. ID uC-osflcyp131g02a1 Method BLASTX NCBI GI g2582822 BLAST score 310 E value 2.0e-28 Match length 69 % identity 83 (Y09987) CDSP32 protein (Chloroplast Drought-induced Stress NCBI Description Protein of 32kDa) [Solanum tuberosum] Seq. No. 413523 Seq. ID uC-osflcyp131g07a1 BLASTX Method NCBI GI g4587989 BLAST score 245

53863

1.0e-20

123

E value Match length

% identity (AF085279) hypothetical Cys-3-His zinc finger protein NCBI Description [Arabidopsis thaliana] 413524 Seq. No. uC-osflcyp131g08a1 Seq. ID BLASTX Method NCBI GI g3023751 BLAST score 270 1.0e-23 E value Match length 64 83 % identity NCBI Description 70 KD PEPTIDYLPROLYL ISOMERASE (PEPTIDYLPROLYL CIS-TRANS ISOMERASE) (CYCLOPHILIN) (PPIASE) >gi_1076772_pir__S55383
peptidylprolyl isomerase (EC 5.2.1.8) - wheat >gi_854626_emb_CAA60505_ (X86903) peptidylprolyl isomerase [Triticum aestivum] 413525 Seq. No. Seq. ID uC-osflcyp131h01a1 Method BLASTN q600766 NCBI GI BLAST score 247 E value 1.0e-136 303 Match length % identity 96 NCBI Description Oryza sativa cyclophilin 2 (Cyp2) gene, complete cds 413526 Seq. No. uC-osflcyp131h06a1 Seq. ID Method BLASTX NCBI GI g2342494 BLAST score 241 E value 2.0e-20 Match length 71 % identity 59 (D14058) bromelain [Ananas comosus] NCBI Description >gi_2463582_dbj_BAA22543_ (D38531) FB31 precursor (FB13 precursor) [Ananas comosus] Seq. No. 413527 Seq. ID uC-osflcyp131h09a1 Method BLASTN NCBI GI g450548 190 BLAST score E value 1.0e-102 Match length 190 100 % identity O.sativa (pRSAM-1) gene for S-adenosyl methionine NCBI Description

synthetase

Seq. No. 413528

Seq. ID uC-osflcyp131h10a1

BLASTX Method g548493 NCBI GI BLAST score 296 E value 1.0e-26

E value

Match length

2.0e-17

59

Match length 69 % identity 74 NCBI Description EXOPOLYGALACTURONASE PRECURSOR (EXOPG) (PECTINASE) (GALACTURAN 1,4-ALPHA-GALACTURONIDASE) >gi 629854 pir S30067 polygalacturonase - maize >gi 288612 emb CAA47052 (X66422) polygalacturonase [Zea mays] Seq. No. 413529 Seq. ID uC-osflcyp132a02a1 Method BLASTX NCBI GI g5441874 BLAST score 173 E value 2.0e-12 Match length 45 69 % identity NCBI Description (AP000366) Similar to maize transposon MuDR mudrA-like protein. (AC002340) [Oryza sativa] Seq. No. 413530 Seq. ID uC-osflcyp132a05a1 Method BLASTN NCBI GI g450548 BLAST score 248 E value 1.0e-137 Match length 255 % identity 100 NCBI Description O.sativa (pRSAM-1) gene for S-adenosyl methionine synthetase Seq. No. 413531 Seq. ID uC-osflcyp132a07a1 Method BLASTN NCBI GI g3273242 BLAST score 373 E value 0.0e+00Match length 413 % identity 98 NCBI Description Oryza sativa mRNA for NLS receptor, complete cds 413532 Seq. No. Seq. ID uC-osflcyp132a08a1 Method BLASTX g2804572 NCBI GI BLAST score 379 E value 2.0e-36 Match length 77 % identity NCBI Description (AB006081) chlorophyll a/b-binding protein [Fagus crenata] Seq. No. 413533 Seq. ID uC-osflcyp132b03a1 Method BLASTX NCBI GI g1362086 BLAST score 157

BLAST score

436

% identity NCBI Description 5-methyltetrahydropteroyltriglutamate--homocysteine S-methyltransferase (EC 2.1.1.14) - Madagascar periwinkle >gi 2129919 pir S65957 5-methyltetrahydropteroyltriglutamate--homocysteine S-methyltransferase (EC 2.1.1.14) - Madagascar periwinkle >gi_886471_emb_CAA58474_ (X83499) methionine synthase [Catharanthus roseus] Seq. No. 413534 Seq. ID uC-osflcyp132b05a1 Method BLASTN NCBI GI g3851004 BLAST score 35 E value 6.0e-10 Match length 127 % identity 83 NCBI Description Zea mays pyruvate dehydrogenase E1 alpha subunit RNA, nuclear gene encoding mitochondrial protein, complete cds Seq. No. 413535 Seq. ID uC-osflcyp132b06a1 Method BLASTX NCBI GI g2827314 BLAST score 247 E value 6.0e-21 Match length 56 % identity 86 NCBI Description (AF042199) casein kinase [Oryza sativa] Seq. No. 413536 Seq. ID uC-osflcyp132b10a1 Method BLASTX NCBI GI g5679838 BLAST score 190 E value 6.0e-19 Match length 117 % identity 44 NCBI Description (AJ243961) has similarity to Arabidopsis thaliana gi 3068705 [Oryza sativa] 413537 Seq. No. Seq. ID uC-osflcyp132b11a1 Method BLASTX NCBI GI g100598 BLAST score 178 9.0e-13 E value 52 Match length % identity 69 NCBI Description ubiquitin / ribosomal protein S27a-1 - barley >gi_167073 (M60175) ubiquitin [Hordeum vulgare] Seq. No. 413538 Seq. ID uC-osflcyp132b12a1 Method BLASTN NCBI GI q4097337

```
0.0e + 00
E value
Match length
                   452
% identity
                   99
                   Oryza sativa metallothionein-like protein mRNA, complete
NCBI Description
Seq. No.
                   413539
Seq. ID
                   uC-osflcyp132c12a1
Method
                   BLASTX
NCBI GI
                   g322854
BLAST score
                   376
                   4.0e-36
E value
                   92
Match length
% identity
                   84
NCBI Description pollen-specific protein - rice >gi 20310 emb CAA78897
                   (Z16402) pollen specific gene [Oryza sativa]
Seq. No.
                   413540
Seq. ID
                   uC-osflcyp132d03a1
Method
                   BLASTX
NCBI GI
                   q2342735
BLAST score
                   318
E value
                   2.0e-31
Match length
                   94
% identity
                   73
NCBI Description (AC002341) unknown protein [Arabidopsis thaliana]
Seq. No.
                   413541
Seq. ID
                   uC-osflcyp132d06a1
Method
                   BLASTX
NCBI GI
                   g421916
BLAST score
                   258
E value
                   3.0e-22
Match length
                   49
% identity
                   98
                   chlorophyll a/b-binding protein - English ivy (fragment)
>gi_12582_emb_CAA48410_ (X68333) light harvesting
NCBI Description
                   chlorophyll a /b binding protein [Hedera helix]
Seq. No.
                   413542
Seq. ID
                   uC-osflcyp132d11a1
Method
                   BLASTX
NCBI GI
                   g3914470
BLAST score
                   413
E value
                   2.0e-40
                   94
Match length
                   79
% identity
NCBI Description PHOTOSYSTEM II 10 KD POLYPEPTIDE PRECURSOR
                   >gi 1321868 emb CAA66373 (X97771) 10kD PSII protein
                   [Hordeum vulgare]
```

413543 Seq. No.

Seq. ID uC-osflcyp132e02a1

Method BLASTN NCBI GI q6063530 BLAST score 393 0.0e + 00E value

421 Match length % identity 98 NCBI Description Oryza sativa genomic DNA, chromosome 3, clone:P0043E01 413544 Seq. No. Seq. ID uC-osflcyp132e04a1 Method BLASTX NCBI GI q2832660 BLAST score 356 E value 1.0e-33 Match length 135 50 % identity NCBI Description (AL021710) lipase-like protein [Arabidopsis thaliana] Seq. No. 413545 uC-osflcyp132e05a1 Seq. ID Method BLASTN NCBI GI g5295936 BLAST score 303 E value 1.0e-170 Match length 315 99 % identity NCBI Description Oryza sativa genomic DNA, chromosome 6, clone:P0681F10, complete sequence Seq. No. 413546 uC-osflcyp132e06a1 Seq. ID BLASTX Method NCBI GI q4314378 BLAST score 148 E value 2.0e-09 Match length 47 % identity 51 NCBI Description (AC006232) putative lipase [Arabidopsis thaliana] >gi 5306262_gb_AAD41994.1_AC006233_5 (AC006233) putative lipase [Arabidopsis thaliana] 413547 Seq. No. Seq. ID uC-osflcyp132e10a1 BLASTX Method NCBI GI g693920 BLAST score 366 E value 8.0e-35 72 Match length % identity 97 (U21113) chlorophyll a/b binding protein [Solanum NCBI Description tuberosum]

Seq. No. 413548

Seq. ID uC-osflcyp132f01a1

Method BLASTN
NCBI GI 9450548
BLAST score 135
E value 8.0e-70
Match length 215
% identity 91

NCBI Description O.sativa (pRSAM-1) gene for S-adenosyl methionine

synthetase 413549 Seq. No. Seq. ID uC-osflcyp132f02a1 Method BLASTX NCBI GI g1170937 BLAST score 241 3.0e-20 E value Match length 47 94 % identity NCBI Description S-ADENOSYLMETHIONINE SYNTHETASE 1 (METHIONINE ADENOSYLTRANSFERASE 1) (ADOMET SYNTHETASE 1) >gi_450549_emb_CAA81481_ (Z26867) S-adenosyl methionine synthetase [Oryza sativa] 413550 Seq. No. uC-osflcyp132f04a1 Seq. ID Method BLASTX g3452497 NCBI GI BLAST score 385 E value 4.0e-37 89 Match length 83

% identity 83
NCBI Description (Y17796) ketol-acid reductoisomerase [Pisum sativum]

Seq. No. 413551
Seq. ID uC-osflcyp132f05a1
Method BLASTX
NCBI GI g2286153

NCBI GI g2286153
BLAST score 217
E value 2.0e-17
Match length 45
% identity 91

NCBI Description (AF007581) cytoplasmic malate dehydrogenase [Zea mays]

Seq. No. 413552

Seq. ID uC-osflcyp132f06a1

Method BLASTX
NCBI GI 94206765
BLAST score 183
E value 2.0e-13
Match length 52
% identity 67

NCBI Description (AF104329) putative type 1 membrane protein [Arabidopsis

thaliana]

Seq. No. 413553

Seq. ID uC-osflcyp132f07a1

Method BLASTN
NCBI GI g20094
BLAST score 378
E value 0.0e+00
Match length 398
% identity 99

NCBI Description O.sativa RSs2 gene for sucrose-UDP glucosyltransferase

(isozyme 2)

Seq. No. 413554 Seq. ID uC-osflcyp132g04a1 Method BLASTX NCBI GI q2505877 BLAST score 375 E value 7.0e - 36Match length 95 75 % identity NCBI Description (Y12776) dehydrogenase [Arabidopsis thaliana] Seq. No. 413555 uC-osflcyp132h03a1 Seq. ID Method BLASTX NCBI GI q1350986 BLAST score 257 3.0e-22 E value Match length 53 % identity 96 NCBI Description 40S RIBOSOMAL PROTEIN S3A (CYC07 PROTEIN) >gi 483431 dbj BAA05059 (D26060) cyc07 [Oryza sativa] 413556 Seq. No. Seq. ID uC-osflcyp132h10a1 Method BLASTX NCBI GI q485518 BLAST score 403 3.0e-39 E value Match length 76 100 % identity ubiquitin / ribosomal protein CEP52 - rice NCBI Description >gi 303857 dbj BAA02154 (D12629) ubiquitin/ribosomal polyprotein [Oryza sativa] Seq. No. 413557 Seq. ID uC-osflcyp134a02a1 Method BLASTN NCBI GI g2613142 BLAST score 247 E value 1.0e-136 Match length 283 % identity 97 NCBI Description Oryza sativa tubulin (RiP3) mRNA, complete cds Seq. No. 413558 Seq. ID uC-osflcyp134a03a1 Method BLASTX NCBI GI q4240031 BLAST score 235 E value 1.0e-19 80 Match length 55 % identity (AB018422) DNA binding zinc finger protein (Pspzf) [Pisum NCBI Description sativum]

Seq. No. 413559

Seq. ID uC-osflcyp134a05a1

Method BLASTN

E value

Match length

2.0e-13

67

```
NCBI GI
                   q218173
BLAST score
                   38
E value
                   5.0e-12
Match length
                   58
                   91
% identity
NCBI Description
                  Oryza sativa mRNA for type II light-harvesting chlorophyll
                   a/b binding protein of photosystem II (LHCPII), complete
                   413560
Seq. No.
Seq. ID
                   uC-osflcyp134a08a1
Method
                   BLASTX
NCBI GI
                   q4240031
BLAST score
                   227
E value
                   1.0e-18
                   77
Match length
% identity
                   56
NCBI Description
                  (AB018422) DNA binding zinc finger protein (Pspzf) [Pisum
                   sativum]
Seq. No.
                   413561
Seq. ID
                   uC-osflcyp134a11a1
Method
                   BLASTN
NCBI GI
                   q1136121
BLAST score
                   144
E value
                   4.0e-75
Match length
                   192
% identity
                   94
NCBI Description O.sativa mRNA for alpha-tubulin (clone OSTA-136)
Seq. No.
                   413562
Seq. ID
                   uC-osflcyp134b06a1
Method
                   BLASTN
NCBI GI
                   q607894
BLAST score
                   304
E value
                   1.0e-170
Match length
                   316
                   99
% identity
NCBI Description Oryza sativa IR54 anther specific (RTS2) gene, complete cds
Seq. No.
                   413563
Seq. ID
                   uC-osflcyp134b09a1
Method
                   {\tt BLASTX}
NCBI GI
                   g4929751
BLAST score
                   220
E value
                   1.0e-17
                   107
Match length
                   36
% identity
NCBI Description (AF151899) CGI-141 protein [Homo sapiens]
Seq. No.
                   413564
Seq. ID
                   uC-osflcyp134b10a1
Method
                   BLASTX
NCBI GI
                   g126386
BLAST score
                   183
```

```
% identity
                   46
                  POLLEN ALLERGEN LOL P 2-A (LOL P II-A)
NCBI Description
                   >gi 82449 pir A34291 pollen allergen Lol p IIA - perennial
                   ryegrass
                   413565
Seq. No.
                  uC-osflcyp134b11a1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1170937
BLAST score
                   296
E value
                   1.0e-26
Match length
                  53
% identity
                   100
                  S-ADENOSYLMETHIONINE SYNTHETASE 1 (METHIONINE
NCBI Description
                  ADENOSYLTRANSFERASE 1) (ADOMET SYNTHETASE 1)
                  >gi 450549 emb CAA81481 (Z26867) S-adenosyl methionine
                   synthetase [Oryza sativa]
                   413566
Seq. No.
Seq. ID
                   uC-osflcyp134c05a1
Method
                  BLASTN
NCBI GI
                  g218160
BLAST score
                   72
E value
                   2.0e-32
Match length
                  148
                   88
% identity
NCBI Description Oryza sativa mRNA for elongation factor 1 beta'
Seq. No.
                   413567
Seq. ID
                  uC-osflcyp134c07a1
Method
                   BLASTX
NCBI GI
                   g1835731
BLAST score
                   465
E value
                   2.0e-46
Match length
                   99
% identity
                   90
NCBI Description (U86018) photosystem II 10 kDa polypeptide [Oryza sativa]
Seq. No.
                   413568
Seq. ID
                   uC-osflcyp134c11a1
Method
                   BLASTN
NCBI GI
                   g2072554
BLAST score
                   202
E value
                   1.0e-109
Match length
                   310
% identity
                   91
NCBI Description
                  Oryza sativa metallothionein-like protein mRNA, complete
                   cds
                   413569
Seq. No.
Seq. ID
                   uC-osflcyp134d03a1
Method
                  BLASTX
NCBI GI
                   g417260
BLAST score
                  319
E value
                   2.0e-29
                  96
Match length
```

53872

66

% identity

Match length

66

```
NCBI Description LIGHT REGULATED PROTEIN PRECURSOR >qi 422003 pir S33632
                   lir1 protein - rice >gi 20263 emb CAA48706 (X68807)
                  light-regulated gene [Oryza sativa]
                   413570
Seq. No.
Seq. ID
                  uC-osflcyp134d07a1
Method
                  BLASTN
NCBI GI
                  q287400
BLAST score
                  242
E value
                   1.0e-133
Match length
                  297
% identity
                  95
NCBI Description Rice mRNA for peroxidase, complete cds
Seq. No.
                   413571
                  uC-osflcyp134d08a1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q439879
BLAST score
                  208
E value
                   2.0e-16
Match length
                   47
% identity
NCBI Description
                  (L15194) [Golden delicious apple fruit expressed mRNA,
                  complete cds.], gene product [Malus domestica]
Seq. No.
                   413572
                  uC-osflcyp134d11a1
Seq. ID
Method
                  BLASTX
NCBI GI
                   g2130073
BLAST score
                   384
E value
                   6.0e-37
Match length
                  74
% identity
                   100
NCBI Description
                  fructose-bisphosphate aldolase (EC 4.1.2.13) isoenzyme C-1,
                   cytosolic - rice >gi_786178_dbj_BAA08845_ (D50307) aldolase
                   C-1 [Oryza sativa] >\overline{g}i 790970 d\overline{b}j BAA08830 (D50301)
                   aldolase C-1 [Oryza sativa]
Seq. No.
                   413573
Seq. ID
                   uC-osflcyp134e01a1
Method
                  BLASTX
NCBI GI
                   g4406807
                   276
BLAST score
E value
                   2.0e-24
Match length
                   66
% identity
                   79
NCBI Description
                  (AC006201) putative elongation factor beta-1 [Arabidopsis
                   thaliana] >gi_4874292_gb_AAD31355.1_AC007212_11 (AC007212)
                   putative elongation factor beta-1 [Arabidopsis thaliana]
                   413574
Seq. No.
Seq. ID
                   uC-osflcyp134e07a1
Method
                  BLASTX
NCBI GI
                  g2293566
BLAST score
                  211
E value
                   1.0e-27
```

Seq. ID

```
% identity
NCBI Description (AF012896) ADP-ribosylation factor 1 [Oryza sativa]
Seq. No.
                  413575
Seq. ID
                  uC-osflcyp134f04a1
Method
                  BLASTN
NCBI GI
                  q607894
BLAST score
                  350
E value
                  0.0e + 00
Match length
                  398
% identity
                  97
NCBI Description Oryza sativa IR54 anther specific (RTS2) gene, complete cds
                  413576
Seq. No.
Seq. ID
                  uC-osflcyp134f07a1
Method
                  BLASTX
NCBI GI
                  q2293566
BLAST score
                  247
                  5.0e-21
E value
Match length
                  59
                  83
% identity
NCBI Description (AF012896) ADP-ribosylation factor 1 [Oryza sativa]
Seq. No.
                  413577
                  uC-osflcyp134g03a1
Seq. ID
Method
                  BLASTN
NCBI GI
                  a5912298
BLAST score
                  98
                  1.0e-47
E value
Match length
                  120
% identity
                  96
NCBI Description Oryza sativa mRNA for gigantea homologue, partial
Seq. No.
                   413578
Seq. ID
                  uC-osflcyp134g05a1
Method
                  BLASTX
NCBI GI
                  g4678949
BLAST score
                  272
E value
                  8.0e-24
                  70
Match length
% identity
                  71
                  (AL049711) dihydrolipoamide S-acetyltransferase precursor
NCBI Description
                   [Arabidopsis thaliana]
                   413579
Seq. No.
Seq. ID
                  uC-osflcyp134g07a1
Method
                  BLASTX
NCBI GI
                  q3914899
                  173
BLAST score
E value
                  2.0e-12
Match length
                  33
                  100
% identity
NCBI Description 40S RIBOSOMAL PROTEIN S4 >gi 2331301 (AF013487) ribosomal
                  protein S4 type I [Zea mays]
Seq. No.
                   413580
```

53874

uC-osflcyp134g08a1

Method BLASTX
NCBI GI g5803254
BLAST score 163
E value 5.0e-11
Match length 64
% identity 55

NCBI Description (AP000399) ESTs C97429(C60159), D22427(C11106),

AU078031(E31854), D15683(C1084) correspond to a region of the predicted gene; hypothetical protein [Oryza sativa]

Seq. No. 413581

Seq. ID uC-osflcyp134g11a1

Method BLASTX
NCBI GI g4531444
BLAST score 201
E value 2.0e-18
Match length 105
% identity 56

NCBI Description (AC006224) putative protein kinase [Arabidopsis thaliana]

Seq. No. 413582

Seq. ID uC-osflcyp134h04a1

Method BLASTX
NCBI GI g4033424
BLAST score 153
E value 7.0e-10
Match length 49
% identity 61

NCBI Description SOLUBLE INORGANIC PYROPHOSPHATASE (PYROPHOSPHATE

PHOSPHO-HYDROLASE) (PPASE) >gi 2668746 (AF034947) inorganic

pyrophosphatase [Zea mays]

Seq. No. 413583

Seq. ID uC-osflcyp134h08a1

Method BLASTX
NCBI GI g2623298
BLAST score 247
E value 7.0e-25
Match length 90
% identity 65

NCBI Description (AC002409) putative 4-alpha-glucanotransferase [Arabidopsis

thaliana]

Seq. No. 413584

Seq. ID uC-osflcyp135a02a1

Method BLASTN
NCBI GI g218156
BLAST score 172
E value 6.0e-92
Match length 195
% identity 97

NCBI Description Oryza sativa gene for cytoplasmic aldolase, complete cds,

clone:AldC-a

Seq. No. 413585

Seq. ID uC-osflcyp135a08a1

Method BLASTN

% identity

100

```
q1835730
NCBI GI
BLAST score
                   244
E value
                   1.0e-135
                   252
Match length
                   99
% identity
                  Oryza sativa photosystem II 10 kDa polypeptide mRNA,
NCBI Description
                   complete cds
Seq. No.
                   413586
Seq. ID
                   uC-osflcyp135c01a1
Method
                   BLASTN
NCBI GI
                   g2662342
BLAST score
                   253
E value
                   1.0e-140
                   273
Match length
                   99
% identity
NCBI Description Oryza sativa mRNA for EF-1 alpha, complete cds
Seq. No.
                   413587
Seq. ID
                   uC-osflcyp135c07a1
Method
                   BLASTN
NCBI GI
                   g2267005
                   271
BLAST score
E value
                   1.0e-151
Match length
                   271
                   100
% identity
NCBI Description Oryza sativa endosperm lumenal binding protein (BiP) mRNA,
                   complete cds
Seq. No.
                   413588
Seq. ID
                   uC-osflcyp135c08a1
Method
                   BLASTN
NCBI GI
                   q4105602
BLAST score
                  50
E value
                   1.0e-19
                  58
Match length
                   97
% identity
NCBI Description Oryza sativa metallothionein (MTe) gene, complete cds
Seq. No.
                   413589
Seq. ID
                   uC-osflcyp135d01a1
Method
                  BLASTX
NCBI GI
                   g4158219
BLAST score
                  230
E value
                   3.0e-19
Match length
                   44
% identity
                   100
NCBI Description (Y18623) amylogenin [Oryza sativa]
Seq. No.
                   413590
Seq. ID
                  uC-osflcyp135d11a1
Method
                  BLASTN
NCBI GI
                  g4574138
BLAST score
                  246
E value
                  1.0e-136
Match length
                   246
```

NCBI Description Oryza sativa cysteine synthase (rcs3) mRNA, complete cds 413591 Seq. No. uC-osflcyp135e09a1 Seq. ID Method BLASTN NCBI GI g2267005 BLAST score 263 E value 1.0e-146 Match length 263 % identity 100 NCBI Description Oryza sativa endosperm lumenal binding protein (BiP) mRNA, complete cds 413592 Seq. No. Seq. ID uC-osflcyp135e10a1 BLASTN Method NCBI GI g2331130 BLAST score 225 E value 1.0e-123 225 Match length % identity 100 NCBI Description Oryza sativa glycine-rich protein (OSGRP1) mRNA, complete Seq. No. 413593 Seq. ID uC-osflcyp135e11a1 Method BLASTN NCBI GI g218188 BLAST score 245 E value 1.0e-135 245 Match length 67 % identity NCBI Description Rice mRNA for poly-ubiquitin, partial sequence Seq. No. 413594 Seq. ID uC-osflcyp135f06a1 BLASTX Method NCBI GI g3005931 BLAST score 154 E value 2.0e-10 Match length 38 % identity NCBI Description (AJ005016) ABC transporter [Homo sapiens] Seq. No. 413595 Seq. ID uC-osflcyp135g08a1 Method BLASTN NCBI GI g303856 BLAST score 38 E value 5.0e-12 Match length 42 98 % identity NCBI Description Rice mRNA for ubiquitin protein fused to a ribosomal protein, complete cds

53877

413596

uC-osflcyp135g11a1

Seq. No. Seq. ID

```
Method
                  BLASTN
NCBI GI
                  q5091597
BLAST score
                  124
E value
                  2.0e-63
Match length
                  237
% identity
NCBI Description Oryza sativa chromosome 1 BAC 10A19I, complete sequence
Seq. No.
                  413597
Seq. ID
                  uC-osflcyp135h07a1
Method
                  BLASTN
NCBI GI
                  q529093
BLAST score
                  238
                  1.0e-131
E value
Match length
                  262
                  98
% identity
NCBI Description Rice mRNA for proteasome C2 subunit, complete cds
                  413598
Seq. No.
Seq. ID
                  uC-osflcyp135h10a1
Method
                  BLASTN
NCBI GI
                  q218188
BLAST score
                  232
E value
                  1.0e-128
Match length
                  236
% identity
                  83
NCBI Description Rice mRNA for poly-ubiquitin, partial sequence
Seq. No.
                  413599
Seq. ID
                  uC-osflcyp135h12a1
Method
                  BLASTN
NCBI GI
                  g538427
BLAST score
                  84
E value
                  2.0e-39
Match length
                  173
% identity
                  88
NCBI Description Oryza sativa ribosomal protein S16 mRNA, complete cds
                  413600
Seq. No.
Seq. ID
                  uC-osflcyp136a04a1
Method
                  BLASTN
NCBI GI
                  g1212995
BLAST score
                  47
E value
                  2.0e-17
Match length
                  67
% identity
                  93
NCBI Description H.vulgare mRNA for UDP-glucose pyrophosphorylase
                  413601
Seq. No.
Seq. ID
                  uC-osflcyp136b03a1
Method
                  BLASTX
NCBI GI
                  g4972094
BLAST score
                  158
E value
                  6.0e-11
Match length
                  35
% identity
NCBI Description (AL078468) hypothetical protein [Arabidopsis thaliana]
```

NCBI GI

413602 Seq. No. Seq. ID uC-osflcyp136b07a1 Method BLASTN NCBI GI g218209 BLAST score 140 7.0e-73 E value Match length 184 % identity 95 NCBI Description Oryza sativa mRNA for the small subunit of ribulose-1,5-bisphosphate carboxylase, complete cds, clone pOSSS2106 Seq. No. 413603 Seq. ID uC-osflcyp136b09a1 Method BLASTN NCBI GI g20280 BLAST score 274 E value 1.0e-153 Match length 278 % identity 100 NCBI Description Rice gene for phenylalanine ammonia-lyase (EC 4.3.1.5) Seq. No. 413604 Seq. ID uC-osflcyp136c01a1 Method BLASTN NCBI GI q4105602 BLAST score 269 E value 1.0e-150 Match length 277 99 % identity NCBI Description Oryza sativa metallothionein (MTe) gene, complete cds Seq. No. 413605 Seq. ID uC-osflcyp136d05a1 Method BLASTN q397615 NCBI GI BLAST score 50 E value 4.0e-19 Match length 66 % identity 94 NCBI Description O.sativa salT gene 413606 Seq. No. Seq. ID uC-osflcyp136d06a1 Method BLASTN NCBI GI g1136121 BLAST score 283 E value 1.0e-158 Match length 283 100 % identity NCBI Description O.sativa mRNA for alpha-tubulin (clone OSTA-136) 413607 Seq. No. Seq. ID uC-osflcyp136d12a1 Method BLASTN

53879

g1136121



BLAST score 257 E value 1.0e-142 Match length 257 % identity 100

NCBI Description O.sativa mRNA for alpha-tubulin (clone OSTA-136)

Seq. No. 413608

Seq. ID uC-osflcyp136e09a1

Method BLASTN
NCBI GI g218146
BLAST score 188
E value 1.0e-101
Match length 258
% identity 94

NCBI Description Rice mRNA for mitochondrial F1-ATPase

Seq. No. 413609

Seq. ID uC-osflcyp136f04a1

Method BLASTN
NCBI GI g508576
BLAST score 265
E value 1.0e-147
Match length 273
% identity 100

NCBI Description Oryza sativa box protein (MADS1) mRNA, complete cds

Seq. No. 413610

Seq. ID uC-osflcyp136f05a1

Method BLASTN
NCBI GI g5670155
BLAST score 181
E value 2.0e-97
Match length 265
% identity 46

NCBI Description Oryza sativa subsp. japonica BAC clone 34K24, complete

sequence

Seq. No. 413611

Seq. ID uC-osflcyp136f12a1

Method BLASTN
NCBI GI g5456937
BLAST score 211
E value 1.0e-115
Match length 211
% identity 100

NCBI Description Oryza sativa rps9 mRNA for ribosomal protein S9, complete

cds

Seq. No. 413612

Seq. ID uC-osflcyp136g04a1

Method BLASTN
NCBI GI g1574943
BLAST score 254
E value 1.0e-141
Match length 277
% identity 98

NCBI Description Oryza sativa polyubiquitin (Rubq1) mRNA, complete cds

413613 Seq. No. uC-osflcyp136g10a1 Seq. ID Method BLASTN NCBI GI q20181 BLAST score 125 E value 6.0e-64 Match length 129 99 % identity NCBI Description Rice cab2R gene for light harvesting chlorophyll a/b-binding protein Seq. No. 413614 uC-osflcyp136h02a1 Seq. ID Method BLASTN q3885881 NCBI GI BLAST score 240 E value 1.0e-132 Match length 288 97 % identity NCBI Description Oryza sativa inorganic pyrophosphatase (IPP) mRNA, complete cds 413615 Seq. No. Seq. ID uC-osflcyp136h12a1 Method BLASTN NCBI GI q639683 BLAST score 80 4.0e-37 E value 221 Match length % identity 83 NCBI Description Rice mRNA for phosphoglucose isomerase (Pgi-a), complete 413616 Seq. No. Seq. ID uC-osflcyp137a05a1 Method BLASTN NCBI GI q5852170 BLAST score 151 E value 2.0e-79 Match length 178 % identity 97 NCBI Description Oryza sativa indica(GLA4) genomic DNA, chromosome 4, BAC clone:t17804 Seq. No. 413617 Seq. ID uC-osflcyp137b02a1 Method BLASTN NCBI GI g606816 BLAST score 134 E value 2.0e-69 Match length 162 96 % identity

Seq. No. 413618

NCBI Description

Oryza sativa chloroplast carbonic anhydrase mRNA, complete

Method

BLASTN

```
uC-osflcyp137b03a1
Seq. ID
Method
                    BLASTN
NCBI GI
                    q218154
BLAST score
                    51
E value
                    1.0e-19
                    67
Match length
                    97
% identity
NCBI Description Oryza sativa gene for cytoplasmic aldolase, complete cds,
                    clone:Aldp
                    413619
Seq. No.
Seq. ID
                    uC-osflcyp137b10a1
Method
                    BLASTN
NCBI GI
                    q1132482
BLAST score
                    152
E value
                    6.0e-80
                    235
Match length
                    94
% identity
NCBI Description Rice mRNA for ADP-ribosylation factor, complete cds
Seq. No.
                    413620
                    uC-osflcyp137d10a1
Seq. ID
Method
                    BLASTX
NCBI GI
                    g2499819
                    189
BLAST score
E value
                    3.0e-14
Match length
                    34
                    100
% identity
                    ASPARTIC PROTEINASE ORYZASIN 1 PRECURSOR
NCBI Description
                    >gi_2130068_pir__S66516 aspartic proteinase 1 precursor - rice >gi_1030715_dbj_BAA06876_ (D32165) aspartic protease [Oryza sativa] >gi_1711289_dbj_BAA06875_ (D32144) aspartic
                    protease [Oryza sativa]
                    413621
Seq. No.
Seq. ID
                    uC-osflcyp137f02a1
Method
                    BLASTN
NCBI GI
                    q4107008
BLAST score
                    60
E value
                    5.0e-25
Match length
                    96
                    91
% identity
NCBI Description Oryza sativa mRNA for OSK1, complete cds
Seq. No.
                     413622
Seq. ID
                    uC-osflcyp137f03a1
Method
                    BLASTN
NCBI GI
                    g11957
BLAST score
                    105
E value
                    4.0e-52
Match length
                    137
                    93
% identity
NCBI Description Rice complete chloroplast genome
Seq. No.
                     413623
Seq. ID
                    uC-osflcyp137f12a1
```

BLAST score

E value

133

1.0e-68

```
NCBI GI
                  q218209
BLAST score
                   68
E value
                  9.0e-30
Match length
                  88
                  97
% identity
NCBI Description
                  Oryza sativa mRNA for the small subunit of
                  ribulose-1,5-bisphosphate carboxylase, complete cds, clone
                  posss2106
                  413624
Seq. No.
Seq. ID
                  uC-osflcyp137h04a1
Method
                  BLASTN
                  q3077789
NCBI GI
BLAST score
                  61
E value
                  2.0e-26
Match length
                  69
                  99
% identity
NCBI Description
                  Oryza sativa RINO1 mRNA for myo-inositol phosphate
                  synthase, complete cds
Seq. No.
                  413625
Seq. ID
                  uC-osflcyp137h05a1
Method
                  BLASTN
NCBI GI
                  q4680488
BLAST score
                  59
E value
                  1.0e-24
                  144
Match length
                  94
% identity
NCBI Description Oryza sativa BAC clone 1.H19, complete sequence
Seq. No.
                   413626
Seq. ID
                  uC-osflcyp138a02a1
Method
                  BLASTX
NCBI GI
                  g289920
BLAST score
                  177
E value
                  5.0e-13
                  33
Match length
% identity
                  100
                  (L07119) chlorophyll A/B binding protein [Gossypium
NCBI Description
                  hirsutum]
                   413627
Seq. No.
Seq. ID
                  uC-osflcyp138a06a1
Method
                  BLASTX
NCBI GI
                  g2293566
                  207
BLAST score
E value
                  2.0e-16
                  38
Match length
                  100
% identity
NCBI Description (AF012896) ADP-ribosylation factor 1 [Oryza sativa]
Seq. No.
                   413628
Seq. ID
                  uC-osflcyp138a11a1
                  BLASTN
Method
NCBI GI
                  g3721941
```

```
274
Match length
                   87
% identity
                   Oryza sativa mRNA for chitinase, complete cds
NCBI Description
                   413629
Seq. No.
                   uC-osflcyp138b01a1
Seq. ID
                   BLASTN
Method
                   g416266
NCBI GI
                   70
BLAST score
                   3.0e-31
E value
                   136
Match length
                   88
% identity
                   Rice mRNA for oxygen-evolving protein, partial sequence
NCBI Description
                   413630
Seq. No.
                   uC-osflcyp138b07a1
Seq. ID
                   BLASTN
Method
                   g5679837
NCBI GI
                   179
BLAST score
                   4.0e-96
E value
                   276
Match length
                   99
% identity
NCBI Description Oryza sativa chromosome 4 BAC 11332 genomic sequences
                   413631
Seq. No.
                   uC-osflcyp138b10a1
Seq. ID
                   BLASTN
Method
                   g167043
NCBI GI
                   36
BLAST score
                   7.0e-11
E value
                   52
Match length
                    92
% identity
NCBI Description Barley glyceraldehyde-3-phosphate dehydrogenase mRNA, 3'
                   end
                    413632
Seq. No.
                    uC-osflcyp138b12a1
Seq. ID
                    BLASTN
Method
                    q4105602
NCBI GI
                    305
BLAST score
                    1.0e-171
E value
Match length
                    305
                    100
% identity
NCBI Description Oryza sativa metallothionein (MTe) gene, complete cds
                    413633
Seq. No.
Seq. ID
                    uC-osflcyp138c02a1
Method
                    BLASTX
NCBI GI
                    g1345809
BLAST score
                    182
                    7.0e-14
E value
Match length
                    50
                    72
 % identity
                    CHALCONE SYNTHASE (NAREGENIN-CHALCONE SYNTHASE)
NCBI Description
                    >gi_2117713_pir__S58190 naringenin-chalcone synthase (EC
2.3.1.74) - rice >gi_927491_emb_CAA61955_ (X89859)
                    naringenin-chalcone synthase [Oryza sativa]
```

```
413634
Seq. No.
                  uC-osflcyp138c05a1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g450548
BLAST score
                  242
                  1.0e-133
E value
Match length
                  242
% identity
                  100
                  O.sativa (pRSAM-1) gene for S-adenosyl methionine
NCBI Description
                  synthetase
Seq. No.
                  413635
                  uC-osflcyp138c06a1
Seq. ID
Method
                  BLASTN
NCBI GI
                   g425794
BLAST score
                  71
                   8.0e-32
E value
                   83
Match length
                   96
% identity
                  Rice mRNA for heat shock protein 82 (gene name AD167),
NCBI Description
                  partial cds
Seq. No.
                   413636
                   uC-osflcyp138c07a1
Seq. ID
Method
                   BLASTN
NCBI GI
                   q425794
BLAST score
                   201
                   1.0e-109
E value
Match length
                   217
% identity
                   98
NCBI Description Rice mRNA for heat shock protein 82 (gene name AD167),
                   partial cds
Seq. No.
                   413637
                   uC-osflcyp138c09a1
Seq. ID
                   BLASTN
Method
                   g3885891
NCBI GI
                   273
BLAST score
                   1.0e-152
E value
                   301
Match length
                   98
% identity
NCBI Description Oryza sativa photosystem-1 F subunit precursor (PSI-F)
                   mRNA, complete cds
Seq. No.
                   413638
                   uC-osflcyp138c10a1
Seq. ID
                   BLASTN
Method
                   g531030
NCBI GI
                   56
BLAST score
E value
                   1.0e-22
                   108
Match length
                   88
% identity
                  Pennisetum ciliare apomixis-associated mRNA
NCBI Description
                   >gi 531483 emb_Z36546 PCAPOSPA3 P.ciliare (Higgins)
                   apospory associated mRNA, 876bp
                   >gi_549985_gb_U13149_PCU13149 Pennisetum ciliare possible
```

apospory-associated mRNA clone pSUB 3-1a, partial cds 413639 Seq. No. uC-osflcyp138d01a1 Seq. ID Method BLASTX NCBI GI g1351014 171 BLAST score 3.0e-12E value 32 Match length 100 % identity 40S RIBOSOMAL PROTEIN S8 >gi 968902 dbj_BAA07207 (D38010) NCBI Description ribosomal protein S8 [Oryza sativa] 413640 Seq. No. uC-osflcyp138d07a1 Seq. ID Method BLASTN NCBI GI q425794 BLAST score 265 1.0e-147 E value 268 Match length 100 % identity Rice mRNA for heat shock protein 82 (gene name AD167), NCBI Description partial cds

Seq. No. 413641

Seq. ID uC-osflcyp138d09a1

Method BLASTN
NCBI GI g3248998
BLAST score 234
E value 1.0e-129
Match length 257
% identity 98

NCBI Description Oryza sativa translation elongation factor mRNA, partial

cds

Seq. No. 413642

Seq. ID uC-osflcyp138d10a1

Method BLASTN
NCBI GI g20328
BLAST score 65
E value 4.0e-28
Match length 65
% identity 100

NCBI Description O.sativa RAc2 gene for actin

Seq. No. 413643

Seq. ID uC-osflcyp138e09a1

Method BLASTN
NCBI GI g968995
BLAST score 209
E value 1.0e-114
Match length 268
% identity 94

NCBI Description Oryza sativa clone glyceraldehyde-3-phosphate dehydrogenase

(Gpc) mRNA, complete cds

Seq. No. 413644

uC-osflcyp138f12a1 Seq. ID Method BLASTN NCBI GI q20321 BLAST score 239 1.0e-132 E value Match length 303 95 % identity NCBI Description Oryza sativa RAc1 mRNA for actin 413645 Seq. No. Seq. ID uC-osflcyp138g01a1 BLASTN Method q4574138 NCBI GI 164 BLAST score E value 3.0e-87 204 Match length 95 % identity NCBI Description Oryza sativa cysteine synthase (rcs3) mRNA, complete cds 413646 Seq. No. uC-osflcyp138g06a1 Seq. ID Method BLASTX NCBI GI q5016095 BLAST score 207 2.0e-16 E value Match length 52 % identity 81 (AF003551) lysine-ketoglutarate reductase/saccharopine NCBI Description dehydrogenase bifunctional enzyme [Zea mays] Seq. No. 413647 Seq. ID uC-osflcyp138g09a1 Method BLASTN NCBI GI q2331130 BLAST score 254 E value 1.0e-141 258 Match length 100 % identity Oryza sativa glycine-rich protein (OSGRP1) mRNA, complete NCBI Description cds 413648 Seq. No. uC-osflcyp139a02b1 Seq. ID Method BLASTX NCBI GI g82080 BLAST score 359 5.0e - 35E value Match length 145 60 % identity

NCBI Description chlorophyll a/b-binding protein type III precursor - tomato >qi 226872 prf 1609235A chlorophyll a/b binding protein

[Lycopersicon esculentum]

Seq. No. 413649

Seq. ID uC-osflcyp139a04b1

Method BLASTX NCBI GI g1929998

% identity

NCBI Description

48

```
309
BLAST score
                    3.0e-28
E value
Match length
                    150
                    48
% identity
                    (U77463) NADPH-dependent HC-toxin reductase [Hordeum
NCBI Description
                    vulgare]
                    413650
Seq. No.
                    uC-osflcyp139a05a1
Seq. ID
                    BLASTN
Method
                    g169806
NCBI GI
                    153
BLAST score
                    1.0e-80
E value
                    193
Match length
                    97
% identity
                    Rice oryzacystatin gene, complete cds
NCBI Description
                    413651
Seq. No.
                    uC-osflcyp139a05b1
Seq. ID
                    BLASTX
Method
NCBI GI
                    q118170
                    283
BLAST score
                    3.0e-25
E value
                    57
Match length
                    96
% identity
                    CYSTEINE PROTEINASE INHIBITOR-I (ORYZACYSTATIN-I)
NCBI Description
                    >gi_82491_pir__A28464 oryzacystatin - rice >gi_169784
(J03469) oryzacystatin [Oryza sativa] >gi_169807 (M29259)
oryzastatin [Oryza sativa] >gi_259137_bbs_120195 (S49967)
                     oryzacystatin=cysteine protease inhibitor [Oryza=rice,
                     Peptide, 102 aa] [Oryza] >gi_1280613 (U54702) oryzacystatin
                     [Oryza sativa]
                    413652
Seq. No.
                    uC-osflcyp139a06b1
Seq. ID
                    BLASTX
Method
NCBI GI
                     q1076800
                     350
BLAST score
                     3.0e-33
E value
                     98
Match length
                     67
% identity
                    L-ascorbate peroxidase (EC 1.11.1.11), cytosolic isozyme -
NCBI Description
                     maize >gi_600116_emb_CAA84406 (Z34934) cytosolic ascorbate
                     peroxidase [Zea mays] >gi 1096503_prf__2111423A ascorbate
                     peroxidase [Zea mays]
Seq. No.
                     413653
Seq. ID
                     uC-osflcyp139a07b1
Method
                     BLASTX
NCBI GI
                     g3776567
                     304
BLAST score
E value
                     1.0e-27
                     145
Match length
```

53888

gene. [Arabidopsis thaliana]

(ACO05388) Strong similarity to F21B7.33 gi_2809264 from A.

thaliana BAC gb_AC002560. EST gb_N65119 comes from this

```
413654
Seq. No.
                  uC-osflcyp139a10a1
Seq. ID
                  BLASTN
Method
NCBI GI
                  g886404
                  83
BLAST score
                  4.0e-39
E value
                  87
Match length
                  99
% identity
NCBI Description Oryza sativa MADS-box protein (MADS3) mRNA, complete cds
                  413655
Seq. No.
                  uC-osflcyp139a10b1
Seq. ID
                  BLASTX
Method
                  q2130078
NCBI GI
                  364
BLAST score
                  1.0e-34
E value
                  86
Match length
                  83
% identity
NCBI Description MADS-box protein 3 - rice >gi_886405 (L37528) MADS box
                  protein [Oryza sativa]
                  413656
Seq. No.
                  uC-osflcyp139a11b1
Seq. ID
                  BLASTX
Method
                  g2369766
NCBI GI
BLAST score
                   549
                   2.0e-56
E value
                   139
Match length
                   73
% identity
NCBI Description (AJ001304) hypothetical protein [Citrus x paradisi]
                   413657
Seq. No.
                   uC-osflcyp139a12b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g5729802
BLAST score
                   615
                   5.0e-64
E value
                   142
Match length
                   77
% identity
NCBI Description similar to S. pombe dim1+ >gi_2565275 (AF023611) Dim1p
                   homolog [Homo sapiens]
                   413658
Seq. No.
                   uC-osflcyp139b04b1
Seq. ID
                   BLASTX
Method
NCBI GI
                   g2952328
BLAST score
                   669
E value
                   2.0e-70
Match length
                   137
                   93
% identity
                   (AF049889) 1-aminocyclopropane-1-carboxylate oxidase [Oryza
NCBI Description
                   sativa]
                   413659
Seq. No.
                   uC-osflcyp139b06b1
Seq. ID
Method
                   BLASTX
```

```
NCBI GI
                  g2072555
BLAST score
                  237
                  9.0e-20
E value
Match length
                  44
                  100
% identity
                   (AF001396) metallothionein-like protein [Oryza sativa]
NCBI Description
                  >gi 6103441_gb_AAF03603.1_ (AF147786) metallothionein-like
                  protein [Oryza sativa]
                  413660
Seq. No.
Seq. ID
                  uC-osflcyp139b07a1
Method
                  BLASTN
                  g2286112
NCBI GI
BLAST score
                  126
E value
                  2.0e-64
                  177
Match length
                   96
% identity
                  Oryza sativa MADS box protein (OsMADS8) mRNA, complete cds
NCBI Description
                   413661
Seq. No.
Seq. ID
                  uC-osflcyp139b07b1
Method
                  BLASTX
NCBI GI
                   g113512
BLAST score
                  158
                   9.0e-11
E value
                   43
Match length
                   79
% identity
                  FLORAL HOMEOTIC PROTEIN AGL2 >gi 81610 pir B39534 floral
NCBI Description
                   homeotic protein AGL2 - Arabidopsis thaliana >gi_166591
                   (M55551) transcription factor [Arabidopsis thaliana]
                   413662
Seq. No.
                   uC-osflcyp139b08a1
Seq. ID
                   BLASTN
Method
NCBI GI
                   g2331132
BLAST score
                   281
E value
                   1.0e-157
Match length
                   333
                   96
% identity
                  Oryza sativa glycine-rich protein (OSGRP2) mRNA, complete
NCBI Description
Seq. No.
                   413663
                   uC-osflcyp139b08b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2293480
BLAST score
                   432
E value
                   1.0e-42
                   84
Match length
                   100
% identity
                  (AF011331) glycine-rich protein [Oryza sativa]
NCBI Description
                   413664
Seq. No.
Seq. ID
                   uC-osflcyp139b09b1
```

BLASTX

g1794137 173

Method NCBI GI

BLAST score

```
E value
                   3.0e-12
Match length
                  71
% identity
                   48
                  (AB000402) DMO25 [Drosophila melanogaster]
NCBI Description
                  413665
Seq. No.
                  uC-osflcyp139b11b1
Seq. ID
                  BLASTX
Method
NCBI GI
                  q4914340
                  341
BLAST score
E value
                   6.0e-32
Match length
                  106
                   60
% identity
                  (AC005489) F14N23.26 [Arabidopsis thaliana]
NCBI Description
                   413666
Seq. No.
Seq. ID
                  uC-osflcyp139c03b1
Method
                  BLASTX
                   g1084455
NCBI GI
BLAST score
                   435
                   5.0e-43
E value
                   120
Match length
% identity
                   72
                  peptidylprolyl isomerase (EC 5.2.1.8) Cyp2 - rice
NCBI Description
                   >gi 600767 (L29469) cyclophilin 2 [Oryza sativa]
                   413667
Seq. No.
                   uC-osflcyp139c04b1
Seq. ID
                   BLASTX
Method
NCBI GI
                   g4895197
BLAST score
                   182
                   3.0e-13
E value
Match length
                   92
                   39
% identity
NCBI Description (AC007661) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   413668
                   uC-osflcyp139c05b1
Seq. ID
Method
                   BLASTN
NCBI GI
                   g21841
BLAST score
                   43
                   9.0e-15
E value
                   108
Match length
                   47
% identity
NCBI Description T.aestivum mRNA for a proline-rich protein
Seq. No.
                   413669
Seq. ID
                   uC-osflcyp139c11b1
                   BLASTX
Method
NCBI GI
                   g2160177
BLAST score
                   433
E value
                   1.0e-42
                   141
Match length
                   60
% identity
                   (AC000132) EST gb_R64758 comes from this gene. [Arabidopsis
NCBI Description
                   thaliana]
```

```
413670
Seq. No.
Seq. ID
                  uC-osflcyp139c12a1
Method
                  BLASTX
NCBI GI
                  g5295971
BLAST score
                  445
E value
                  3.0e-44
Match length
                  110
                  83
% identity
                  (AB026295) EST D24315(R1718) corresponds to a region of the
NCBI Description
                  predicted gene.; Similar to Tobacco DNA for retroviral-like
                  transposon Tnt 1-94.(X13777) [Oryza sativa]
Seq. No.
                  413671
                  uC-osflcyp139c12b1
Seq. ID
Method
                  BLASTX
                  g5295971
NCBI GI
BLAST score
                  768
E value
                  5.0e-82
                  149
Match length
                  99
% identity
NCBI Description
                  (AB026295) EST D24315(R1718) corresponds to a region of the
                  predicted gene.; Similar to Tobacco DNA for retroviral-like
                  transposon Tnt 1-94.(X13777) [Oryza sativa]
Seq. No.
                  413672
                  uC-osflcyp139d01b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g283464
BLAST score
                  142
E value
                  9.0e-09
Match length
                  119
% identity
NCBI Description sporozoite surface protein 2 - Plasmodium yoelii (fragment)
                   413673
Seq. No.
Seq. ID
                  uC-osflcyp139d03b1
Method
                  BLASTX
NCBI GI
                   q2154609
BLAST score
                   316
                   5.0e-29
E value
Match length
                   79
% identity
                   73
NCBI Description
                   (D63509) endoxyloglucan transferase related protein
                   [Arabidopsis thaliana] >gi_4522010_gb_AAD21783.1
                   (AC007069) endoxyloglucan transferase [Arabidopsis
                   thaliana]
Seq. No.
                   413674
                   uC-osflcyp139d04b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q543711
BLAST score
                  619
                   1.0e-64
E value
Match length
                  147
                   88
% identity
NCBI Description 14-3-3-LIKE PROTEIN S94 >gi_419796_pir__S30927 14-3-3
                  protein homolog - rice >gi_303859_dbj_BAA03711_ (D16140)
```





413675 Seq. No. uC-osflcyp139d05b1 Seq. ID Method BLASTX g3334123 NCBI GI 238 BLAST score 4.0e-21 E value 81 Match length 73 % identity ATP SYNTHASE GAMMA CHAIN, MITOCHONDRIAL PRECURSOR NCBI Description >gi_1655480_dbj_BAA13599_ (D88374) gamma subunit of mitochondrial F1-ATPase [Arabidopsis thaliana] >gi_2924787 (AC002334) mitochondrial F1-ATPase, gamma subunit [Arabidopsis thaliana] Seq. No. 413676 uC-osflcyp139d06b1 Seq. ID BLASTX Method q3885894 NCBI GI 432 BLAST score 1.0e-42 E value 97 Match length 87 % identity (AF093635) photosystem-1 H subunit GOS5 [Oryza sativa] NCBI Description Seq. No. 413677 uC-osflcyp139d09b1 Seq. ID BLASTX Method g530207 NCBI GI BLAST score 529 E value 5.0e-54149 Match length 66 % identity (L35272) heat shock protein [Glycine max] NCBI Description Seq. No. 413678 uC-osflcyp139d10b1 Seq. ID Method BLASTX q1708424 NCBI GI 432 BLAST score 1.0e-43 E value 137 Match length % identity NCBI Description ISOFLAVONE REDUCTASE HOMOLOG >gi 1230614 (U48590) isoflavone reductase-like protein [Lupinus albus] Seq. No. 413679 uC-osflcyp139d11b1 Seq. ID

Method BLASTX
NCBI GI g2894607
BLAST score 461
E value 5.0e-46
Match length 135
% identity 61

NCBI Description (AL021889) NAM (no apical meristem)-like protein

[Arabidopsis thaliana]

```
413680
Seq. No.
                  uC-osflcyp139e02b1
Seq. ID
                  BLASTX
Method
                  g231509
NCBI GI
                  494
BLAST score
                  6.0e-50
E value
                  108
Match length
                  85
% identity
                  ACTIN DEPOLYMERIZING FACTOR (ADF) >gi_419809_pir__S30935
NCBI Description
                  actin-depolymerizing factor - trumpet lily
                  >gi 22748 emb_CAA78483_ (Z14110) actin depolymerizing
                  factor [Lilium longiflorum]
                  413681
Seq. No.
                  uC-osflcyp139e03b1
Seq. ID
                  BLASTX
Method
                  g1652164
NCBI GI
                  195
BLAST score
                  8.0e-15
E value
                  83
Match length
                   47
% identity
                  (D90903) hypothetical protein [Synechocystis sp.]
NCBI Description
                   413682
Seq. No.
                  uC-osflcyp139e07b1
Seq. ID
                  BLASTN
Method
                   g2286108
NCBI GI
                   39
BLAST score
                   2.0e-12
E value
                   84
Match length
                   98
% identity
NCBI Description Oryza sativa MADS box protein (OsMADS6) mRNA, complete cds
                   413683
Seq. No.
                   uC-osflcyp139e08b1
Seq. ID
Method
                   BLASTX
                   q1370188
NCBI GI
                   472
BLAST score
                   2.0e-47
E value
Match length
                   101
% identity
                   87
NCBI Description (Z73943) RAB7D [Lotus japonicus]
                   413684
Seq. No.
                   uC-osflcyp139e10b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g1917019
BLAST score
                   621
                   8.0e-65
E value
                   140
Match length
% identity
NCBI Description (U92045) ribosomal protein S6 RPS6-1 [Zea mays]
                   413685
Seq. No.
                   uC-osflcyp139e11b1
Seq. ID
Method
                   BLASTX
```

```
g3122673
NCBI GI
                   371
BLAST score
E value
                   2.0e-35
                   132
Match length
                   60
% identity
                   60S RIBOSOMAL PROTEIN L15 >gi 2245027 emb CAB10447.1_
NCBI Description
                   (Z97341) ribosomal protein [Arabidopsis thaliana]
                   413686
Seq. No.
                   uC-osflcyp139e12b1
Seq. ID
                   BLASTX
Method
                   g464986
NCBI GI
BLAST score
                   256
                   3.0e-22
E value
                   51
Match length
                   92
% identity
                   UBIQUITIN-CONJUGATING ENZYME E2-17 KD 9 (UBIQUITIN-PROTEIN
NCBI Description
                   LIGASE 9) (UBIQUITIN CARRIER PROTEIN 9) (UBCAT4B)
                   >gi_421857_pir__S32674 ubiquitin--protein ligase (EC 6.3.2.19) UBC9 - Arabidopsis thaliana
                   >gi_297884_emb_CAA78714_ (Z14990) ubiquitin conjugating
                   enzyme homolog [Arabidopsis thaliana] >gi 349211 (L00639)
                   ubiquitin conjugating enzyme [Arabidopsis thaliana]
                   >gi_600391_emb_CAA51201_ (X72626) ubiquitin conjugating
                   enzyme E2 [Arabidopsis Thaliana]
                   >gi_4455355_emb_CAB36765.1_ (AL035524) ubiquitin-protein
                   ligase UBC9 [Arabidopsis thaliana]
                   413687
Seq. No.
                   uC-osflcyp139f02a1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g5640155
                   200
BLAST score
                   1.0e-15
E value
                   111
Match length
                   48
% identity
NCBI Description (AJ242530) gibberellin response modulator [Zea mays]
Seq. No.
                   413688
                   uC-osflcyp139f02b1
Seq. ID
                   BLASTX
Method
NCBI GI
                   g5640155
BLAST score
                   326
                   3.0e - 30
E value
Match length
                   145
                   57
% identity
NCBI Description (AJ242530) gibberellin response modulator [Zea mays]
Seq. No.
                   413689
                   uC-osflcyp139f03b1
Seq. ID
Method
                   BLASTN
NCBI GI
                   g2462784
                   34
BLAST score
                   2.0e-09
E value
                   50
Match length
                   92
% identity
```

NCBI Description Streptococcus equi M-like protein (szPSe) gene, complete

```
cds
```

413690 Seq. No. Seq. ID uC-osflcyp139f04b1 Method BLASTX NCBI GI g320618 BLAST score 402 2.0e-46 E value Match length 114 % identity NCBI Description chlorophyll a/b-binding protein I precursor - rice >gi_218172_dbj_BAA00536_ (D00641) type I light-harvesting chlorophyll a/b-binding protein [Oryza sativa] >gi_227611_prf__1707316A chlorophyll a/b binding protein 1 [Oryza sativa] 413691 Seq. No. uC-osflcyp139f07b1 Seq. ID Method BLASTX NCBI GI q1706260 374 BLAST score 3.0e-42E value Match length 101 89 % identity CYSTEINE PROTEINASE 1 PRECURSOR >gi 2118131 pir S59597 NCBI Description cysteine proteinase 1 precursor - maize >gi 643597_dbj_BAA08244_ (D45402) cysteine proteinase [Zea mays] 413692 Seq. No. Seq. ID uC-osflcyp139f08b1 BLASTN Method NCBI GI q6016845 BLAST score 42 3.0e-14 E value Match length 66 % identity NCBI Description Oryza sativa genomic DNA, chromosome 1, clone:P0711E10 Seq. No. 413693 Seq. ID uC-osflcyp139f09b1 Method BLASTX NCBI GI g417488 BLAST score 581 4.0e-60 E value Match length 151 % identity 72 ALPHA-GLUCAN PHOSPHORYLASE, H ISOZYME (STARCH PHOSPHORYLASE NCBI Description H) >gi_100452_pir__A40995 starch phosphorylase (EC 2.4.1.1) H - potato >qi 169473 (M69038) alpha-glucan phosphorylase type H isozyme [Solanum tuberosum] 413694 Seq. No.

Seq. ID uC-osflcyp139f10b1

 ${\tt BLASTX}$ Method NCBI GI q2088647 BLAST score 422

2.0e-41 E value Match length 147 54 % identity (AF002109) hypothetical protein [Arabidopsis thaliana] NCBI Description >gi 3158394 (AF036340) LRR-containing F-box protein [Arabidopsis thaliana] 413695 Seq. No. Seq. ID uC-osflcyp139f11b1 Method BLASTX NCBI GI q4165488 BLAST score 697 2.0e-73 E value Match length 146 % identity 99 (AJ132399) alpha-tubulin 3 [Hordeum vulgare] NCBI Description 413696 Seq. No. uC-osflcyp139f12b1 Seq. ID Method BLASTX q1053047 NCBI GI 205 BLAST score E value 4.0e-16 Match length 95 % identity 51 NCBI Description (U38425) histone H3 [Glycine max] >gi 1053049 (U38426) histone H3 [Glycine max] >gi 1053051 (U38427) histone H3 [Glycine max] 413697 Seq. No. Seq. ID uC-osflcyp139g01b1 BLASTN Method NCBI GI g596077 BLAST score 41 E value 9.0e-14Match length 65 % identity 91 Zea mays thiamine biosynthetic enzyme (thi1-1) mRNA, NCBI Description complete cds Seq. No. 413698 uC-osflcyp139g04a1 Seq. ID Method BLASTN NCBI GI g435465 214 BLAST score E value 1.0e-117 Match length 444 91 % identity Rice mRNA for calcium-dependent protein kinase, complete NCBI Description cds 413699 Seq. No.

Seq. ID uC-osflcyp139g04b1

Method BLASTX
NCBI GI g1705733
BLAST score 485
E value 7.0e-49

Method

NCBI GI

BLASTX

g1184776

```
104
Match length
% identity
                   CALCIUM-DEPENDENT PROTEIN KINASE, ISOFORM 1 (CDPK 1)
NCBI Description
                   >gi_542156_pir__JC1515 calcium-dependent protein kinase (EC 2.7.1.-) - rice >gi_435466_dbj_BAA02698_ (D13436)
                   calcium-dependent protein kinase [Oryza sativa]
                   413700
Seq. No.
Seq. ID
                   uC-osflcyp139g09b1
Method
                   BLASTX
NCBI GI
                   g3242705
BLAST score
                   182
                   2.0e-13
E value
                   90
Match length
                   43
% identity
NCBI Description
                   (AC003040) putative nicotinate phosphoribosyltransferase
                   [Arabidopsis thaliana]
                   413701
Seq. No.
Seq. ID
                   uC-osflcyp139g10b1
Method
                   BLASTX
NCBI GI
                   g4056503
BLAST score
                   167
E value
                   1.0e-11
Match length
                   36
                   89
% identity
NCBI Description
                   (AC005896) unknown protein [Arabidopsis thaliana]
Seq. No.
                   413702
                   uC-osflcyp139g11b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2501189
BLAST score
                   240
E value
                   3.0e - 34
Match length
                   120
% identity
                   72
                   THIAMINE BIOSYNTHETIC ENZYME 1-1 PRECURSOR
NCBI Description
                   >qi 2130146 pir S61419 thiamine biosynthetic enzyme thil-1
                    - maize >gi_596\overline{07}8 (U17350) thiamine biosynthetic enzyme
                    [Zea mays]
                    413703
Seq. No.
Seq. ID
                   uC-osflcyp139g12a1
Method
                   BLASTN
NCBI GI
                   g218171
BLAST score
                   96
E value
                   8.0e-47
Match length
                   120
                   96
% identity
                   Oryza sativa mRNA for type I light-harvesting chlorophyll
NCBI Description
                   a/b binding protein of photosystem II (LHCPII), complete
                   cds
                   413704
Seq. No.
Seq. ID
                   uC-osflcyp139g12b1
```

BLAST score 390 9.0e-38 E value Match length 111 72 % identity (U45857) cytosolic glyceroldehyde-3-phosphate dehydrogenase NCBI Description GAPC4 [Zea mays] 413705 Seq. No. Seq. ID uC-osflcyp139h02b1 Method BLASTX NCBI GI q6065740 213 BLAST score 5.0e-30 E value Match length 118 56 % identity (AJ012758) nucleotide diphosphate kinase Ia [Arabidopsis NCBI Description thaliana] 413706 Seq. No. uC-osflcyp139h04b1 Seq. ID Method BLASTX NCBI GI g2130069 BLAST score 335 3.0e - 31E value Match length 72 90 % identity catalase (EC 1.11.1.6) catA - rice NCBI Description >gi_1261858_dbj_BAA06232 (D29966) catalase [Oryza sativa] Seq. No. Seq. ID uC-osflcyp139h05b1 BLASTX Method NCBI GI g5702186 BLAST score 338 E value 5.0e-37 Match length 131 % identity 65 (AF106085) 4-coumarate:CoA ligase 2 [Arabidopsis thaliana] NCBI Description >gi_5702188_gb_AAD47193.1_AF106086_1 (AF106086) 4-coumarate:CoA ligase 2 [Arabidopsis thaliana] 413708 Seq. No. uC-osflcyp139h06a1 Seq. ID Method BLASTX NCBI GI g482311 BLAST score 313 E value 1.0e-28 Match length 65 97 % identity photosystem II oxygen-evolving complex protein 1 - rice

NCBI Description

(strain Nihonbare) >gi_739292_prf__2002393A oxygen-evolving

complex protein 1 [Oryza sativa]

413709 Seq. No.

Seq. ID uC-osflcyp139h06b1

BLASTX Method g482311 NCBI GI

Seq. ID Method

BLASTX

```
564
BLAST score
                  2.0e-68
E value
                  137
Match length
                  97
% identity
                  photosystem II oxygen-evolving complex protein 1 - rice
NCBI Description
                   (strain Nihonbare) >gi_739292_prf__2002393A oxygen-evolving
                  complex protein 1 [Oryza sativa]
                  413710
Seq. No.
                  uC-osflcyp139h07b1
Seq. ID
                  BLASTX
Method
                  g1706260
NCBI GI
BLAST score
                  396
                  1.0e-38
E value
                  85
Match length
                  89
% identity
                  CYSTEINE PROTEINASE 1 PRECURSOR >gi 2118131_pir__S59597
NCBI Description
                  cysteine proteinase 1 precursor - maize
                  >gi 643597 dbj BAA08244_ (D45402) cysteine proteinase [Zea
                  mays]
                   413711
Seq. No.
                  uC-osflcyp139h10a1
Seq. ID
                  BLASTX
Method
NCBI GI
                  g2351580
                  181
BLAST score
E value
                   3.0e-13
                  43
Match length
                   79
% identity
NCBI Description
                  (U82433) thymidine diphospho-glucose 4-6-dehydratase
                   homolog [Prunus armeniaca]
                   413712
Seq. No.
                   uC-osflcyp139h10b1
Seq. ID
Method
                  BLASTX
NCBI GI
                   q3927825
BLAST score
                   261
                   7.0e-40
E value
Match length
                   114
                   71
% identity
                   (AC005727) putative dTDP-glucose 4-6-dehydratase
NCBI Description
                   [Arabidopsis thaliana]
                   413713
Seq. No.
                   uC-osflcyp140a01b1
Seq. ID
                   BLASTX
Method
NCBI GI
                   q3183106
BLAST score
                   237
E value
                   1.0e-19
Match length
                   108
% identity
                   45
NCBI Description PROBABLE OXALYL-COA DECARBOXYLASE >gi_1788716 (AE000325)
                   putative enzyme [Escherichia coli]
                   413714
Seq. No.
                   uC-osflcyp140a02a1
```

```
NCBI GI
                   g5031275
BLAST score
                   218
E value
                   1.0e-17
Match length
                   52
                   77
% identity
NCBI Description (AF139496) unknown [Prunus armeniaca]
Seq. No.
                   413715
Seq. ID
                   uC-osflcyp140a02b1
Method
                   BLASTX
NCBI GI
                   g2293480
BLAST score
                   290
E value
                   4.0e-36
Match length
                   87
% identity
                   94
NCBI Description (AF011331) glycine-rich protein [Oryza sativa]
                   413716
Seq. No.
Seq. ID
                   uC-osflcyp140a05b1
Method
                   BLASTX
NCBI GI
                   g2130069
BLAST score
                   289
E value
                   4.0e-34
Match length
                   126
% identity
                   65
NCBI Description catalase (EC 1.11.1.6) catA - rice
                   >gi_1261858_dbj_BAA06232_ (D29966) catalase [Oryza sativa]
Seq. No.
                   413717
Seq. ID
                   uC-osflcyp140a07b1
Method
                   BLASTX
NCBI GI
                   g4104931
BLAST score
                   487
E value
                   5.0e-49
Match length
                   160
% identity
                   61
NCBI Description (AF042196) auxin response factor 8 [Arabidopsis thaliana]
Seq. No.
                   413718
Seq. ID
                   uC-osflcyp140a08b1
Method
                   BLASTX
NCBI GI
                   g5031275
BLAST score
                   661
E value
                   2.0e-69
Match length
                   162
% identity
                   77
NCBI Description (AF139496) unknown [Prunus armeniaca]
Seq. No.
                   413719
Seq. ID
                   uC-osflcyp140a09a1
                   BLASTN
Method
NCBI GI
                   g218171
BLAST score
                   79
E value
                   2.0e-36
Match length
                   135
% identity
                   90
NCBI Description Oryza sativa mRNA for type I light-harvesting chlorophyll
```

Seq. No.

Seq. ID

413725

uC-osflcyp140b04a1

```
Seq. No.
                   413720
                   uC-osflcyp140a10a1
Seq. ID
Method
                   BLASTN
NCBI GI
                   g3885887
                   307
BLAST score
E value
                   1.0e-172
Match length
                   375
                   95
% identity
NCBI Description
                  Oryza sativa high mobility group protein (HMG) mRNA,
                   complete cds
                   413721
Seq. No.
                   uC-osflcyp140a10b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3885888
BLAST score
                   273
E value
                   7.0e-24
Match length
                   98
                   62
% identity
NCBI Description
                  (AF093632) high mobility group protein [Oryza sativa]
Seq. No.
                   413722
                   uC-osflcyp140a11b1
Seq. ID
                   BLASTX
Method
                   g3953465
NCBI GI
                   383
BLAST score
E value
                   8.0e-37
Match length
                   129
% identity
                   52
NCBI Description (AC002328) F20N2.10 [Arabidopsis thaliana]
                   413723
Seq. No.
Seq. ID
                   uC-osflcyp140b02b1
Method
                   BLASTX
NCBI GI
                   q5281051
BLAST score
                   368
E value
                   5.0e-35
Match length
                   87
% identity
                   79
NCBI Description
                  (AL080318) stress-induced protein stil-like protein
                   [Arabidopsis thaliana]
Seq. No.
                   413724
Seq. ID
                   uC-osflcyp140b03b1
Method
                   BLASTX
NCBI GI
                   g1587206
BLAST score
                   669
E value
                   2.0e-70
Match length
                   166
                   79
% identity
NCBI Description T complex protein [Cucumis sativus]
```

a/b binding protein of photosystem II (LHCPII), complete

Method BLASTN
NCBI GI g218154
BLAST score 54
E value 1.0e-21
Match length 62
% identity 98

NCBI Description Oryza sativa gene for cytoplasmic aldolase, complete cds,

clone:Aldp

Seq. No. 413726

Seq. ID uC-osflcyp140b04b1

Method BLASTX
NCBI GI g3913018
BLAST score 748
E value 1.0e-79
Match length 151
% identity 100

NCBI Description FRUCTOSE-BISPHOSPHATE ALDOLASE, CHLOROPLAST PRECURSOR

(ALDP) >gi 218155_dbj_BAA02730_ (D13513) chloroplastic

aldolase [Oryza sativa]

Seq. No. 413727

Seq. ID uC-osflcyp140b06b1

Method BLASTX
NCBI GI g3860333
BLAST score 382
E value 8.0e-37
Match length 100
% identity 66

NCBI Description (AJ012693) basic blue copper protein [Cicer arietinum]

Seq. No. 413728

Seq. ID uC-osflcyp140b10a1

Method BLASTX
NCBI GI g5922625
BLAST score 607
E value 4.0e-63
Match length 112
% identity 97

NCBI Description (AP000492) ESTs AU065732(E51179), AU030519(E51179)

correspond to a region of the predicted gene.; similar to epoxide hydrolases; coded for by A. thaliana cDNA T04215. (AF069298) [Oryza sativa] >gi_6016858_dbj_BAA85201.1_ (AP000570) ESTs AU065732(E51179),AU030519(E51179)

correspond to a region of the predicted gene.; Similar to epoxide hydrolases; coded for by A. thaliana cDNA T04215.

(AF069298) [Oryza sativa]

Seq. No. 413729

Seq. ID uC-osflcyp140b10b1

Method BLASTN
NCBI GI g6016845
BLAST score 489
E value 0.0e+00
Match length 574
% identity 96

NCBI Description Oryza sativa genomic DNA, chromosome 1, clone:P0711E10

413730 Seq. No. Seq. ID uC-osflcyp140c03b1 Method BLASTX NCBI GI g1708236 BLAST score 520 7.0e-53 E value Match length 158 % identity 62 NCBI Description HYDROXYMETHYLGLUTARYL-COA SYNTHASE (HMG-COA SYNTHASE) (3-HYDROXY-3-METHYLGLUTARYL COENZYME A SYNTHASE) >qi 2129617 pir JC4567 hydroxymethylglutaryl-CoA synthase (EC 4.1.3.5) - Arabidopsis thaliana >gi_1143390_emb_CAA58763_ (X83882)
hydroxymethylglutaryl-CoA synthase [Arabidopsis thaliana] >gi 1586548 prf 2204245A hydroxy methylglutaryl CoA synthase [Arabidopsis thaliana] Seq. No. 413731 uC-osflcyp140c04b1 Seq. ID Method BLASTX NCBI GI q1658313 BLAST score 818 E value 8.0e-88 Match length 150 % identity NCBI Description (Y08987) osr40g2 [Oryza sativa] Seq. No. 413732 Seq. ID uC-osflcyp140c06a1 Method BLASTX NCBI GI g3252807 BLAST score 181 E value 9.0e-14 Match length 49 78 % identity NCBI Description (AC004705) hypothetical protein [Arabidopsis thaliana] 413733 Seq. No. Seq. ID uC-osflcyp140c07b1 BLASTX Method NCBI GI g1296955 BLAST score 271 E value 8.0e-24 Match length 99 % identity 31 NCBI Description (X95402) duplicated domain structure protein [Oryza sativa] 413734 Seq. No. Seq. ID uC-osflcyp140c08a1 BLASTN Method NCBI GI g2570504 BLAST score 206 E value 1.0e-112 Match length 266 % identity 94 NCBI Description Oryza sativa proteasome component mRNA, complete cds

BLAST score

E value

314

1.0e-28

Seq. No. 413735 Seq. ID uC-osflcyp140c08b1 Method BLASTX NCBI GI g3121825 BLAST score 323 E value 7.0e-30 Match length 105 % identity 63 2-CYS PEROXIREDOXIN BAS1 PRECURSOR (THIOL-SPECIFIC NCBI Description ANTIOXIDANT PROTEIN) >gi_1498247_emb_CAA63910_ (X94219) bas1 protein [Spinacia oleracea] 413736 Seq. No. Seq. ID uC-osflcyp140c09b1 BLASTX Method NCBI GI q6093778 BLAST score 453 E value 4.0e-45 Match length 97 95 % identity NCBI Description PROTEASOME COMPONENT C3 (MACROPAIN SUBUNIT C3) (MULTICATALYTIC ENDOPEPTIDASE COMPLEX SUBUNIT C3) >gi_2511574_emb_CAA73619.1_ (Y13176) multicatalytic
endopeptidase [Arabidopsis thaliana] >gi_3421075 (AF043520) 20S proteasome subunit PAB1 [Arabidopsis thaliana] >gi_4966368_gb_AAD34699.1_AC006341_27 (AC006341) Identical
to gb_Y13176 Arabidopsis thaliana mRNA for proteasome subunit prc3. ESTs gb H36972, gb T22551 and gb T13800 come from this gene Seq. No. 413737 uC-osflcyp140c11b1 Seq. ID Method BLASTX NCBI GI q4539009 BLAST score 577 2.0e-59 E value Match length 174 61 % identity NCBI Description (AL049481) putative protein [Arabidopsis thaliana] 413738 Seq. No. Seq. ID uC-osflcyp140c12b1 Method BLASTX NCBI GI g3046731 927 BLAST score 1.0e-100 E value 193 Match length 89 % identity NCBI Description (AJ005373) protein kinase [Craterostigma plantagineum] 413739 Seq. No. Seq. ID uC-osflcyp140d04b1 BLASTX Method NCBI GI q4512703

Match length 106 55 % identity (AC006569) unknown protein [Arabidopsis thaliana] NCBI Description 413740 Seq. No. uC-osflcyp140d05b1 Seq. ID BLASTX Method NCBI GI g1352469 BLAST score 553 E value 9.0e-57 129 Match length 82 % identity BETA-FRUCTOFURANOSIDASE, CELL WALL ISOZYME PRECURSOR NCBI Description (SUCROSE-6-PHOSPHATE HYDROLASE) (INVERTASE) >gi 736359 (U17695) invertase [Zea mays] >gi_1582380_prf__2118364A cell wall invertase [Zea mays] 413741 Seq. No. uC-osflcyp140d07b1 Seq. ID BLASTX Method g1184774 NCBI GI 576 BLAST score 2.0e-59 E value 131 Match length 85 % identity (U45856) cytosolic glyceroldehyde-3-phosphate dehydrogenase NCBI Description GAPC3 [Zea mays] Seq. No. 413742 uC-osflcyp140d08b1 Seq. ID Method BLASTX g2493318 NCBI GI 246 BLAST score 1.0e-20 E value Match length 86 % identity 55 NCBI Description BLUE COPPER PROTEIN PRECURSOR >gi_562779_emb_CAA80963_ (Z25471) blue copper protein [Pisum sativum] >gi_1098264_prf__2115352A blue Cu protein [Pisum sativum] 413743 Seq. No. Seq. ID uC-osflcyp140d09b1 Method BLASTX NCBI GI g4585882 BLAST score 662 E value 2.0e-69 Match length 172 73 % identity

NCBI Description (AC005850) PSI type III chlorophyll a/b-binding protein

[Arabidopsis thaliana]

Seq. No. 413744

Seq. ID uC-osflcyp140d11b1

Method BLASTX
NCBI GI g2435517
BLAST score 250
E value 4.0e-21

Match length % identity NCBI Description

(AF024504) contains similarity to peptidase family A1 [Arabidopsis thaliana]

413745 Seq. No.

uC-osflcyp140e02b1 Seq. ID

Method BLASTX NCBI GI g2130073 BLAST score 225 2.0e-18 E value 47 Match length 96 % identity

fructose-bisphosphate aldolase (EC 4.1.2.13) isoenzyme C-1, cytosolic - rice >gi_786178_dbj_BAA08845_ (D50307) aldolase NCBI Description

C-1 [Oryza sativa] >gi 790970 dbj_BAA08830_ (D50301)

aldolase C-1 [Oryza sativa]

413746 Seq. No.

uC-osflcyp140e05b1 Seq. ID

Method BLASTX NCBI GI q5668762 BLAST score 276 3.0e-24E value 174 Match length 39 % identity

(AC005916) EST gb N65787 comes from this gene. [Arabidopsis NCBI Description

thaliana]

413747 Seq. No.

Seq. ID uC-osflcyp140e06b1

Method BLASTX q3600033 NCBI GI BLAST score 672 1.0e-70 E value Match length 167

% identity (AF080119) contains similarity to the N terminal domain of NCBI Description

the E1 protein (Pfam: E1 N.hmm, score: 12.36) [Arabidopsis

thaliana]

Seq. No. 413748

uC-osflcyp140e07b1 Seq. ID

Method BLASTX NCBI GI g320618 BLAST score 780 E value 2.0e-83 Match length 161 % identity 92

chlorophyll a/b-binding protein I precursor - rice NCBI Description

>gi_218172_dbj_BAA00536_ (D00641) type I light-harvesting chlorophyll a/b-binding protein [Oryza sativa]

>gi 227611 prf 1707316A chlorophyll a/b binding protein 1

[Oryza sativa]

413749 Seq. No.

uC-osflcyp140e11b1 Seq. ID

```
Method
                  BLASTX
                  g1353352
NCBI GI
                  276
BLAST score
                  3.0e-24
E value
Match length
                  84
                   64
% identity
                  (U31975) alanine aminotransferase [Chlamydomonas
NCBI Description
                  reinhardtii]
                  413750
Seq. No.
                  uC-osflcyp140f02b1
Seq. ID
Method
                  BLASTX
                  q4138732
NCBI GI
BLAST score
                  150
                  2.0e-09
E value
Match length
                  102
                   42
% identity
                  (Y17332) proline-rich protein [Zea mays]
NCBI Description
                   413751
Seq. No.
                  uC-osflcyp140f03b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2980788
BLAST score
                  203
E value
                   9.0e-16
Match length
                  100
% identity
                   45
                  (AL022197) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   413752
                  uC-osflcyp140f04a1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g5091608
BLAST score
                  185
                   1.0e-13
E value
Match length
                   39
% identity
                   95
NCBI Description
                  (AC007858) Identical to gb_D50317 ADP glucose
                   pyrophosphorylase large subunit from Oryza sativa.
                                                                        ESTs
                   dbj_D22125 and dbj_D15718 come from
Seq. No.
                   413753
                  uC-osflcyp140f04b1
Seq. ID
Method
                  BLASTX
NCBI GI
                   g1213073
BLAST score
                   247
E value
                   4.0e-21
Match length
                  80
% identity
                   68
NCBI Description
                  (X75616) heat shock protein 17.8 [Oryza sativa]
                   413754
Seq. No.
```

Seq. ID uC-osflcyp140f05b1

Method BLASTX NCBI GI g2501850 BLAST score 739 E value 2.0e-78

```
Match length
                  183
% identity
                   75
NCBI Description
                 (AF012823) GDP dissociation inhibitor [Nicotiana tabacum]
Seq. No.
                   413755
Seq. ID
                  uC-osflcyp140f06a1
Method
                  BLASTX
NCBI GI
                  g3319774
BLAST score
                  203
E value
                  8.0e-16
Match length
                  59
% identity
                  59
NCBI Description (Y16228) TOM7 protein [Solanum tuberosum]
Seq. No.
                   413756
Seq. ID
                  uC-osflcyp140f06b1
Method
                  BLASTX
NCBI GI
                  g6015065
BLAST score
                  717
E value
                   6.0e - 76
Match length
                  153
% identity
                  90
NCBI Description ELONGATION FACTOR 2 (EF-2) >gi_2369714_emb_CAB09900_
                  (Z97178) elongation factor 2 [Beta vulgaris]
Seq. No.
                  413757
Seq. ID
                  uC-osflcyp140f08a1
Method
                  BLASTX
NCBI GI
                  g3608495
BLAST score
                  193
E value
                  1.0e-14
Match length
                  69
% identity
                   61
NCBI Description
                  (AF089738) plastid division protein FtsZ [Arabidopsis
                  thaliana] >gi_4510351_gb_AAD21440.1_ (AC006921) plastid
                  division protein FtsZ [Arabidopsis thaliana]
Seq. No.
                   413758
Seq. ID
                  uC-osflcyp140f08b1
Method
                  BLASTX
NCBI GI
                  g1321661
BLAST score
                  605
E value
                  6.0e-63
Match length
                  123
% identity
                  97
NCBI Description (D45423) ascorbate peroxidase [Oryza sativa]
Seq. No.
                  413759
Seq. ID
                  uC-osflcyp140f10b1
Method
                  BLASTX
NCBI GI
                  g2627058
BLAST score
                  951
E value
                  1.0e-103
Match length
                  182
% identity
                  98
NCBI Description
                  (D50317) ADP glucose pyrophosphorylase large subunit [Oryza
                  sativa]
```

413760 Seq. No. Seq. ID uC-osflcyp140f11b1 Method BLASTX NCBI GI g1173347 BLAST score 395 E value 4.0e-38 Match length 84 % identity 96 NCBI Description SEDOHEPTULOSE-1,7-BISPHOSPHATASE, CHLOROPLAST PRECURSOR (SEDOHEPTULOSE-BISPHOSPHATASE) (SBPASE) (SED(1,7)P2ASE) >gi_100803_pir__S23452 sedoheptulose-bisphosphatase (EC 3.1.3.37) precursor - wheat >gi_14265_emb_CAA46507_ (X65540) sedoheptulose-1,7-bisphosphatase [Triticum aestivum] 413761 Seq. No. Seq. ID uC-osflcyp140g01b1 Method BLASTX NCBI GI q4038471 BLAST score 384 E value 5.0e-37 Match length 86 % identity 85 NCBI Description (AF111029) 40S ribosomal protein S27 homolog [Zea mays] 413762 Seq. No. Seq. ID uC-osflcyp140g02b1 Method BLASTX NCBI GI g1890575 BLAST score 479 E value 4.0e-48Match length 98 % identity 90 NCBI Description (X93174) xyloglucan endotransglycosylase (XET) [Hordeum vulgare] 413763 Seq. No. Seq. ID uC-osflcyp140g03b1 Method BLASTX NCBI GI g4760700 BLAST score 251 E value 2.0e-21 Match length 101 % identity 52 NCBI Description (AB024437) peroxidase 1 [Scutellaria baicalensis] Seq. No. 413764 Seq. ID uC-osflcyp140g04b1 Method BLASTX NCBI GI q141305 BLAST score 261 E value 2.0e-22 95 Match length % identity 56 NCBI Description YPT1-RELATED PROTEIN 2 >gi_101034_pir S12790 GTP-binding protein ypt2 - fission yeast (Schizosaccharomyces pombe)

>gi_5144_emb_CAA36707_ (X52469) ypt2 gene product (AA
1-200) [Schizosaccharomyces pombe] >gi_5150_emb_CAA37045_
(X52864) ypt-related protein (AA 1-200)
[Schizosaccharomyces pombe] >gi_2414662_emb_CAB16405.1_
(Z99262) ypt1-related protein 2 [Schizosaccharomyces pombe]

Seq. No. 413765

Seq. ID uC-osflcyp140g05b1

Method BLASTX
NCBI GI g3885888
BLAST score 316
E value 7.0e-29
Match length 107
% identity 65

NCBI Description (AF093632) high mobility group protein [Oryza sativa]

Seq. No. 413766

Seq. ID uC-osflcyp140g06b1

Method BLASTX
NCBI GI g4107001
BLAST score 694
E value 3.0e-73
Match length 135
% identity 99

NCBI Description (D82035) OSK4 [Oryza sativa]

Seq. No. 413767

Seq. ID uC-osflcyp140g07b1

Method BLASTN
NCBI GI g2760169
BLAST score 35
E value 5.0e-10
Match length 143
% identity 81

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MFB13, complete sequence

Seq. No. 413768

Seq. ID uC-osflcyp140g10b1

Method BLASTX
NCBI GI g131225
BLAST score 632
E value 8.0e-68
Match length 158
% identity 86

NCBI Description PHOTOSYSTEM I REACTION CENTRE SUBUNIT XI PRECURSOR (SUBUNIT

V) (PSI-L) >gi_100605_pir__A39759 photosystem I 18K protein

precursor - barley >gi_167087 (M61146) photosystem I

hydrophobic protein [Hordeum vulgare]

Seq. No. 413769

Seq. ID uC-osflcyp140h01a1

Method BLASTN
NCBI GI g3582315
BLAST score 37
E value 2.0e-11

Match length 45

% identity NCBI Description Arabidopsis thaliana chromosome II BAC T27A16 genomic

sequence, complete sequence [Arabidopsis thaliana]

413770 Seq. No.

Seq. ID uC-osflcyp140h01b1

Method BLASTX NCBI GI q1706260 BLAST score 444 E value 4.0e-44 Match length 99 % identity 88

NCBI Description CYSTEINE PROTEINASE 1 PRECURSOR >gi_2118131_pir__S59597

cysteine proteinase 1 precursor - maize

>gi 643597_dbj_BAA08244_ (D45402) cysteine proteinase [Zea

mays]

413771 Seq. No.

Seq. ID uC-osflcyp140h02b1

Method BLASTX g1388088 NCBI GI BLAST score 192 E value 8.0e-15 Match length 59 % identity 59

NCBI Description (U35831) thioredoxin m [Pisum sativum]

413772 Seq. No.

uC-osflcyp140h03b1 Seq. ID

Method BLASTX NCBI GI q2435519 BLAST score 380 E value 1.0e-36 Match length 118 % identity

NCBI Description (AF024504) similar to mouse MEM3 (GB:U47024 and S.

cerevisiae vacuolar sorting protein 35 (SW; P34110)

[Arabidopsis thaliana]

Seq. No. 413773

Seq. ID uC-osflcyp140h04a1

Method BLASTX NCBI GI g115787 BLAST score 439 E value 2.0e-43 Match length 83 % identity 100

CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I NCBI Description

CAB-2) (LHCP) >gi_82461_pir__S03706 chlorophyll a/b-binding protein 2R precursor - rice >gi_20182_emb_CAA32109_

(X13909) chlorophyll a/b-binding preprotein (AA -28 to 235)

[Oryza sativa]

Seq. No. 413774

Seq. ID uC-osflcyp140h04b1

Method BLASTX NCBI GI g3892722

```
BLAST score
                  143
                  8.0e-09
E value
Match length
                  42
% identity
                  57
NCBI Description (AL033545) putative protein [Arabidopsis thaliana]
                  413775
Seq. No.
Seq. ID
                  uC-osflcyp140h05b1
Method
                  BLASTX
NCBI GI
                  g1076722
BLAST score
                  533
E value
                  2.0e-54
Match length
                  119
                  87
% identity
NCBI Description hypothetical protein - barley (fragment)
                  413776
Seq. No.
Seq. ID
                  uC-osflcyp140h06b1
Method
                  BLASTX
NCBI GI
                  g2293480
BLAST score
                  170
E value
                  3.0e-12
Match length
                  41
                  83
% identity
NCBI Description (AF011331) glycine-rich protein [Oryza sativa]
Seq. No.
                  413777
Seq. ID
                  uC-osflcyp140h07b1
Method
                  BLASTX
NCBI GI
                  g3582335
BLAST score
                  703
E value
                  2.0e-74
Match length
                  149
% identity
NCBI Description (AC005496) unknown protein [Arabidopsis thaliana]
Seq. No.
                  413778
Seq. ID
                  uC-osflcyp140h08b1
Method
                  BLASTX
NCBI GI
                  q4115914
BLAST score
                  510
E value
                  9.0e-52
Match length
                  152
% identity
                  59
NCBI Description
                  (AF118222) contains similarity to Iron/Ascorbate family of
                  oxidoreductases (Pfam: PF00671, Score=297.8, E=1.3e-85,
                  N=1) [Arabidopsis thaliana] >gi_4539410_emb CAB40043.1
                  (ALO49524) putative Fe(II)/ascorbate oxidase [Arabidopsis
                  thaliana]
Seq. No.
                  413779
Seq. ID
                  uC-osflcyp140h09a1
Method
                  BLASTX
NCBI GI
                  g3687240
BLAST score
                  143
E value
                  9.0e-09
Match length
                  84
```

% identity

58

% identity NCBI Description (AC005169) extensin-like protein [Arabidopsis thaliana] Seq. No. 413780 Seq. ID uC-osflcyp140h10a1 Method BLASTN NCBI GI q218171 BLAST score 103 E value 6.0e-51Match length 187 % identity 94 NCBI Description Oryza sativa mRNA for type I light-harvesting chlorophyll a/b binding protein of photosystem II (LHCPII), complete 413781 Seq. No. Seq. ID uC-osflcyp140h10b1 Method BLASTX NCBI GI g320618 BLAST score 724 E value 8.0e-77Match length 156 % identity 89 NCBI Description chlorophyll a/b-binding protein I precursor - rice >gi_218172_dbj_BAA00536_ (D00641) type I light-harvesting chlorophyll a/b-binding protein [Oryza sativa] >gi_227611_prf__1707316A chlorophyll a/b binding protein 1 [Oryza sativa] 413782 Seq. No. Seq. ID uC-osflcyp140h11b1 Method BLASTX NCBI GI q2832625 BLAST score 267 E value 4.0e-23 Match length 64 % identity NCBI Description (AL021711) putative protein [Arabidopsis thaliana] Seq. No. 413783 Seq. ID uC-osflcyp141a01b1 Method BLASTX NCBI GI g2829887 BLAST score 390 E value 1.0e-37 Match length 148 % identity 56 NCBI Description (AC002396) Hypothetical protein [Arabidopsis thaliana] Seq. No. 413784 Seq. ID uC-osflcyp141a02b1 Method BLASTX NCBI GI g4263704 BLAST score 185 E value 9.0e-14 Match length 62

```
NCBI Description (AC006223) putative sugar starvation-induced protein
                   [Arabidopsis thaliana]
Seq. No.
                   413785
Seq. ID
                   uC-osflcyp141a03a1
Method
                   BLASTN
NCBI GI
                   g310322
BLAST score
                   214
E value
                   1.0e-117
Match length
                   222
% identity
                   99
NCBI Description Oryza sativa triosephosphate isomerase (Rictipi2) gene,
                   exons 1-9
Seq. No.
                   413786
Seq. ID
                   uC-osflcyp141a03b1
Method
                   BLASTX
NCBI GI
                   g1351270
BLAST score
                   751
E value
                   5.0e-80
Match length
                   163
% identity
                   90
NCBI Description
                   TRIOSEPHOSPHATE ISOMERASE, CYTOSOLIC (TIM)
                   >gi_478410_pir__JQ2255 triose-phosphate isomerase (EC
                   5.3.1.1) - rice >gi_169821 (M87064) triosephosphate
                   isomerase [Oryza sativa]
Seq. No.
                   413787
Seq. ID
                   uC-osflcyp141a06a1
Method
                   BLASTX
NCBI GI
                   g4588906
BLAST score
                   312
E value
                   1.0e-28
Match length
                  71
% identity
NCBI Description (AF118149) ribosomal protein S7 [Secale cereale]
Seq. No.
                   413788
Seq. ID
                  uC-osflcyp141a06b1
Method
                  BLASTX
NCBI GI
                  g4588906
BLAST score
                  357
E value
                  3.0e-34
Match length
                  84
% identity
NCBI Description (AF118149) ribosomal protein S7 [Secale cereale]
Seq. No.
                  413789
Seq. ID
                  uC-osflcyp141a08b1
Method
                  BLASTX
NCBI GI
                  g3935147
BLAST score
                  552
E value
                  1.0e-56
Match length
                  178
% identity
                  58
NCBI Description (AC005106) T25N20.11 [Arabidopsis thaliana]
```

Seq. No. 413790 Seq. ID uC-osflcyp141a09a1 Method BLASTX NCBI GI g3335359 BLAST score 246 E value 8.0e-21 Match length 63 % identity 76 NCBI Description (AC003028) unknown protein [Arabidopsis thaliana] Seq. No. 413791 Seq. ID uC-osflcyp141a10b1 Method BLASTX NCBI GI q3913427 BLAST score 497 E value 2.0e-50 Match length 126 % identity 75 NCBI Description S-ADENOSYLMETHIONINE DECARBOXYLASE PROENZYME (ADOMETDC) (SAMDC) >gi_1532073_emb_CAA69075_ (Y07767) S-adenosylmethionine decarboxylase [Zea mays] Seq. No. 413792 Seq. ID uC-osflcyp141a11b1 Method BLASTX NCBI GI q4539314 BLAST score 236 E value 5.0e-20 Match length 85 % identity 55 NCBI Description (AL035679) kinesin like protein [Arabidopsis thaliana] Seq. No. 413793 Seq. ID uC-osflcyp141b01a1 Method BLASTN NCBI GI q4887615 BLAST score 361 E value 0.0e + 00Match length 381 % identity 99 NCBI Description Oryza sativa HOS58 mRNA, partial cds Seq. No. 413794 Seq. ID uC-osflcyp141b01b1 Method BLASTX NCBI GI g3122572 BLAST score 223 E value 9.0e-27 Match length 124 % identity 57 NCBI Description NADH-UBIQUINONE OXIDOREDUCTASE 75 KD SUBUNIT PRECURSOR (COMPLEX I-75KD) (CI-75KD) (76 KD MITOCHONDRIAL COMPLEX I

SUBUNIT) >gi_1084434_pir__ S52737 NADH dehydrogenase (ubiquinone) (EC 1.6.5.3) 76K chain precursor - potato >gi_758340_emb_CAA59818_ (X85808) 76 kDa mitochondrial complex I subunit [Solanum tuberosum]

Seq. No.

413800

413795 Seq. No. Seq. ID uC-osflcyp141b02b1 Method BLASTX NCBI GI g4678209 BLAST score 288 E value 1.0e-33 Match length 149 % identity NCBI Description (AC007134) putative sugar transporter [Arabidopsis thaliana] Seq. No. 413796 Seq. ID uC-osflcyp141b03b1 Method BLASTX NCBI GI q1184774 BLAST score 604 E value 1.0e-62 Match length 148 % identity NCBI Description (U45856) cytosolic glyceroldehyde-3-phosphate dehydrogenase GAPC3 [Zea mays] Seq. No. 413797 Seq. ID uC-osflcyp141b04b1 Method BLASTX NCBI GI q4079798 BLAST score 320 E value 2.0e-30 Match length 153 % identity NCBI Description (AF052203) 23 kDa polypeptide of photosystem II [Oryza sativa] Seq. No. 413798 Seq. ID uC-osflcyp141b05a1 Method BLASTX NCBI GI g1345809 BLAST score 329 E value 3.0e-50Match length 109 % identity 86 NCBI Description CHALCONE SYNTHASE (NAREGENIN-CHALCONE SYNTHASE) >gi_2117713_pir__S58190 naringenin-chalcone synthase (EC 2.3.1.74) - rice >gi_927491_emb_CAA61955_ (X89859) naringenin-chalcone synthase [Oryza sativa] Seq. No. 413799 Seq. ID uC-osflcyp141b05b1 Method BLASTX NCBI GI g1816444 BLAST score 397 E value 8.0e-42 Match length 114 % identity 82 NCBI Description (AB000801) chalcone synthase [Oryza sativa]

Seq. No.

413805

Seq. ID uC-osflcyp141b08b1 Method BLASTX NCBI GI q4646206 BLAST score 666 E value 6.0e-70 Match length 178 % identity NCBI Description (AC007230) Contains similarity to gb_D13630 KIAA0005 gene from Homo sapiens. ESTs gb_T45345, gb_T21086, gb_R90360, gb_T20468, gb_T45191 and gb_AI100459 come from this gene. [Arabidopsis thaliana] Seq. No. 413801 Seq. ID uC-osflcyp141b10a1 Method BLASTN NCBI GI g1778820 BLAST score 152 E value 7.0e-80 Match length 351 % identity NCBI Description Oryza sativa S-adenosyl-L-methionine synthetase (pOS-SAMS2) mRNA, complete cds Seq. No. 413802 Seq. ID uC-osflcyp141b10b1 Method BLASTX NCBI GI q3024122 BLAST score 612 E value 2.0e-64 Match length 131 % identity 98 S-ADENOSYLMETHIONINE SYNTHETASE 2 (METHIONINE NCBI Description ADENOSYLTRANSFERASE 2) (ADOMET SYNTHETASE 2) >gi_1778821 (U82833) S-adenosyl-L-methionine synthetase [Oryza sativa] Seq. No. 413803 Seq. ID uC-osflcyp141c05b1 Method BLASTX NCBI GI q4539004 BLAST score 163 E value 3.0e-11 Match length 42 % identity 69 NCBI Description (AL049481) putative protein kinase [Arabidopsis thaliana] Seq. No. 413804 Seq. ID uC-osflcyp141c06a1 Method BLASTX NCBI GI g2982268 BLAST score 477 E value 7.0e-4896 Match length % identity NCBI Description (AF051217) probable 40S ribosomal protein S15 [Picea mariana]

NCBI GI

```
Seq. ID
                   uC-osflcyp141c06b1
Method
                   BLASTX
NCBI GI
                   g2982268
BLAST score
                   579
E value
                   7.0e-60
Match length
                   123
 % identity
NCBI Description
                  (AF051217) probable 40S ribosomal protein S15 [Picea
                   mariana]
Seq. No.
                   413806
Seq. ID
                   uC-osflcyp141c10a1
Method
                   BLASTN
NCBI GI
                   q3859567
BLAST score
                   206
E value
                   1.0e-112
Match length
                   257
% identity
                   95
NCBI Description Oryza sativa clone FIL1 unknown mRNA
Seq. No.
                   413807
Seq. ID
                   uC-osflcyp141d01b1
Method
                   BLASTX
NCBI GI
                   g5107819
BLAST score
                   186
E value
                   9.0e-14
Match length
                   100
% identity
                   40
NCBI Description
                  (AF149413) contains similarity to arabinosidase
                   [Arabidopsis thaliana]
Seq. No.
                   413808
Seq. ID
                   uC-osflcyp141d02a1
Method
                   BLASTX
NCBI GI
                   g1084455
BLAST score
                   278
E value
                   1.0e-24
Match length
                   55
% identity
                   96
NCBI Description peptidylprolyl isomerase (EC 5.2.1.8) Cyp2 - rice
                  >gi 600767 (L29469) cyclophilin 2 [Oryza sativa]
Seq. No.
                   413809
Seq. ID
                  uC-osflcyp141d02b1
Method
                  BLASTX
NCBI GI
                  g1084455
BLAST score
                  367
E value
                  2.0e-61
Match length
                  120
% identity
NCBI Description peptidylprolyl isomerase (EC 5.2.1.8) Cyp2 - rice
                  >gi_600767 (L29469) cyclophilin 2 [Oryza sativa]
Seq. No.
                  413810
Seq. ID
                  uC-osflcyp141d03b1
Method
                  BLASTX
```

g3024871

Method

NCBI GI

BLAST score

BLASTX

503

g2723471

```
BLAST score
                   494
E value
                   8.0e-50
Match length
                   160
% identity
                   55
NCBI Description
                  HYPOTHETICAL 77.3 KD PROTEIN SLL0005
                   >gi_1001579_dbj BAA10206 (D64000) ABC1-like [Synechocystis
                   sp.]
Seq. No.
                   413811
Seq. ID
                   uC-osflcyp141d05a1
Method
                  BLASTX
NCBI GI
                   g2723471
BLAST score
                   290
E value
                   2.0e-26
Match length
                   66
% identity
                   83
NCBI Description (D87819) sucrose transporter [Oryza sativa]
Seq. No.
                   413812
Seq. ID
                  uC-osflcyp141d05b1
Method
                  BLASTX
                  g119958
NCBI GI
BLAST score
                   232
E value
                  2.0e-19
Match length
                  86
% identity
                   57
NCBI Description FERREDOXIN III PRECURSOR (FD III) >gi_168473 (M73831)
                   ferredoxin [Zea mays] >gi 1864001 dbj BAA19251 (AB001387)
                   Fd III [Zea mays] >gi_444686_prf__1907324C
                   ferredoxin:ISOTYPE=III [Zea mays]
Seq. No.
                  413813
Seq. ID
                  uC-osflcyp141d08b1
Method
                  BLASTX
NCBI GI
                  q3790188
BLAST score
                  382
E value
                  2.0e-39
Match length
                  100
% identity
NCBI Description
                  (Y14431) NAD-dependent isocitrate dehydrogenase [Nicotiana
                  tabacum]
Seq. No.
                  413814
Seq. ID
                  uC-osflcyp141d09b1
Method
                  BLASTX
NCBI GI
                  g4586058
BLAST score
                  370
E value
                  5.0e-36
Match length
                  166
% identity
                  50
NCBI Description (AC007020) unknown protein [Arabidopsis thaliana]
Seq. No.
                  413815
Seq. ID
                  uC-osflcyp141d10b1
```

```
7.0e-51
E value
Match length
                    141
 % identity
                    68
NCBI Description (D87819) sucrose transporter [Oryza sativa]
Seq. No.
                    413816
Seq. ID
                    uC-osflcyp141d11a1
Method
                    BLASTX
NCBI GI
                    g119958
BLAST score
                    304
E value
                    1.0e-27
Match length
                    59
% identity
                    95
NCBI Description FERREDOXIN III PRECURSOR (FD III) >gi_168473 (M73831)
                    ferredoxin [Zea mays] >gi_1864001_dbj_BAA19251_ (AB001387) Fd III [Zea mays] >gi_444686_prf_1907324C
                    ferredoxin:ISOTYPE=III [Zea mays]
Seq. No.
                    413817
Seq. ID
                   uC-osflcyp141e02b1
Method
                   BLASTX
NCBI GI
                   g5901808
BLAST score
                   180
E value
                   5.0e-13
Match length
                   139
% identity
                   32
NCBI Description (AF181626) BcDNA.GH03694 [Drosophila melanogaster]
Seq. No.
                   413818
Seq. ID
                   uC-osflcyp141e04b1
Method
                   BLASTX
NCBI GI
                   g3600033
BLAST score
                   439
E value
                   2.0e-43
Match length
                   146
% identity
                   62
NCBI Description
                   (AF080119) contains similarity to the N terminal domain of
                   the El protein (Pfam: El_N.hmm, score: 12.36) [Arabidopsis
                   thaliana]
Seq. No.
                   413819
Seq. ID
                   uC-osflcyp141e09b1
Method
                   BLASTX
NCBI GI
                   g485517
BLAST score
                   499
E value
                   1.0e-50
Match length
                   98
% identity
                   99
NCBI Description ADP, ATP carrier protein - rice
Seq. No.
                   413820
Seq. ID
                   uC-osflcyp141f01a1
Method
                   BLASTX
NCBI GI
                   g2911053
BLAST score
                   278
E value
                   1.0e-24
Match length
                   84
```

Seq. No.

```
% identity
 NCBI Description
                  (AL021961) hypothetical protein [Arabidopsis thaliana]
 Seq. No.
                   413821
 Seq. ID
                   uC-osflcyp141f02b1
Method
                   BLASTX
NCBI GI
                   g1261917
BLAST score
                   339
E value
                   1.0e-31
Match length
                   90
 % identity
NCBI Description (X96979) lipid transfer protein 7a2b [Hordeum vulgare]
Seq. No.
                   413822
Seq. ID
                   uC-osflcyp141f03a1
Method
                   BLASTX
NCBI GI
                   g3256035
BLAST score
                   195
E value
                   8.0e-15
Match length
                   67
% identity
                   55
NCBI Description
                   (Y14274) putative serine/threonine protein kinase [Sorghum
                   bicolor]
Seq. No.
                   413823
Seq. ID
                   uC-osflcyp141f05a1
Method
                   BLASTN
NCBI GI
                   q425794
BLAST score
                   244
E value
                   1.0e-135
Match length
                   267
% identity
                   98
NCBI Description Rice mRNA for heat shock protein 82 (gene name AD167),
                   partial cds
Seq. No.
                   413824
Seq. ID
                   uC-osflcyp141f05b1
Method
                   BLASTX
NCBI GI
                   g5123910
BLAST score
                   508
E value
                   3.0e-55
Match length
                  122
% identity
                   93
NCBI Description (X98582) HSP80-2 [Triticum aestivum]
Seq. No.
                  413825
Seq. ID
                  uC-osflcyp141f08b1
Method
                  BLASTX
NCBI GI
                  g129591
BLAST score
                  583
E value
                  2.0e-60
Match length
                  118
% identity
                  97
NCBI Description PHENYLALANINE AMMONIA-LYASE >gi 295824 emb CAA34226
                  (X16099) phenylalanine ammonia-lyase [Oryza sativa]
```

BLAST score

215

```
Seq. ID
                    uC-osflcyp141f10a1
 Method
                   BLASTX
 NCBI GI
                   g3913426
 BLAST score
                   212
 E value
                   7.0e-17
 Match length
                   39
 % identity
                   100
 NCBI Description
                   S-ADENOSYLMETHIONINE DECARBOXYLASE PROENZYME (ADOMETDC)
                    (SAMDC) >gi_1532048_emb_CAA69074 (Y07766)
                   S-adenosylmethionine decarboxylase [Oryza sativa]
 Seq. No.
                   413827
 Seq. ID
                   uC-osflcyp141f10b1
 Method
                   BLASTX
 NCBI GI
                   g2129921
 BLAST score
                   179
E value
                   6.0e-13
Match length
                   51
 % identity
                   67
NCBI Description hypothetical protein 1 - Madagascar periwinkle >gi_758694
                   (U12573) putative [Catharanthus roseus]
Seq. No.
                   413828
Seq. ID
                   uC-osflcyp141f11b1
Method
                   BLASTX
NCBI GI
                   q3126854
BLAST score
                   598
E value
                   2.0e-76
Match length
                   152
% identity
                   89
NCBI Description (AF061577) chlorophyll a/b binding protein [Oryza sativa]
Seq. No.
                   413829
Seq. ID
                   uC-osflcyp141g02b1
Method
                   BLASTX
NCBI GI
                   q4049346
BLAST score
                   248
E value
                   4.0e-21
Match length
                   106
% identity
                   51
NCBI Description (AL034567) putative protein [Arabidopsis thaliana]
Seq. No.
                   413830
Seq. ID
                   uC-osflcyp141g04b1
Method
                   BLASTX
NCBI GI
                   g4490306
BLAST score
                  163
E value
                   4.0e-19
Match length
                  138
% identity
                  42
NCBI Description (AL035678) putative protein [Arabidopsis thaliana]
Seq. No.
                  413831
Seq. ID
                  uC-osflcyp141g05a1
Method
                  BLASTX
NCBI GI
                  g6006848
```

BLAST score

```
E value
                     3.0e-17
 Match length
                     47
 % identity
                     87
 NCBI Description
                    (AC009540) unknown protein, 5' partial [Arabidopsis
                     thaliana]
 Seq. No.
                     413832
 Seq. ID
                    uC-osflcyp141g05b1
 Method
                    BLASTX
 NCBI GI
                    g114268
 BLAST score
                    546
 E value
                    6.0e-56
 Match length
                    139
 % identity
                    68
NCBI Description L-ASCORBATE OXIDASE HOMOLOG PRECURSOR (ASCORBASE)
                    >gi_541907_pir__S23763 gene Bp10 protein - rape
                    >gi_17789_emb_CAA45554_ (X64257) protein homologous to
                    ascorbate oxidase [Brassica napus]
Seq. No.
                    413833
Seq. ID
                    uC-osflcyp141g07b1
Method
                    BLASTX
NCBI GI
                    q4204257
BLAST score
                    393
E value
                    4.0e-38
Match length
                    118
% identity
                    61
NCBI Description (AC005223) 5493 [Arabidopsis thaliana]
Seq. No.
                    413834
Seq. ID
                    uC-osflcyp141g09a1
Method
                    BLASTN
NCBI GI
                    g5051932
BLAST score
                    200
E value
                    1.0e-108
Match length
                    254
% identity
                    100
NCBI Description Oryza sativa MADS-box protein FDRMADS8 mRNA, complete cds
Seq. No.
                    413835
Seq. ID
                   uC-osflcyp141g10a1
Method
                   BLASTX
NCBI GI
                   g128592
BLAST score
                   217
E value
                   2.0e-17
Match length
                   58
% identity
                   67
NCBI Description
                   POLLEN-SPECIFIC PROTEIN NTP303 PRECURSOR
                   >gi_82190_pir__S22495 pollen-specific protein precursor -
common tobacco >gi_19902_emb_CAA43454_ (X61146) pollen
                   specific protein [Nicotiana Tabacum]
Seq. No.
                   413836
Seq. ID
                   uC-osflcyp141g11a1
Method
                   BLASTX
NCBI GI
                   g2598049
```

Method

BLASTX

```
E value
                      9.0e-20
 Match length
                      61
 % identity
                      (Y15269) chloroplast drought-induced stress protein, 34 kD)
 NCBI Description
                      [Solanum tuberosum]
 Seq. No.
                      413837
 Seq. ID
                     uC-osflcyp141g11b1
Method
                     BLASTX
 NCBI GI
                     g6006848
 BLAST score
                     453
E value
                     8.0e-73
Match length
                     173
 % identity
                     86
NCBI Description (AC009540) unknown protein, 5' partial [Arabidopsis
                     thaliana]
Seq. No.
                     413838
Seq. ID
                     uC-osflcyp141h01b1
Method
                     BLASTX
NCBI GI
                     g1845195
BLAST score
                     338
E value
                     1.0e-31
Match length
                     71
% identity
                     92
NCBI Description (Y08297) HMGcl [Zea mays] >gi_5441504_emb_CAB46753.1_
                     (AJ131374) HMGc1 protein [Zea mays]
Seq. No.
                     413839
Seq. ID
                     uC-osflcyp141h02b1
Method
                     BLASTX
NCBI GI
                     g1197461
BLAST score
                     746
E value
                     2.0e-79
Match length
                     148
% identity
                     94
NCBI Description (X78819) casein kinase I [Arabidopsis thaliana]
Seq. No.
                     413840
Seq. ID
                     uC-osflcyp141h06a1
Method
                     BLASTX
NCBI GI
                     g122090
BLAST score
                     191
E value
                     2.0e-14
Match length
                     46
% identity
                     87
NCBI Description
HISTONE H3 >gi_81287_pir__S00940 histone H3 - Volvox carteri >gi_2119017_pir__S59581 histone H3 (clone CH-II) - Chlamydomonas reinhardtii >gi_21985_emb_CAA30035_ (X06963)
                    put. histone H3 [Volvox carteri] >gi_21988_emb_CAA30037_
                     (X06964) put. histone H3 [Volvox car\overline{\text{teri}}] \overline{>}gi\overline{\_5}71470
                     (U16724) histone H3 [Chlamydomonas reinhardtii] >gi_571475
                     (U16725) histone H3 [Chlamydomonas reinhardtii]
                     413841
Seq. No.
Seq. ID
                    uC-osflcyp141h09b1
```

NCBI GI g3858935 BLAST score 386 E value 4.0e-37 Match length 123 % identity 61

NCBI Description (AL021636) synaptobrevin-like protein [Arabidopsis

thaliana] >gi_4103357 (AF025332) vesicle-associated membrane protein 7C; synaptobrevin 7C [Arabidopsis

thaliana]

Seq. No. 413842

Seq. ID uC-osflcyp141h12b1

Method BLASTX
NCBI GI 9417103
BLAST score 630
E value 8.0e-66
Match length 127
% identity 99

NCBI Description HISTONE H3.2, MINOR >gi_282871_pir__S24346 histone

H3.3-like protein - Arabidopsis thaliana

>gi_16324_emb_CAA42957_ (X60429) histone H3.3 like protein [Arabidopsis thaliana] >gi_404825_emb_CAA42958_ (X60429) histone H3.3 like protein [Arabidopsis thaliana] >gi_488563 (U09458) histone H3.2 [Medicago sativa] >gi_488567 (U09460) histone H3.2 [Medicago sativa] >gi_488569 (U09461) histone H3.2 [Medicago sativa] >gi_488575 (U09464) histone H3.2

[Medicago sativa] >gi_488577 (U09465) histone H3.2

[Medicago sativa] >gi_510911 emb_CAA56153 (X79714) histone H3 [Lolium temulentum] >gi_1435157 emb_CAA58445 (X83422)

histone H3 variant H3.3 [Lycopersicon esculentum]
>gi_2558944 (AF024716) histone 3 [Gossypium hirsutum]
>gi_3273350_dbj_BAA31218_ (AB015760) histone H3 [Nicotiana tabacum] >gi_3885890 (AF093633) histone H3 [Oryza sativa]
>gi_4038469_gb_AAC97380_ (AF109910) histone H3 [Porteresia coarctata] >gi_4490754_emb_CAB38916.1_ (AL035708) histone H3.3 [Arabidopsis thaliana] >gi_4490755_emb_CAB38917.1_

(AL035708) Histon H3 [Arabidopsis thaliana]

>gi_6006364_dbj_BAA84794.1_ (AP000559) EST D15300(C0425) corresponds to a region of the predicted gene.; Similar to

histone H3 (AB015760) [Oryza sativa]

Seq. No. 413843

Seq. ID uC-osflcyp142a02b1

Method BLASTX
NCBI GI g2995384
BLAST score 190
E value 6.0e-15
Match length 44
% identity 86

NCBI Description (AJ004810) cytochrome P450 monooxygenase [Zea mays]

Seq. No. 413844

Seq. ID uC-osflcyp142a04b1

Method BLASTN
NCBI GI g5410347
BLAST score 98
E value 1.0e-47

Match length 258 % identity 84 NCBI Description Sorghum bicolor BAC clone 110K5, partial sequence Seq. No. 413845 Seq. ID uC-osflcyp142a06b1 Method BLASTX NCBI GI g2435519 BLAST score 419 E value 4.0e-41 Match length 143 % identity 57 NCBI Description (AF024504) similar to mouse MEM3 (GB:U47024 and S. cerevisiae vacuolar sorting protein 35 (SW; P34110) [Arabidopsis thaliana] Seq. No. 413846 Seq. ID uC-osflcyp142a07b1 Method BLASTX NCBI GI g548603 BLAST score 353 E value 2.0e-33 Match length 110 % identity 67 NCBI Description PHOTOSYSTEM I REACTION CENTRE SUBUNIT II PRECURSOR (PHOTOSYSTEM I 20 KD SUBUNIT) (PSI-D) >gi_478404_pir__JQ2247 photosystem I chain D precursor barley >gi_167085 (M98254) PSI-D subunit [Hordeum vulgare] Seq. No. 413847 Seq. ID uC-osflcyp142a08b1 Method BLASTX NCBI GI g4678342 BLAST score 364 E value 1.0e-34 Match length 149 % identity 44 NCBI Description (AL049659) lipase-like protein [Arabidopsis thaliana] Seq. No. 413848 Seq. ID uC-osflcyp142a09b1 Method BLASTX NCBI GI g6014904 BLAST score 191 E value 2.0e-14 Match length 35 % identity 94

NCBI Description DAG PROTEIN, CHLOROPLAST PRECURSOR

>gi_1200205_emb_CAA65064_ (X95753) DAG [Antirrhinum majus]

Seq. No. 413849

Seq. ID uC-osflcyp142a10b1

Method BLASTX NCBI GI g2809245 BLAST score 141 E value 9.0e-09 Match length 43

```
% identity
NCBI Description (AC002560) F21B7.14 [Arabidopsis thaliana]
                  413850
Seq. No.
Seq. ID
                  uC-osflcyp142a12b1
                  BLASTX
Method
NCBI GI
                  g3915037
                  509
BLAST score
                  7.0e-52
E value
                  109
Match length
                  86
% identity
NCBI Description SUCROSE SYNTHASE 2 (SUCROSE-UDP GLUCOSYLTRANSFERASE 2)
                  >gi_2570067_emb_CAA04512_ (AJ001071) second sucrose
                  synthase [Pisum sativum]
                  413851
Seq. No.
Seq. ID
                  uC-osflcyp142b01b1
Method
                  BLASTX
NCBI GI
                  q4006978
BLAST score
                  152
                  9.0e-10
E value
Match length
                  83
% identity
                  40
NCBI Description (AJ131335) pollen allergen (group II) [Cynodon dactylon]
                  413852
Seq. No.
                  uC-osflcyp142b07b1
Seq. ID
Method
                  BLASTX
                  g121349
NCBI GI
BLAST score
                  732
E value
                  8.0e-78
                  137
Match length
                  100
% identity
NCBI Description GLUTAMINE SYNTHETASE SHOOT ISOZYME (GLUTAMATE--AMMONIA
                  LIGASE) (CLONE LAMBDA-GS28) >gi_20368_emb_CAA32461
                  (X14245) cytosolic glutamine synthetase (AA 1-356) [Oryza
                  sativa]
Seq. No.
                  413853
Seq. ID
                  uC-osflcyp142b08b1
Method
                  BLASTX
                  g3894176
NCBI GI
BLAST score
                  488
E value
                  2.0e-49
Match length
                  94
                  89
% identity
NCBI Description (AC005312) putative NAM (no apical meristem) protein
                  [Arabidopsis thaliana]
Seq. No.
                  413854
Seq. ID
                  uC-osflcyp142b10b1
Method
                  BLASTN
NCBI GI
                  g5777612
BLAST score
                  303
                  1.0e-170
E value
Match length
                  395
                  94
% identity
```

Method

NCBI Description Oryza sativa chromosome 4 BAC q3037-207F1 complete genome 413855 Seq. No. uC-osflcyp142b12b1 Seq. ID Method BLASTN q5091597 NCBI GI 164 BLAST score 4.0e-87 E value Match length 269 90 % identity NCBI Description Oryza sativa chromosome 1 BAC 10A19I, complete sequence 413856 Seq. No. uC-osflcyp142c05b1 Seq. ID BLASTX Method q3258575 NCBI GI BLAST score 337 2.0e-31 E value Match length 112 64 % identity NCBI Description (U89959) Hypothetical protein [Arabidopsis thaliana] 413857 Seq. No. uC-osflcyp142c06b1 Seq. ID BLASTX Method q3885492 NCBI GI 688 BLAST score 1.0e-72 E value Match length 153 % identity 82 NCBI Description (AF063865) tapetum specific protein [Zea mays] 413858 Seq. No. uC-osflcyp142c07b1 Seq. ID BLASTX Method g3914140 NCBI GI 359 BLAST score 4.0e-34 E value 111 Match length % identity 68 NCBI Description NONSPECIFIC LIPID-TRANSFER PROTEIN 5 PRECURSOR (LTP 5) >gi_3172343 (AF051369) lipid transfer protein [Oryza satīva] 413859 Seq. No. uC-osflcyp142c08b1 Seq. ID BLASTN Method g1208445 NCBI GI 35 BLAST score 5.0e-10 E value 59 Match length 90 % identity NCBI Description Rice (YK426) mRNA, complete cds 413860 Seq. No. uC-osflcyp142c12b1 Seq. ID BLASTX

NCBI GI g2370253 384 BLAST score 6.0e-37 E value 161 Match length 50 % identity (Y13273) putative protein kinase [Lycopersicon esculentum] NCBI Description >qi 5669642 qb AAD46406.1 AF096250 1 (AF096250) ethylene-responsive protein kinase TCTR1 [Lycopersicon esculentum] 413861 Seq. No. uC-osflcyp142d02b1 Seq. ID BLASTX Method g3377797 NCBI GI BLAST score 374 8.0e-36 E value 117 Match length % identity 64 (AF075597) Similar to 60S ribosome protein L19; coded for NCBI Description by A. thaliana cDNA T04719; coded for by A. thaliana cDNA H36046; coded for by A. thaliana cDNA T44067; coded for by A. thaliana cDNA T14056; coded for by A. thaliana cDNA R90691 [Ara 413862 Seq. No. uC-osflcyp142d09b1 Seq. ID BLASTN Method NCBI GI g4097337 139 BLAST score 3.0e-72E value 249 Match length 96 % identity NCBI Description Oryza sativa metallothionein-like protein mRNA, complete cds 413863 Seq. No. uC-osflcyp142e02b1 Seq. ID Method BLASTX

NCBI GI g283008 BLAST score 705 E value 1.0e-74 Match length 136 % identity 99

NCBI Description sucrose synthase (EC 2.4.1.13) - rice

>gi 20366 emb CAA46017 (X64770) sucrose synthase [Oryza

sativa]

Seq. No. 413864

Seq. ID uC-osflcyp142e04b1

Method BLASTN
NCBI GI g4097337
BLAST score 303
E value 1.0e-170
Match length 370
% identity 100

NCBI Description Oryza sativa metallothionein-like protein mRNA, complete

cds

```
413865
Seq. No.
                  uC-osflcyp142e06b1
Seq. ID
Method
                  BLASTX
                  g4415992
NCBI GI
                  725
BLAST score
                  2.0e-90
E value
                  168
Match length
                   97
% identity
                  (AF059288) beta-tubulin 2 [Eleusine indica]
NCBI Description
Seq. No.
                   413866
                   uC-osflcyp142e07b1
Seq. ID
                   BLASTX
Method
NCBI GI
                   g1706260
BLAST score
                   518
                   7.0e-74
E value
Match length
                   150
                   86
% identity
                  CYSTEINE PROTEINASE 1 PRECURSOR >gi_2118131_pir__S59597
NCBI Description
                   cysteine proteinase 1 precursor - maize
                   >gi_643597_dbj_BAA08244_ (D45402) cysteine proteinase [Zea
                   mays]
                   413867
Seq. No.
                   uC-osflcyp142e08b1
Seq. ID
                   BLASTX
Method
NCBI GI
                   g4982479
                   570
BLAST score
                   8.0e-59
E value
                   141
Match length
                   76
% identity
                  (AF069441) predicted protein of unknown function
NCBI Description
                   [Arabidopsis thaliana]
                   413868
Seq. No.
                   uC-osflcyp142e10b1
Seq. ID
Method
                   BLASTX
                   g3915102
NCBI GI
                   155
BLAST score
                   5.0e-10
E value
                   50
Match length
                   50
% identity
                  GAMMA-THIONIN HOMOLOG PPT PRECURSOR >gi 1076652_pir__S52634
NCBI Description
                   gamma-thionin - Petunia inflata >gi 499655 (L27173)
                   gamma-thionin homolog [Petunia inflata]
Seq. No.
                   413869
                   uC-osflcyp142e11b1
Seq. ID
                   BLASTX
Method
                   q1632768
NCBI GI
                   472
BLAST score
E value
                   2.0e-47
                   114
Match length
                   79
 % identity
```

NCBI Description (D84408) calcium dependent protein kinase [Zea mays]

```
413870
Seq. No.
                  uC-osflcyp142e12b1
Seq. ID
                  BLASTX
Method
                  g3550483
NCBI GI
BLAST score
                  296
                  1.0e-26
E value
Match length
                  67
% identity
                  42
                  (AJ224324) cp31BHv [Hordeum vulgare]
NCBI Description
                  413871
Seq. No.
Seq. ID
                  uC-osflcyp142f02b1
Method
                  BLASTX
                  q283008
NCBI GI
BLAST score
                  574
                  3.0e-59
E value
Match length
                  130
% identity
                  88
                  sucrose synthase (EC 2.4.1.13) - rice
NCBI Description
                  >qi 20366 emb CAA46017 (X64770) sucrose synthase [Oryza
                   sativa]
Seq. No.
                   413872
                  uC-osflcyp142f03b1
Seq. ID
                   BLASTX
Method
NCBI GI
                   g551288
BLAST score
                   694
                   2.0e-73
E value
Match length
                   141
                   93
% identity
                  (Z33611) phosphoglycerate mutase [Zea mays]
NCBI Description
                   413873
Seq. No.
                   uC-osflcyp142f04b1
Seq. ID
                   BLASTX
Method
                   g3522929
NCBI GI
                   823
BLAST score
                   2.0e-88
E value
                   158
Match length
                   98
% identity
                  (AC002535) putative dTDP-glucose 4-6-dehydratase
NCBI Description
                   [Arabidopsis thaliana] >gi_3738279 (AC005309) putative
                   dTDP-glucose 4-6-dehydratase [Arabidopsis thaliana]
                   413874
Seq. No.
                   uC-osflcyp142f05b1
Seq. ID
                   BLASTX
Method
                   g4510385
NCBI GI
                   640
BLAST score
                   6.0e-67
E value
                   181
Match length
                   69
% identity
                  (AC007017) unknown protein [Arabidopsis thaliana]
NCBI Description
                   413875
Seq. No.
                   uC-osflcyp142f09b1
Seq. ID
                   BLASTX
Method
```

q4510377 NCBI GI 443 BLAST score 7.0e-44E value 113 Match length 77 % identity (AC007017) putative RNA helicase A [Arabidopsis thaliana] NCBI Description 413876 Seq. No. uC-osflcyp142f11b1 Seq. ID BLASTX Method g5902359 NCBI GI 548 BLAST score 3.0e-56 E value Match length 168 64 % identity (AC009322) Heat-shock protein [Arabidopsis thaliana] NCBI Description 413877 Seq. No. uC-osflcyp142f12b1 Seq. ID BLASTX Method q2407281 NCBI GI 521 BLAST score 3.0e-53 E value 102 Match length 98 % identity (AF017363) ribulose 1,5-bisphosphate carboxylase small NCBI Description subunit [Oryza sativa] 413878 Seq. No. uC-osflcyp142g01b1 Seq. ID BLASTX Method g2498576 NCBI GI 481 BLAST score 2.0e-48E value 107 Match length 75 % identity MAJOR POLLEN ALLERGEN PHA A 1 PRECURSOR (PHA A I) NCBI Description >gi_1246116_bbs_174854 (S80654) major allergen Pha a 1 [Phalaris aquatica=canary grass, pollen, Peptide, 269 aa] [Phalaris aquatica] 413879 Seq. No. uC-osflcyp142g03b1 Seq. ID BLASTX Method q3025188 NCBI GI 210 BLAST score E value 8.0e-17 Match length 73

42 % identity

HYPOTHETICAL 11.9 KD PROTEIN SLR1846 NCBI Description

>gi 1652154 dbj BAA17078_ (D90903) hypothetical protein

[Synechocystis sp.]

413880 Seq. No.

uC-osflcyp142g04b1 Seq. ID

BLASTN Method NCBI GI g6041757 BLAST score 309 E value 1.0e-173 Match length 326 % identity 98

NCBI Description Genomic Sequence For Oryza sativa Clone 10P20, Lemont

Strain, Complete Sequence, complete sequence

Seq. No. 413881

Seq. ID uC-osflcyp142g05b1

Method BLASTX
NCBI GI g629858
BLAST score 637
E value 9.0e-67
Match length 129
% identity 93

NCBI Description protein kinase C inhibitor - maize

Seq. No. 413882

Seq. ID uC-osflcyp142g06b1

Method BLASTX
NCBI GI g3046731
BLAST score 299
E value 1.0e-56
Match length 132
% identity 84

NCBI Description (AJ005373) protein kinase [Craterostigma plantagineum]

Seq. No. 413883

Seq. ID uC-osflcyp142g07b1

Method BLASTX
NCBI GI g2618704
BLAST score 362
E value 2.0e-34
Match length 97
% identity 72

NCBI Description (AC002510) putative thioredoxin reductase [Arabidopsis

thaliana]

Seq. No. 413884

Seq. ID uC-osflcyp142g08b1

Method BLASTX
NCBI GI g1352461
BLAST score 528
E value 7.0e-54
Match length 121
% identity 81

NCBI Description IN2-2 PROTEIN

Seq. No. 413885

Seq. ID uC-osflcyp142g10b1

Method BLASTX
NCBI GI g2267006
BLAST score 605
E value 7.0e-63
Match length 151
% identity 81

NCBI Description (AF006825) endosperm lumenal binding protein [Oryza sativa]

NCBI GI

```
413886
Seq. No.
                  uC-osflcyp142g12b1
Seq. ID
                  BLASTX
Method
                  g1136120
NCBI GI
                  709
BLAST score
                  5.0e-75
E value
                  164
Match length
                  85
% identity
NCBI Description (X91806) alpha-tubulin [Oryza sativa]
                  413887
Seq. No.
                  uC-osflcyp142h03b1
Seq. ID
                  BLASTX
Method
                  g3080436
NCBI GI
                  249
BLAST score
                  2.0e-21
E value
                  92
Match length
                  58
% identity
NCBI Description (AL022605) putative protein [Arabidopsis thaliana]
                   413888
Seq. No.
                  uC-osflcyp142h05b1
Seq. ID
                  BLASTN
Method
                  q4097337
NCBI GI
                   276
BLAST score
                   1.0e-154
E value
Match length
                   353
                   100
% identity
NCBI Description Oryza sativa metallothionein-like protein mRNA, complete
                   413889
Seq. No.
                   uC-osflcyp142h08b1
Seq. ID
                   BLASTX
Method
                   g3063469
NCBI GI
                   255
BLAST score
E value
                   9.0e-22
                   152
Match length
                   42
% identity
NCBI Description (AC003981) F22013.31 [Arabidopsis thaliana]
                   413890
Seq. No.
                   uC-osflcyp142h09b1
Seq. ID
                   BLASTX
Method
                   g1353352
NCBI GI
                   253
BLAST score
E value
                   1.0e-21
                   82
Match length
                   61
% identity
NCBI Description (U31975) alanine aminotransferase [Chlamydomonas
                   reinhardtii]
                   413891
Seq. No.
                   uC-osflcyp142h10b1
Seq. ID
                   BLASTN
Method
```

53935

g1212993

Match length

% identity

271 97

```
BLAST score
                  53
                  8.0e-21
E value
                  113
Match length
% identity
                  87
                  H.vulgare mRNA for coproporphyrinogen oxidase
NCBI Description
Seq. No.
                  413892
                  uC-osflcyp142h11b1
Seq. ID
Method
                  BLASTX
                  g1917019
NCBI GI
                  580
BLAST score
                  5.0e-60
E value
                  135
Match length
                  84
% identity
                  (U92045) ribosomal protein S6 RPS6-1 [Zea mays]
NCBI Description
Seq. No.
                  413893
                  uC-osflcyp143a04b1
Seq. ID
Method
                  BLASTX
                  q585551
NCBI GI
BLAST score
                  416
                  9.0e-41
E value
Match length
                  76
% identity
                  100
                  NUCLEOSIDE DIPHOSPHATE KINASE I (NDK I) (NDP KINASE I)
NCBI Description
                  >gi_629798_pir__S43330 nucleoside-diphosphate kinase (EC
                   2.7.4.6) - rice >gi_303849_dbj_BAA03798_ (D16292)
                  nucleoside diphosphate kinase [Oryza sativa]
                   413894
Seq. No.
                  uC-osflcyp143a07b1
Seq. ID
                  BLASTX
Method
NCBI GI
                   g4567247
                   303
BLAST score
                   2.0e-27
E value
                   101
Match length
                   59
% identity
NCBI Description (AC007070) unknown protein [Arabidopsis thaliana]
                   413895
Seq. No.
                   uC-osflcyp143a10b1
Seq. ID
Method
                   BLASTX
                   q3738306
NCBI GI
BLAST score
                   432
                   1.0e-45
E value
                   153
Match length
                   60
% identity
NCBI Description (AC005309) unknown protein [Arabidopsis thaliana]
Seq. No.
                   413896
                   uC-osflcyp143a11b1
Seq. ID
                   BLASTN
Method
NCBI GI
                   q3618319
                   235
BLAST score
                   1.0e-129
E value
```

```
NCBI Description Oryza sativa mRNA for zinc finger protein, complete cds,
                  clone:S3574
                   413897
Seq. No.
                  uC-osflcyp143b02b1
Seq. ID
                  BLASTX
Method
                   g4585882
NCBI GI
                   644
BLAST score
                   1.0e-67
E value
                   135
Match length
                   83
% identity
                  (AC005850) PSI type III chlorophyll a/b-binding protein
NCBI Description
                   [Arabidopsis thaliana]
                   413898
Seq. No.
                   uC-osflcyp143b06b1
Seq. ID
                   BLASTX
Method
NCBI GI
                   g1053063
                   343
BLAST score
                   2.0e-32
E value
Match length
                   89
                   79
% identity
NCBI Description (U38464) small GTP-binding protein [Solanum lycopersicum]
                   413899
Seq. No.
                   uC-osflcyp143b07b1
Seq. ID
                   BLASTX
Method
NCBI GI
                   q3850063
BLAST score
                   242
                   3.0e-20
E value
                   160
Match length
                   34
% identity
NCBI Description (AJ223830) ARE1 [Rattus norvegicus]
                   413900
 Seq. No.
                   uC-osflcyp143b08b1
 Seq. ID
                   BLASTX
Method
                   g231587
 NCBI GI
                   416
 BLAST score
                   9.0e-41
 E value
                   140
 Match length
                    65
 % identity
                   ATP SYNTHASE BETA CHAIN, MITOCHONDRIAL PRECURSOR
 NCBI Description
                   >gi_283001_pir__S25304 H+-transporting ATP synthase (EC
                    3.6\overline{.}1.34) beta chain precursor, mitochondrial - rice
                   >gi_218147_dbj_BAA01372_ (D10491) mitochondrial F1-ATPase
                    [Oryza satīva]
                    413901
 Seq. No.
                    uC-osflcyp143b10b1
 Seq. ID
                    BLASTX
 Method
 NCBI GI
                    q4415912
                    189
 BLAST score
                    2.0e-14
 E value
                   110
 Match length
                    40
 % identity
 NCBI Description (AC006282) putative protease [Arabidopsis thaliana]
```

```
413902
Seq. No.
                  uC-osflcyp143b11b1
Seq. ID
                  BLASTX
Method
                  q4584539
NCBI GI
                  284
BLAST score
                  2.0e-25
E value
                  131
Match length
                  44
% identity
                  (AL049608) extensin-like protein [Arabidopsis thaliana]
NCBI Description
                  413903
Seq. No.
                  uC-osflcyp143b12b1
Seq. ID
                  BLASTX
Method
                  g3335374
NCBI GI
BLAST score
                  172
                   3.0e-12
E value
Match length
                   64
                   55
% identity
                  (AC003028) glutaredoxin-like protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   413904
                   uC-osflcyp143c02b1
Seq. ID
                   BLASTX
Method
                   g1653655
NCBI GI
                   330
BLAST score
                   1.0e-30
E value
Match length
                   159
% identity
                   41
                  (D90915) ATP-dependent Clp protease proteolytic subunit
NCBI Description
                   [Synechocystis sp.]
                   413905
Seq. No.
                   uC-osflcyp143c08b1
Seq. ID
                   BLASTX
Method
                   g4741931
NCBI GI
                   448
BLAST score
                   1.0e-44
E value
                   109
Match length
                   78
% identity
NCBI Description (AF130975) plasma membrane intrinsic protein [Zea mays]
                   413906
Seq. No.
                   uC-osflcyp143c09b1
Seq. ID
                   BLASTX
Method
                   g4006978
NCBI GI
                   188
BLAST score
                   6.0e-14
E value
                   87
Match length
                   43
% identity
NCBI Description (AJ131335) pollen allergen (group II) [Cynodon dactylon]
                   413907
Seq. No.
                   uC-osflcyp143d03b1
Seq. ID
                   BLASTX
Method
                   g538430
NCBI GI
```

338

BLAST score

8.0e-32 E value Match length 84 77 % identity (L36320) superoxide dismutase [Oryza sativa] NCBI Description 413908 Seq. No. uC-osflcyp143d04b1 Seq. ID Method BLASTX NCBI GI q3096949 BLAST score 587 E value 8.0e-61 Match length 152 69 % identity (Y16328) putative cyclic nucleotide-regulated ion channel NCBI Description [Arabidopsis thaliana] >gi_3894399 (AF067798) cyclic nucleotide-gated cation channel [Arabidopsis thaliana] 413909 Seq. No. Seq. ID uC-osflcyp143d05b1 Method BLASTX q4539417 NCBI GI 169 BLAST score E value 6.0e-12 Match length 42 % identity 69 NCBI Description (AL049171) putative protein [Arabidopsis thaliana] 413910 Seq. No. uC-osflcyp143d08b1 Seq. ID Method BLASTX NCBI GI g2500959 BLAST score 285 E value 2.0e-25 Match length 156 % identity 40 ALANYL-TRNA SYNTHETASE (ALANINE--TRNA LIGASE) (ALARS) NCBI Description >qi 1653611 dbj BAA18523 (D90915) alanyl-tRNA synthetase [Synechocystis sp.] 413911 Seq. No. Seq. ID uC-osflcyp143d09b1 Method BLASTX NCBI GI g21695 237 BLAST score 1.0e-19 E value Match length 76 % identity 61 NCBI Description (X66014) cathepsin B [Triticum aestivum] Seq. No. 413912 uC-osflcyp143d12b1 Seq. ID Method BLASTX g4204265 NCBI GI BLAST score 184

53939

7.0e-14

64 55

E value Match length

% identity

```
NCBI Description (AC005223) 45643 [Arabidopsis thaliana]
                  413913
Seq. No.
                  uC-osflcyp143e01b1
Seq. ID
                  BLASTX
Method
                  g2459429
NCBI GI
                  284
BLAST score
                  3.0e-25
E value
                  73
Match length
                  68
% identity
                  (AC002332) unknown protein [Arabidopsis thaliana]
NCBI Description
                  413914
Seq. No.
                  uC-osflcyp143e04b1
Seq. ID
                  BLASTX
Method
                  g4415996
NCBI GI
                  299
BLAST score
                   2.0e-27
E value
                   60
Match length
                   90
% identity
                  (AF059290) beta-tubulin 4 [Eleusine indica]
NCBI Description
                   413915
Seq. No.
                   uC-osflcyp143e07b1
Seq. ID
                   BLASTN
Method
                   g3885887
NCBI GI
                   216
BLAST score
                   1.0e-118
E value
                   272
Match length
                   95
% identity
NCBI Description Oryza sativa high mobility group protein (HMG) mRNA,
                   complete cds
                   413916
Seq. No.
                   uC-osflcyp143e08b1
Seq. ID
                   BLASTX
Method
                   q232031
NCBI GI
BLAST score
                   476
                   8.0e-48
E value
Match length
                   134
                   71
% identity
NCBI Description ELONGATION FACTOR 1-BETA' (EF-1-BETA')
                   >gi_322851_pir__S29224 translation elongation factor eEF-1
                   beta' chain - rice >gi_218161_dbj_BAA02253_ (D12821)
                   elongation factor 1 beta' [Oryza sativa]
                   413917
Seq. No.
Seq. ID
                   uC-osflcyp143e09b1
Method
                   BLASTX
                   g129231
NCBI GI
                   632
BLAST score
                   4.0e-66
E value
Match length
                   133
                   87
 % identity
                   ORYZAIN ALPHA CHAIN PRECURSOR >gi_67644 pir_KHRZOA oryzain
NCBI Description
                    (EC 3.4.22.-) alpha precursor - rice
                   >gi 218181_dbj_BAA14402_ (D90406) oryzain alpha precursor
```

```
413918
Seq. No.
                  uC-osflcyp143e11b1
Seq. ID
                  BLASTX
Method
                  g4417283
NCBI GI
BLAST score
                  364
                  1.0e-34
E value
                  153
Match length
                  44
% identity
                  (AC007019) putative cytochrome p450 [Arabidopsis thaliana]
NCBI Description
                  413919
Seq. No.
                  uC-osflcyp143e12b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3915008
                  310
BLAST score
                  2.0e-28
E value
Match length
                  61
                  100
% identity
                  SUPEROXIDE DISMUTASE [CU-ZN], CHLOROPLAST PRECURSOR
NCBI Description
                   >gi_1805502_dbj_BAA12745.1_ (D85239) superoxide dismutase
                  precusor [Oryza sativa]
                   413920
Seq. No.
                   uC-osflcyp143f01b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   q6018193
BLAST score
                   326
                   4.0e-30
E value
                   163
Match length
                   44
% identity
                  (AF114170) nucleotide-binding protein long form [Mus
NCBI Description
                   musculus]
                   413921
Seq. No.
                   uC-osflcyp143f03b1
Seq. ID
                   BLASTX
Method
                   g3386621
NCBI GI
                   503
BLAST score
                   6.0e-51
E value
                   158
Match length
                   63
% identity
NCBI Description (AC004665) unknown protein [Arabidopsis thaliana]
                   413922
Seq. No.
                   uC-osflcyp143f04b1
Seq. ID
                   BLASTX
Method
                   g3023713
NCBI GI
BLAST score
                   320
                   2.0e-29
E value
Match length
                   144
                   73
% identity
NCBI Description ENOLASE (2-PHOSPHOGLYCERATE DEHYDRATASE)
                   (2-PHOSPHO-D-GLYCERATE HYDRO-LYASE) (OSE1) >gi_780372
```

[Oryza sativa]

(U09450) enolase [Oryza sativa]

```
. 413923
Seq. No.
                  uC-osflcyp143f05b1
Seq. ID
Method
                  BLASTX
                  q4585884
NCBI GI
                  277
BLAST score
                  2.0e-24
E value
Match length
                  129
                  43
% identity
                  (AC005850) Hypothetical protein [Arabidopsis thaliana]
NCBI Description
                  413924
Seq. No.
                  uC-osflcyp143f06b1
Seq. ID
Method
                  BLASTX
                  g3043426
NCBI GI
BLAST score
                  394
E value
                  3.0e-38
                  117
Match length
% identity
                   63
                  (AJ005345) hypothetical protein [Cicer arietinum]
NCBI Description
                   413925
Seq. No.
                   uC-osflcyp143f07b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g404688
BLAST score
                  174
                   2.0e-12
E value
Match length
                   60
                   50
% identity
                  (L19074) cytochrome P450 [Catharanthus roseus]
NCBI Description
                   413926
Seq. No.
                   uC-osflcyp143f08b1
Seq. ID
                   BLASTX
Method
                   g2190547
NCBI GI
                   547
BLAST score
                   5.0e-56
E value
                   158
Match length
% identity
                   64
                   (AC001229) ESTs
NCBI Description
                   gb_T43256,gb_46316,gb_N64930,gb_AA395255,gb AA404382 come
                   from this gene. [Arabidopsis thaliana]
Seq. No.
                   413927
                   uC-osflcyp143f09b1
Seq. ID
Method
                   BLASTX
                   g1084457
NCBI GI
                   440
BLAST score
E value
                   2.0e-43
Match length
                   89
% identity
                   100
NCBI Description elongation factor 1-beta - Rice >gi_432368 dbj BAA04903_
                   (D23674) elongation factor 1 beta [Oryza sativa]
Seq. No.
                   413928
Seq. ID
                   uC-osflcyp143f10b1
                   BLASTX
Method
NCBI GI
                   g3184288
```

```
BLAST score
                  218
E value
                   2.0e-17
Match length
                  62
% identity
                   60
                 (AC004136) unknown protein [Arabidopsis thaliana]
NCBI Description
                  413929
Seq. No.
                  uC-osflcyp143f11b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1519251
BLAST score
                  798
                  2.0e-85
E value
                  171
Match length
% identity
NCBI Description (U65957) GF14-c protein [Oryza sativa]
                   413930
Seq. No.
                  uC-osflcyp143f12b1
Seq. ID
Method
                  BLASTX
NCBI GI
                   q5668644
                   394
BLAST score
                   4.0e-38
E value
Match length
                   92
                   78
% identity
NCBI Description (AL109619) putative protein [Arabidopsis thaliana]
Seq. No.
                   413931
                  uC-osflcyp143g02b1
Seq. ID
                  BLASTX
Method
NCBI GI
                   g3695403
BLAST score
                   496
E value
                   3.0e-50
Match length
                   135
                   70
% identity
NCBI Description
                   (AF096373) contains similarity to the pfkB family of
                   carbohydrate kinases (Pfam: PF00294, E=1.6e-75)
                   [Arabidopsis thaliana] >gi 4538955 emb CAB39779.1
                   (AL049488) fructokinase-like protein [Arabidopsis thaliana]
                   413932
Seq. No.
Seq. ID
                   uC-osflcyp143g10b1
Method
                   BLASTX
NCBI GI
                   g5733874
BLAST score
                   187
E value
                   5.0e-14
Match length
                   101
% identity
                   42
NCBI Description (AC007932) F11A17.8 [Arabidopsis thaliana]
                   413933
Seq. No.
Seq. ID
                   uC-osflcyp143g12b1
Method
                   BLASTX
NCBI GI
                   g3738230
                   175
BLAST score
                   2.0e-12
E value
Match length
                   88
```

45

% identity

```
(AB007790) DREB2A [Arabidopsis thaliana]
NCBI Description
                  >gi_4126706_dbj_BAA36705_ (AB016570) DREB2A [Arabidopsis
                  thaliana]
                  413934
Seq. No.
                  uC-osflcyp143h04b1
Seq. ID
                  BLASTX
Method
                  g2253411
NCBI GI
                  158
BLAST score
                  4.0e-14
E value
                  83
Match length
                  42
% identity
                  (AF007219) PP2A inhibitor [Tetraodon fluviatilis]
NCBI Description
                  413935
Seq. No.
                  uC-osflcyp143h05b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q5902445
                  168
BLAST score
                  6.0e-12
E value
                  75
Match length
                  49
% identity
                 (AB030283) GAG-POL precursor [Oryza sativa]
NCBI Description
                   413936
Seq. No.
                  uC-osflcyp143h06b1
Seq. ID
                  BLASTN
Method
                  g498737
NCBI GI
                  52
BLAST score
                   3.0e-20
E value
                  180
Match length
                   82
% identity
NCBI Description H.vulgare (pMaW21) pseudo mRNA for beta-ketoacyl-ACP
                   synthase (partial)
                   413937
Seq. No.
                   uC-osflcyp143h07b1
Seq. ID
Method
                   BLASTX
                   q1651828
NCBI GI
                   432
BLAST score
                   1.0e-42
E value
                   143
Match length
% identity
NCBI Description (D90900) dihydrolipoamide dehydrogenase [Synechocystis sp.]
                   413938
Seq. No.
                   uC-osflcyp143h09b1
Seq. ID
Method
                   BLASTX
                   q4097522
NCBI GI
BLAST score
                   392
                   6.0e-38
E value
Match length
                   117
% identity
                   60
                  (U63534) cinnamyl alcohol dehydrogenase [Fragaria x
NCBI Description
                   ananassa]
```

Seq. No.

Method

BLASTX

```
uC-osflcyp143h11b1
Seq. ID
                  BLASTN
Method
                  g3859567
NCBI GI
                  159
BLAST score
                  3.0e-84
E value
Match length
                  202
                  94
% identity
NCBI Description Oryza sativa clone FIL1 unknown mRNA
                  413940
Seq. No.
                  uC-osflcyp143h12b1
Seq. ID
Method
                  BLASTX
                  g4220511
NCBI GI
                  146
BLAST score
                  1.0e-09
E value
Match length
                  59
                  59
% identity
                  (AL035356) DNA polymerase III like protein [Arabidopsis
NCBI Description
                  thaliana]
                  413941
Seq. No.
                  uC-osflcyp144a01b1
Seq. ID
Method
                  BLASTX
                  g1825645
NCBI GI
                  307
BLAST score
                  5.0e-28
E value
                  72
Match length
% identity
                  76
                  (U88173) weak similarity to Arabidopsis thaliana
NCBI Description
                  ubiquitin-like protein 8 [Caenorhabditis elegans]
                   413942
Seq. No.
                  uC-osflcyp144a04b1
Seq. ID
                  BLASTN
Method
NCBI GI
                   q2780342
                   56
BLAST score
E value
                   9.0e-23
Match length
                   140
                   85
% identity
                  Oryza sativa gene for PBZ1, complete cds
NCBI Description
                   >gi_3251321_dbj_E12488_E12488 Nucleotide sequence of Oryza
                   sativa PBZ1 gene
                   413943
Seq. No.
                   uC-osflcyp144a05b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   q2407281
BLAST score
                   764
E value
                   1.0e-81
Match length
                   144
                   99
% identity
                   (AF017363) ribulose 1,5-bisphosphate carboxylase small
NCBI Description
                   subunit [Oryza sativa]
                   413944
Seq. No.
                   uC-osflcyp144a06b1
Seq. ID
```

```
g2660669
NCBI GI
BLAST score
                  263
                  7.0e-23
E value
Match length
                  105
                  54
% identity
                  (ACO02342) human Mi-2 autoantigen-like protein [Arabidopsis
NCBI Description
                  thaliana]
                  413945
Seq. No.
                  uC-osflcyp144a07b1
Seq. ID
                  BLASTX
Method
                  g1136120
NCBI GI
                  504
BLAST score
                  4.0e-51
E value
                  96
Match length
                  97
% identity
                  (X91806) alpha-tubulin [Oryza sativa]
NCBI Description
                  413946
Seq. No.
                  uC-osflcyp144a09b1
Seq. ID
                  BLASTX
Method
NCBI GI
                  g4586253
                  205
BLAST score
                   5.0e-16
E value
                  143
Match length
                   41
% identity
NCBI Description (AL049640) auxilin-like protein [Arabidopsis thaliana]
                   413947
Seq. No.
                   uC-osflcyp144a10b1
Seq. ID
                  BLASTN
Method
NCBI GI
                   g20276
BLAST score
                   273
E value
                   1.0e-152
                   379
Match length
                   94
% identity
NCBI Description O.sativa oryzacystatin-II gene
                   413948
Seq. No.
                   uC-osflcyp144b02b1
Seq. ID
                   BLASTX
Method
                   g3075488
NCBI GI
                   712
BLAST score
                   2.0e-75
E value
Match length
                   136
% identity
NCBI Description (AF058796) chlorophyll a/b-binding protein [Oryza sativa]
Seq. No.
                   413949
Seq. ID
                   uC-osflcyp144b03b1
Method
                   BLASTX
NCBI GI
                   q6063542
BLAST score
                   598
E value
                   1.0e-75
Match length
                   152
% identity
                   99
                  (AP000615) EST C74302(E30840) corresponds to a region of
NCBI Description
```

the predicted gene.; similar to glyceraldehyde-3-phosphate dehydrogenase. (M64118) [Oryza sativa]

413950 Seq. No. uC-osflcyp144b06b1 Seq. ID BLASTX Method g133867 NCBI GI 504 BLAST score 5.0e-51E value 120 Match length 80 % identity 40S RIBOSOMAL PROTEIN S11 >gi 82722_pir__S16577 ribosomal NCBI Description protein S11 - maize >gi_22470_emb_CAA39438_ (X55967) ribosomal protein S11 [Zea mays] Seq. No. 413951 uC-osflcyp144b09b1 Seq. ID Method BLASTX q3914431 NCBI GI 350 BLAST score 6.0e-33 E value 124 Match length % identity 61 PROTEASOME COMPONENT C8 (MACROPAIN SUBUNIT C8) NCBI Description (MULTICATALYTIC ENDOPEPTIDASE COMPLEX SUBUNIT C8) >gi_2285802_dbj_BAA21651_ (D78173) 26S proteasome alpha subunit [Spinacia oleracea] 413952 Seq. No. uC-osflcyp144b10b1 Seq. ID BLASTX Method g4588906 NCBI GI BLAST score 604 9.0e-63 E value 137 Match length 88 % identity NCBI Description (AF118149) ribosomal protein S7 [Secale cereale] 413953 Seq. No. uC-osflcyp144b11b1 Seq. ID Method BLASTX NCBI GI q5596468 531 BLAST score E value 4.0e-54174 Match length % identity NCBI Description (AL096882) putative protein [Arabidopsis thaliana] 413954 Seq. No. Seq. ID uC-osflcyp144b12b1 Method BLASTN q1215811 NCBI GI BLAST score 464 0.0e + 00E value

NCBI Description Rice mRNA for probenazole-inducible protein PBZ1, complete

464

100

Match length

% identity

NCBI GI

cds

```
413955
Seq. No.
                  uC-osflcyp144c04b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g551288
BLAST score
                  691
                  5.0e-73
E value
                  141
Match length
                  92
% identity
                  (Z33611) phosphoglycerate mutase [Zea mays]
NCBI Description
                  413956
Seq. No.
                  uC-osflcyp144c05b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1438883
                  291
BLAST score
                   3.0e-26
E value
Match length
                  103
                   54
% identity
                  (U43840) GmCK3p [Glycine max]
NCBI Description
                   413957
Seq. No.
                  uC-osflcyp144c08b1
Seq. ID
                  BLASTX
Method
NCBI GI
                  g5931765
BLAST score
                   231
                   5.0e-19
E value
                  83
Match length
                   53
% identity
NCBI Description (AJ244024) phragmoplastin [Nicotiana tabacum]
                   413958
Seq. No.
                   uC-osflcyp144c09b1
Seq. ID
Method
                  BLASTX
NCBI GI
                   g4539404
BLAST score
                   174
E value
                   2.0e-12
Match length
                   81
% identity
                   47
NCBI Description (AL049524) putative protein [Arabidopsis thaliana]
Seq. No.
                   413959
                   uC-osflcyp144c11b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g4567268
BLAST score
                   675
                   4.0e-71
E value
Match length
                   161
% identity
                   88
                  (AC006841) putative fructose biphosphate aldolase
NCBI Description
                   [Arabidopsis thaliana]
                   413960
Seq. No.
                   uC-osflcyp144d01b1
Seq. ID
                   BLASTX
Method
```

g5816996

```
198
BLAST score
                  2.0e-15
E value
                  43
Match length
                  91
% identity
                  (AL110123) ribosomal protein L32-like protein [Arabidopsis
NCBI Description
                  thaliana]
                  413961
Seq. No.
                  uC-osflcyp144d02b1
Seq. ID
                  BLASTN
Method
                  g20203
NCBI GI
BLAST score
                  71
                  7.0e-32
E value
                  95
Match length
                  94
% identity
NCBI Description Rice mRNA for fructose-diphosphate aldolase (EC 4.1.2.13)
Seq. No.
                  413962
                  uC-osflcyp144d03b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3776003
                  295
BLAST score
                  2.0e-26
E value
                  152
Match length
                  42
% identity
                  (AJ010465) RNA helicase [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  413963
                  uC-osflcyp144d04b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3242075
BLAST score
                   730
                  1.0e-77
E value
Match length
                  144
                   97
% identity
NCBI Description
                  (Z97059) S-adenosyl-L-homocysteine hydrolase [Arabidopsis
                  thaliana]
                   413964
Seq. No.
Seq. ID
                  uC-osflcyp144d06b1
Method
                  BLASTN
                   g3850817
NCBI GI
BLAST score
                   171
E value
                   4.0e-91
Match length
                   267
                   91
% identity
NCBI Description
                  Oryza sativa mRNA for U2 snRNP auxiliary factor, small
                   subunit 35a
Seq. No.
                   413965
                   uC-osflcyp144d07b1
Seq. ID
Method
                  BLASTX
NCBI GI
                   q5669640
BLAST score
                   689
E value
                   1.0e-72
Match length
                   156
% identity
                   88
```

```
(AF096249) ethylene-responsive small GTP-binding protein
NCBI Description
                  [Lycopersicon esculentum]
                  413966
Seq. No.
                  uC-osflcyp144d08b1
Seq. ID
                  BLASTX
Method
NCBI GI
                  g2624326
BLAST score
                  337
                  1.0e-31
E value
                  84
Match length
                  80
% identity
                 (AJ002893) OsGRP1 [Oryza sativa]
NCBI Description
                  413967
Seq. No.
                  uC-osflcyp144d09b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3435096
BLAST score
                  254
                  9.0e-22
E value
                  98
Match length
                  54
% identity
NCBI Description (AF033587) SRZ21 [Arabidopsis thaliana]
                  413968
Seq. No.
                  uC-osflcyp144d10b1
Seq. ID
                  BLASTX
Method
NCBI GI
                  g3980378
BLAST score
                  510
                  9.0e-52
E value
                  142
Match length
% identity
                  67
NCBI Description
                 (AC004561) putative RNA binding protein [Arabidopsis
                  thaliana]
                  413969
Seq. No.
                  uC-osflcyp144d11b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2582971
BLAST score
                  631
                  5.0e-66
E value
Match length
                  146
% identity
                  86
NCBI Description (D83711) TKRP125 [Nicotiana tabacum]
                  413970
Seq. No.
Seq. ID
                  uC-osflcyp144d12b1
Method
                  BLASTX
NCBI GI
                  q417154
BLAST score
                  470
E value
                  3.0e-47
Match length
                  96
% identity
                  95
NCBI Description HEAT SHOCK PROTEIN 82 >gi 100685 pir S25541 heat shock
                  protein 82 - rice (strain Taichung Native One)
                  >gi_20256_emb_CAA77978_ (Z11920) heat shock protein 82
```

(HSP82) [Oryza sativa]

Match length

% identity

50 98

413971 Seq. No. uC-osflcyp144e03b1 Seq. ID Method BLASTX NCBI GI g2493131 BLAST score 726 4.0e-77E value 161 Match length 91 % identity VACUOLAR ATP SYNTHASE SUBUNIT B ISOFORM 1 (V-ATPASE B NCBI Description SUBUNIT) >gi 167108 (L11862) vacuolar ATPase B subunit [Hordeum vulgare] 413972 Seq. No. uC-osflcyp144e04b1 Seq. ID BLASTX Method NCBI GI g113172 389 BLAST score 9.0e-38 E value 89 Match length 83 % identity ACYL CARRIER PROTEIN III PRECURSOR (ACP III) NCBI Description >gi_100561_pir__S17928 acyl carrier protein 3 - barley >gi 166971 (M58754) acyl carrier protein III [Hordeum vulgare] 413973 Seq. No. uC-osflcyp144e06b1 Seq. ID Method BLASTX g6056418 NCBI GI BLAST score 286 2.0e-25 E value Match length 139 40 % identity (AC009525) Similar to beta-glucosidases [Arabidopsis NCBI Description thaliana] Seq. No. 413974 uC-osflcyp144e08b1 Seq. ID Method BLASTX NCBI GI q3176690 582 BLAST score E value 2.0e-68 Match length 155 % identity (AC003671) Similar to ubiquitin ligase gb_D63905 from S. NCBI Description cerevisiae. EST gb_R65295 comes from this gene. [Arabidopsis thaliana] Seq. No. 413975 uC-osflcyp144e10b1 Seq. ID Method BLASTX NCBI GI q2497904 BLAST score 257 E value 4.0e-22

NCBI Description METALLOTHIONEIN-LIKE PROTEIN TYPE 2 >gi 1667588 (U77294)

metallothionein-like protein [Oryza sativa] >gi_2326785_emb_CAA69845_ (Y08529) metallothionein-like protein [Oryza sativa] >gi_4097338 (U57638) metallothionein-like protein [Oryza sativa] >gi_4105603 (AF048750) metallothionein [Oryza sativa]

Seq. No. 413976

Seq. ID uC-osflcyp144e12b1

Method BLASTX
NCBI GI g3023816
BLAST score 530
E value 6.0e-59
Match length 125
% identity 94

NCBI Description GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC

>gi 968996 (U31676) glyceraldehyde-3-phosphate

dehydrogenase [Oryza sativa]

Seq. No. 413977

Seq. ID uC-osflcyp144f02b1

Method BLASTX
NCBI GI g2493494
BLAST score 491
E value 1.0e-66
Match length 165
% identity 74

NCBI Description SERINE CARBOXYPEPTIDASE II-2 PRECURSOR (CP-MII.2)

>gi_619351_bbs_153537 CP-MII.2=serine carboxypeptidase
[Hordeum vulgare=barley, cv. Alexis, aleurone, Peptide, 436
aa] >gi_6102957_emb_CAB59202.1_ (X78878) serine carboxylase

II-2 [Hordeum vulgare]

Seq. No. 413978

Seq. ID uC-osflcyp144f03b1

Method BLASTX
NCBI GI g2293480
BLAST score 449
E value 1.0e-44
Match length 89
% identity 98

NCBI Description (AF011331) glycine-rich protein [Oryza sativa]

Seq. No. 413979

Seq. ID uC-osflcyp144f05b1

Method BLASTX
NCBI GI g4886271
BLAST score 529
E value 4.0e-54
Match length 123
% identity 80

NCBI Description (AL050300) putative protein [Arabidopsis thaliana]

Seq. No. 413980

Seq. ID uC-osflcyp144f06b1

Method BLASTX
NCBI GI g4680212
BLAST score 173

```
3.0e-12
E value
Match length
                  95
                  44
% identity
                  (AF114171) hypothetical protein [Sorghum bicolor]
NCBI Description
                  413981
Seq. No.
                  uC-osflcyp144f07b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g6015058
BLAST score
                  801
                  7.0e-86
E value
Match length
                  151
                  100
% identity
                  ELONGATION FACTOR 1-ALPHA (EF-1-ALPHA) >gi 2791834
NCBI Description
                   (AF041463) elongation factor 1-alpha [Manihot esculenta]
                  413982
Seq. No.
                  uC-osflcyp144f08b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2213629
BLAST score
                  384
                  5.0e-37
E value
                  102
Match length
                  70
% identity
                  (AC000103) F21J9.21 [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   413983
                  uC-osflcyp144f09b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4581108
BLAST score
                  280
                  1.0e-24
E value
                  165
Match length
                   38
% identity
                   (AC005825) putative chloroplast outer membrane protein
NCBI Description
                   86, also very similar to GTP-inding protein from pea
                   (GB:L36857) [Arabidopsis thaliana]
                   413984
Seq. No.
                  uC-osflcyp144f10b1
Seq. ID
Method
                  BLASTX
NCBI GI
                   g170354
BLAST score
                   571
E value
                   5.0e-59
Match length
                   118
% identity
                   21
NCBI Description (M74156) pentameric polyubiquitin [Nicotiana sylvestris]
Seq. No.
                   413985
Seq. ID
                   uC-osflcyp144f11b1
Method
                  BLASTX
NCBI GI
                   g1002800
BLAST score
                   174
E value
                   2.0e-15
Match length
                   52
% identity
NCBI Description (U33917) Cpm7 [Craterostigma plantagineum]
```

NCBI GI

```
413986
Seq. No.
                  uC-osflcyp144g01b1
Seq. ID
Method
                  BLASTX
                  q3885513
NCBI GI
                  205
BLAST score
                   3.0e-16
E value
                   49
Match length
                   67
% identity
NCBI Description
                  (AF084201) similar to chloroplast 50S ribosomal protein L31
                   [Medicago sativa]
Seq. No.
                   413987
                  uC-osflcyp144g02b1
Seq. ID
Method
                  BLASTX
                  q4104220
NCBI GI
                   204
BLAST score
                   4.0e-16
E value
                   91
Match length
                   55
% identity
NCBI Description
                  (AF033538) caffeic acid O-methyltransferase; LPOMT1 [Lolium
                  perenne]
                   413988
Seq. No.
                   uC-osflcyp144g03b1
Seq. ID
Method
                  BLASTX
NCBI GI
                   g537437
                   318
BLAST score
                   3.0e-29
E value
Match length
                   139
% identity
                   48
NCBI Description (U12637) cysteine proteinase [Hemerocallis hybrid cultivar]
                   413989
Seq. No.
Seq. ID
                   uC-osflcyp144g04b1
Method
                   BLASTX
NCBI GI
                   g4586058
BLAST score
                   207
E value
                   3.0e-16
                   91
Match length
% identity
                   46
NCBI Description (AC007020) unknown protein [Arabidopsis thaliana]
Seq. No.
                   413990
Seq. ID
                   uC-osflcyp144g07b1
Method
                   BLASTX
NCBI GI
                   g2293480
BLAST score
                   394
                   2.0e-38
E value
                   80
Match length
                   94
% identity
NCBI Description (AF011331) glycine-rich protein [Oryza sativa]
                   413991
Seq. No.
                   uC-osflcyp144g10b1
Seq. ID
Method
                   BLASTX
```

53954

g4056507

```
BLAST score
                  265
                   6.0e-23
E value
Match length
                  85
                   62
% identity
                   (AC005896) putative RNA binding protein [Arabidopsis
NCBI Description
                  thaliana]
                   413992
Seq. No.
Seq. ID
                  uC-osflcyp144g11b1
Method
                  BLASTX
NCBI GI
                  q3789952
                   796
BLAST score
                   3.0e-85
E value
                  157
Match length
                   97
% identity
                  (AF094775) chlorophyll a/b-binding protein presursor [Oryza
NCBI Description
                   sativa]
                   413993
Seq. No.
Seq. ID
                  uC-osflcyp144h02b1
Method
                  BLASTX
NCBI GI
                   g4220481
BLAST score
                   243
E value
                   1.0e-20
                   105
Match length
% identity
                   50
                  (AC006069) unknown protein [Arabidopsis thaliana]
NCBI Description
                   413994
Seq. No.
                   uC-osflcyp144h04b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   q4884932
BLAST score
                   360
                   3.0e - 34
E value
Match length
                   88
% identity
                   73
                   (AF141659) AtHVA22a [Arabidopsis thaliana]
NCBI Description
                   >qi 4884944 gb AAD31885.1 AF141977 1 (AF141977) AtHVA22a
                   [Arabidopsis thaliana]
                   413995
Seq. No.
                   uC-osflcyp144h08b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3868853
BLAST score
                   171
E value
                   1.0e-20
Match length
                   80
% identity
                   62
NCBI Description (AB013853) GPI-anchored protein [Vigna radiata]
                   413996
Seq. No.
Seq. ID
                   uC-osflcyp144h09b1
                   BLASTX
Method
NCBI GI
                   g2492519
BLAST score
                   526
                   7.0e-54
E value
                   108
Match length
```

Seq. No.

414002

```
94
% identity
                  26S PROTEASE REGULATORY SUBUNIT 7 (26S PROTEASOME SUBUNIT
NCBI Description
                  7) >gi 1395191_dbj_BAA13021_ (D86121) 26S proteasome ATPase
                  subunit [Spinacia oleracea]
                  413997
Seq. No.
                  uC-osflcyp144h12b1
Seq. ID
                  BLASTX
Method
                  g2244765
NCBI GI
                  160
BLAST score
                  1.0e-10
E value
                  66
Match length
                  48
% identity
                  (Z97335) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                  413998
Seq. No.
                  uC-osflcyp149a02a1
Seq. ID
Method
                  BLASTX
                  g829283
NCBI GI
                  268
BLAST score
                  1.0e-23
E value
Match length
                  53
                  98
% identity
                  (Z15018) heat shock protein hsp82 [Oryza sativa]
NCBI Description
                  413999
Seq. No.
                  uC-osflcyp149a10a1
Seq. ID
Method
                  BLASTN
                  g6006355
NCBI GI
                  114
BLAST score
                  1.0e-57
E value
                  122
Match length
                  98
% identity
NCBI Description Oryza sativa genomic DNA, chromosome 6, clone:P0493C11
                  414000
Seq. No.
                  uC-osflcyp149b07a1
Seq. ID
Method
                  BLASTN
NCBI GI
                  q5803242
BLAST score
                   35
E value
                   5.0e-10
                  43
Match length
                   95
% identity
NCBI Description Oryza sativa genomic DNA, chromosome 6, clone:P0535G04
                   414001
Seq. No.
                  uC-osflcyp149b08a1
Seq. ID
Method
                  BLASTX
NCBI GI
                   q733454
                   191
BLAST score
                   2.0e-14
E value
                   38
Match length
% identity
                   97
                  (U23188) chlorophyll a/b-binding apoprotein CP26 precursor
NCBI Description
                   [Zea mays]
```

```
uC-osflcyp149c02a1
Seq. ID
                  BLASTN
Method
                  q1304214
NCBI GI
                  44
BLAST score
                  3.0e-16
E value
                  64
Match length
                  92
% identity
                  Rice mRNA for precursor of 22 kDa protein of photosystem II
NCBI Description
                  (PSII-S), complete cds
                  414003
Seq. No.
                  uC-osflcyp149c08a1
Seq. ID
                  BLASTX
Method
                  g462195
NCBI GI
                  219
BLAST score
                  8.0e-18
E value
Match length
                  43
                  100
% identity
                  PROTEIN TRANSLATION FACTOR SUI1 HOMOLOG (GOS2 PROTEIN)
NCBI Description
                  >gi 100682 pir S21636 GOS2 protein - rice
                  >gi 20238 emb CAA36190 (X51910) GOS2 [Oryza sativa]
                  >gi_3789950 (AF094774) translation initiation factor [Oryza
                  satīva]
                  414004
Seq. No.
                  uC-osflcyp149c12a1
Seq. ID
                  BLASTN
Method
NCBI GI
                  g2570496
                  138
BLAST score
                  2.0e-71
E value
                  138
Match length
                  100
% identity
                  Oryza sativa H protein subunit of glycine decarboxylase
NCBI Description
                  mRNA, complete cds
                   414005
Seq. No.
                  uC-osflcyp149d01a1
Seq. ID
Method
                  BLASTN
                  g20365
NCBI GI
BLAST score
                   59
                   5.0e-25
E value
Match length
                  91
                   91
% identity
NCBI Description O.sativa RSs1 gene for sucrose synthase
                   414006
Seq. No.
                   uC-osflcyp149d02a1
Seq. ID
Method
                  BLASTX
NCBI GI
                   q4337196
                   163
BLAST score
                   4.0e-11
E value
Match length
                   55
% identity
                   56
                  (AC006403) putative serine/threonine receptor kinase
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                   414007
```

NCBI GI

```
uC-osflcyp149e04a1
Seq. ID
Method
                  BLASTN
                  q435648
NCBI GI
BLAST score
                  106
                  7.0e-53
E value
Match length
                  106
                  100
% identity
NCBI Description Rice mRNA for gamma-Tip, complete cds
                  414008
Seq. No.
                  uC-osflcyp149e10a1
Seq. ID
Method
                  BLASTN
NCBI GI
                  q4426561
                  93
BLAST score
E value
                  1.0e-44
Match length
                  186
                  96
% identity
NCBI Description Oryza sativa mRNA for chitinase IIb, complete cds
                  414009
Seq. No.
                  uC-osflcyp149f09a1
Seq. ID
                  BLASTN
Method
                  g2331130
NCBI GI
                  43
BLAST score
E value
                  2.0e-15
                  51
Match length
% identity
                  98
NCBI Description Oryza sativa glycine-rich protein (OSGRP1) mRNA, complete
Seq. No.
                  414010
                  uC-osflcyp149h03a1
Seq. ID
Method
                  BLASTN
NCBI GI
                  q436782
BLAST score
                  143
E value
                  2.0e-74
Match length
                  222
                  98
% identity
NCBI Description Rice mRNA for cyc07, complete cds
Seq. No.
                   414011
                  uC-osflcyp150h08a1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2118130
BLAST score
                  193
E value
                   1.0e-14
Match length
                  39
                   87
% identity
NCBI Description cysteine proteinase (EC 3.4.22.-), glucose
                   starvation-induced - maize (fragment)
                   >gi 559532_emb_CAA57675_ (X82185) cysteine proteinase [Zea
                  mays]
                   414012
Seq. No.
Seq. ID
                  uC-osflcyp151a03a1
Method
                  BLASTX
```

53958

g4582787

```
BLAST score
                  190
                  2.0e-14
E value
Match length
                  48
% identity
                  77
                  (AJ012281) adenosine kinase [Zea mays]
NCBI Description
Seq. No.
                  414013
Seq. ID
                  uC-osflcyp151a03b1
Method
                  BLASTX
NCBI GI
                  g4582787
BLAST score
                  654
                  1.0e-68
E value
Match length
                  130
% identity
                  95
                  (AJ012281) adenosine kinase [Zea mays]
NCBI Description
Seq. No.
                  414014
                  uC-osflcyp151a05b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4567286
BLAST score
                  503
                  7.0e-51
E value
                  133
Match length
% identity
                  70
NCBI Description
                  (AC006841) putative coatomer alpha subunit [Arabidopsis
                  thaliana]
                  414015
Seq. No.
                  uC-osflcyp151a10b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4679028
BLAST score
                  299
E value
                  5.0e-27
Match length
                  129
                  44
% identity
NCBI Description
                  (AF077207) HSPC021 [Homo sapiens]
                  >gi_5106781_gb_AAD39841.1_ (AF083243) HSPC025 [Homo
                  sapiens]
Seq. No.
                  414016
Seq. ID
                  uC-osflcyp151b01a1
Method
                  BLASTN
NCBI GI
                  g487321
BLAST score
                  85
E value
                  7.0e-40
Match length
                  125
% identity
                  94
NCBI Description Rice mRNA EN77, partial sequence
Seq. No.
                  414017
Seq. ID
                  uC-osflcyp151b01b1
Method
                  BLASTX
NCBI GI
                  q729842
BLAST score
                  447
E value
                  8.0e-45
Match length
                  100
% identity
                  87
```

E value

9.0e-69

```
CHLOROPLAST MEMBRANE-ASSOCIATED 30 KD PROTEIN PRECURSOR
NCBI Description
                   (M30) >gi_1076532_pir__S47966 probable lipid transfer protein M30 precursor - garden pea >gi_169107 (M73744) IM30
                   [Pisum sativum]
                   414018
Seq. No.
                   uC-osflcyp151b04b1
Seq. ID
                   BLASTX
Method
                   g1730512
NCBI GI
BLAST score
                   200
                   2.0e-26
E value
                   97
Match length
                   71
% identity
                   PHOSPHOGLYCERATE KINASE, CHLOROPLAST
NCBI Description
                   >gi_2129669_pir__S71368 phosphoglycerate kinase -
                   Arabidopsis thaliana (fragment) >gi_1022805_gb_AAB60303.1_
                   (U37701) phosphoglycerate kinase [Arabidopsis thaliana]
                   414019
Seq. No.
                   uC-osflcyp151b05b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g5923669
BLAST score
                   224
                   4.0e-18
E value
                   170
Match length
% identity
NCBI Description
                   (AC009326) hypothetical protein [Arabidopsis thaliana]
                   414020
Seq. No.
                   uC-osflcyp151b07a1
Seq. ID
Method
                   BLASTN
NCBI GI
                   g218209
BLAST score
                   117
E value
                   5.0e-59
                   213
Match length
% identity
                   Oryza sativa mRNA for the small subunit of
NCBI Description
                   ribulose-1,5-bisphosphate carboxylase, complete cds, clone
                   posss2106
                   414021
Seq. No.
Seq. ID
                   uC-osflcyp151b07b1
Method
                   BLASTX
NCBI GI
                   g2407281
                   647
BLAST score
                   7.0e-68
E value
Match length
                   121
% identity
                   (AF017363) ribulose 1,5-bisphosphate carboxylase small
NCBI Description
                   subunit [Oryza sativa]
Seq. No.
                    414022
Seq. ID
                   uC-osflcyp151b08b1
                   BLASTX
Method
NCBI GI
                   g3806016
BLAST score
                   653
```

```
158
Match length
                  82
% identity
                  (AF053104) peroxisomal targeting signal 1 receptor; PTS1
NCBI Description
                  receptor; Pex5p [Nicotiana tabacum]
                  414023
Seq. No.
                  uC-osflcyp151b10b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q401190
BLAST score
                  491
                  1.0e-49
E value
Match length
                  105
                  86
% identity
                  THAUMATIN-LIKE PROTEIN PRECURSOR >gi 100715 pir S25551
NCBI Description
                  thaumatin-like protein - rice >gi_20376_emb_CAA48278_
                  (X68197) thaumatin-like protein [Oryza sativa]
                  414024
Seq. No.
                  uC-osflcyp151b11b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g115525
                  469
BLAST score
                  5.0e-47
E value
Match length
                  128
                  71
% identity
NCBI Description CALMODULIN >gi_71685_pir__MCSP calmodulin - spinach
Seq. No.
                  414025
                  uC-osflcyp151b12b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4835759
BLAST score
                  564
E value
                  4.0e-58
Match length
                  153
% identity
                  17
NCBI Description (AC007202) T8K14.9 [Arabidopsis thaliana]
                  414026
Seq. No.
                  uC-osflcyp151c02b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1907270
BLAST score
                   529
E value
                   7.0e-54
Match length
                   147
                   73
% identity
                  (X96761) sulphate transporter protein [Sporobolus
NCBI Description
                   stapfianus]
Seq. No.
                   414027
Seq. ID
                   uC-osflcyp151c04a1
Method
                  BLASTX
NCBI GI
                   g1136122
BLAST score
                   209
E value
                   1.0e-16
Match length
                   47
                   79
% identity
```

NCBI Description (X91807) alfa-tubulin [Oryza sativa]

```
Seq. No.
                   414028
                   uC-osflcyp151c04b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g542179
BLAST score
                   776
                   6.0e-83
E value
                   151
Match length
                   99
% identity
                   alpha tubulin - maize >gi_629837_pir__S39998 tubulin alpha
NCBI Description
                   chain - maize (fragment) >gi_393401_emb_CAA52158_ (X73980)
                   alpha tubulin [Zea mays]
                   414029
Seq. No.
Seq. ID
                   uC-osflcyp151c06b1
Method
                   BLASTX
                   q2498586
NCBI GI
BLAST score
                   579
                   7.0e-60
E value
Match length
                   127
                   85
% identity
NCBI Description
                  MAJOR POLLEN ALLERGEN ORY S 1 PRECURSOR (ORY S I)
                   >gi_1173557 (U31771) Ory s 1 [Oryza sativa]
                   414030
Seq. No.
                   uC-osflcyp151c07b1
Seq. ID
                   BLASTX
Method
NCBI GI
                   g3935185
                   180
BLAST score
                   6.0e-13
E value
                   87
Match length
                   43
% identity
                  (AC004557) F17L21.28 [Arabidopsis thaliana]
NCBI Description
                   414031
Seq. No.
                   uC-osflcyp151c08b1
Seq. ID
Method
                   BLASTX
                   g4337175
NCBI GI
                   224
BLAST score
E value
                   3.0e-18
                   74
Match length
                   55
% identity
                   (AC006416) ESTs gb T20589, gb T04648, gb AA597906,
NCBI Description
                   gb_T04111, gb_R841\(\overline{8}\)0, gb_R654\(\overline{2}\)8, gb_T444\(\overline{3}\)9, gb_T76570,
                   gb_R90004, gb_T45020, gb_T42457, gb_T20921, gb_AA042762 and
                   gb AA720210 come from this gene. [Arabidopsis thaliana]
Seq. No.
                   414032
Seq. ID
                   uC-osflcyp151c10a1
Method
                   BLASTX
NCBI GI
                   q1351222
BLAST score
                   144
E value
                   4.0e-09
Match length
                   31
                   81
% identity
                   TRANSCRIPTION INITIATION FACTOR IIB (TFIIB) >gi 945087
NCBI Description
```

(U31097) transcription factor TFIIB [Glycine max]

Method

NCBI GI

BLASTX

g729668

414033 Seq. No. uC-osflcyp151c10b1 Seq. ID BLASTX Method NCBI GI g1351222 765 BLAST score 1.0e-81 E value 176 Match length 86 % identity TRANSCRIPTION INITIATION FACTOR IIB (TFIIB) >gi 945087 NCBI Description (U31097) transcription factor TFIIB [Glycine max] 414034 Seq. No. uC-osflcyp151c12a1 Seq. ID Method BLASTN NCBI GI g2613142 BLAST score 306 1.0e-172 E value 338 Match length 98 % identity NCBI Description Oryza sativa tubulin (RiP3) mRNA, complete cds 414035 Seq. No. uC-osflcyp151c12b1 Seq. ID ${\tt BLASTX}$ Method NCBI GI g1136120 BLAST score 687 2.0e-72 E value 130 Match length 98 % identity NCBI Description (X91806) alpha-tubulin [Oryza sativa] 414036 Seq. No. uC-osflcyp151d01a1 Seq. ID Method BLASTX NCBI GI q2129825 BLAST score 240 3.0e-20 E value 58 Match length 83 % identity NCBI Description dynamin-like protein phragmoplastin 12 - soybean >gi 1217994 (U25547) SDL [Glycine max] 414037 Seq. No. uC-osflcyp151d01b1 Seq. ID Method BLASTX NCBI GI q5931765 BLAST score 830 E value 3.0e-89 Match length 178 % identity NCBI Description (AJ244024) phragmoplastin [Nicotiana tabacum] 414038 Seq. No. Seq. ID uC-osflcyp151d04b1

```
BLAST score
                  232
                  4.0e-19
E value
Match length
                  66
                  62
% identity
                  HISTONE H1 >gi_2147479_pir__S65059 histone H1,
NCBI Description
                  drought-inducible - Lycopersicon pennellii >gi_436823
                   (U01890) Solanum pennellii histone H1 [Solanum pennellii]
                  414039
Seq. No.
                  uC-osflcyp151d05b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4996604
BLAST score
                  365
E value
                  1.0e-34
                  79
Match length
                  84
% identity
                  (AB022274) stromal ascorbate peroxidase [Nicotiana tabacum]
NCBI Description
                  414040
Seq. No.
                  uC-osflcyp151d07a1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g320569
                  168
BLAST score
                  8.0e-12
E value
Match length
                  73
                  48
% identity
NCBI Description
                 transposon TNT1 - Arabidopsis thaliana (fragment)
                   414041
Seq. No.
                  uC-osflcyp151d08a1
Seq. ID
Method
                  BLASTN
NCBI GI
                  q20262
BLAST score
                   65
                   3.0e-28
E value
                  89
Match length
% identity
                   94
NCBI Description O.sativa light-induced mRNA
Seq. No.
                   414042
Seq. ID
                  uC-osflcyp151d09b1
Method
                  BLASTX
NCBI GI
                  g6091733
BLAST score
                   219
E value
                   1.0e-17
Match length
                   65
                   62
% identity
NCBI Description
                  (AC010797) unknown protein [Arabidopsis thaliana]
Seq. No.
                   414043
Seq. ID
                  uC-osflcyp151d12b1
Method
                  BLASTX
NCBI GI
                  g5732069
BLAST score
                  228
E value
                   9.0e-19
Match length
                  100
                   48
% identity
                  (AF147263) contains similarity to Pfam family PF00036 - EF
NCBI Description
```

hand; score=11.7, E=0.66, N=1 [Arabidopsis thaliana] 414044 Seq. No. uC-osflcyp151e02b1 Seq. ID ${\tt BLASTX}$ Method NCBI GI g6094242 606 BLAST score 8.0e-79E value 171 Match length 78 % identity NCBI Description PUTATIVE SELENIUM-BINDING PROTEIN >gi 2244759 emb CAB10182.1 (Z97335) selenium-binding protein like [Arabidopsis thaliana] 414045 Seq. No. uC-osflcyp151e04b1 Seq. ID Method BLASTX NCBI GI q2494320 BLAST score 205 5.0e-16 E value 124 Match length 46 % identity EUKARYOTIC TRANSLATION INITIATION FACTOR 5 (EIF-5) NCBI Description >gi_1806575_emb_CAA67868_ (X99517) Eukaryotic initiation factor-5 [Zea mays] 414046 Seq. No. Seq. ID uC-osflcyp151e05a1 Method BLASTX NCBI GI g3023818 BLAST score 281 4.0e-25 E value 64 Match length 78 % identity GLUCOSE-6-PHOSPHATE 1-DEHYDROGENASE, CHOLOROPLAST ISOFORM NCBI Description PRECURSOR (G6PD) >gi_1197385_emb_CAA58775_ (X83923) glucose-6-phosphate dehydrogenase [Solanum tuberosum] 414047 Seq. No. uC-osflcyp151e05b1 Seq. ID Method BLASTX NCBI GI q5734502 315 BLAST score 7.0e-29 E value 66 Match length 91 % identity NCBI Description (AJ010712) glucose-6-phosphate 1-dehydrogenase [Solanum tuberosum]

Seq. No. 414048

Seq. ID uC-osflcyp151e08b1

Method BLASTX
NCBI GI g3337091
BLAST score 199
E value 3.0e-15
Match length 104
% identity 43

```
(AB016204) polygalacturonase inhibitor (PGIP) [Citrus
NCBI Description
                  unshiu]
                  414049
Seq. No.
                  uC-osflcyp151e09b1
Seq. ID
                  BLASTX
Method
                  g3386614
NCBI GI
                  452
BLAST score
                  6.0e-45
E value
                  139
Match length
                  41
% identity
                  (AC004665) putative transcription factor SF3 [Arabidopsis
NCBI Description
                  thaliana]
                  414050
Seq. No.
                  uC-osflcyp151e12a1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1236961
                  274
BLAST score
                   4.0e-24
E value
                  69
Match length
                   62
% identity
                  (U50201) prunasin hydrolase precursor [Prunus serotina]
NCBI Description
                   414051
Seq. No.
                  uC-osflcyp151e12b1
Seq. ID
                  BLASTX
Method
NCBI GI
                  g1311386
                   395
BLAST score
                  5.0e-38
E value
                  117
Match length
                   66
% identity
NCBI Description Cyanogenic Beta-Glucosidase Mol_id: 1; Molecule: Cyanogenic
                   Beta-Glucosidase; Chain: Null; Ec: 3.2.1.21
                   414052
Seq. No.
Seq. ID
                   uC-osflcyp151f02b1
Method
                   BLASTX
NCBI GI
                   a2286153
BLAST score
                   329
                   9.0e - 31
E value
Match length
                   82
% identity
                   77
NCBI Description (AF007581) cytoplasmic malate dehydrogenase [Zea mays]
                   414053
Seq. No.
Seq. ID
                   uC-osflcyp151f05b1
Method
                   BLASTX
NCBI GI
                   q4678323
BLAST score
                   235
E value
                   2.0e-19
Match length
                   122
% identity
NCBI Description (AL049658) putative protein [Arabidopsis thaliana]
Seq. No.
                   414054
Seq. ID
                   uC-osflcyp151f06b1
```

```
Method
                  BLASTX
                  g3426051
NCBI GI
BLAST score
                  284
                  3.0e-25
E value
Match length
                  82
                  72
% identity
                  (AC005168) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                  414055
Seq. No.
Seq. ID
                  uC-osflcyp151f09a1
                  BLASTX
Method
NCBI GI
                  g1707642
BLAST score
                  337
                  2.0e-31
E value
Match length
                  80
                  86
% identity
NCBI Description (Y07748) TMK [Oryza sativa]
Seq. No.
                  414056
                  uC-osflcyp151f09b1
Seq. ID
                  BLASTX
Method
NCBI GI
                  g1707642
BLAST score
                  916
                  3.0e-99
E value
Match length
                  179
                  99
% identity
NCBI Description (Y07748) TMK [Oryza sativa]
Seq. No.
                   414057
                  uC-osflcyp151f11b1
Seq. ID
Method
                  BLASTX
                  q1350548
NCBI GI
                  189
BLAST score
                  5.0e-14
E value
                  64
Match length
                  59
% identity
NCBI Description (L47609) heat shock-like protein [Picea glauca]
                   414058
Seq. No.
                  uC-osflcyp151f12a1
Seq. ID
                  BLASTX
Method
                  g444790
NCBI GI
BLAST score
                   212
                   7.0e-17
E value
                   59
Match length
                   75
% identity
NCBI Description nucleotide translocator [Arabidopsis thaliana]
                   414059
Seq. No.
                   uC-osflcyp151f12b1
Seq. ID
                   BLASTX
Method
NCBI GI
                   q485517
BLAST score
                   671
E value
                   1.0e-70
                   157
Match length
                   80
% identity
NCBI Description ADP, ATP carrier protein - rice
```

```
414060
Seq. No.
                  uC-osflcyp151g02b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3115237
BLAST score
                  716
                  8.0e-76
E value
Match length
                  161
                  84
% identity
                  (Y12957) ribulose-bisphosphate carboxylase large subunit
NCBI Description
                   [Lepironia articulata]
Seq. No.
                   414061
                  uC-osflcyp151g04b1
Seq. ID
Method
                  BLASTX
                  g2673912
NCBI GI
BLAST score
                  152
                   6.0e-10
E value
Match length
                   41
                   68
% identity
                  (AC002561) unknown protein [Arabidopsis thaliana]
NCBI Description
                   414062
Seq. No.
                  uC-osflcyp151g05b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g21699
                  299
BLAST score
                   6.0e-27
E value
                  100
Match length
% identity
                   60
NCBI Description (X66013) cathepsin B [Triticum aestivum]
                   414063
Seq. No.
                  uC-osflcyp151g07a1
Seq. ID
Method
                  BLASTX
NCBI GI
                   q2586082
BLAST score
                   174
E value
                   5.0e-13
Match length
                   48
% identity
NCBI Description (U72725) retrofit [Oryza longistaminata]
Seq. No.
                   414064
                   uC-osflcyp151g07b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2586082
BLAST score
                   263
E value
                   9.0e-23
                  126
Match length
% identity
NCBI Description (U72725) retrofit [Oryza longistaminata]
                   414065
Seq. No.
Seq. ID
                   uC-osflcyp151g08a1
Method
                   BLASTN
NCBI GI
                   g218178
                   37
BLAST score
```

NCBI GI

```
E value
                  2.0e-11
Match length
                  105
                  84
% identity
NCBI Description Oryza sativa OSA1 mRNA for H-ATPase, complete cds
                  414066
Seq. No.
                  uC-osflcyp151g08b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g218179
BLAST score
                  290
E value
                  6.0e-26
                  80
Match length
                  71
% identity
NCBI Description
                  (D10207) H-ATPase [Oryza sativa] >gi 444339 prf 1906387A H
                  ATPase [Oryza sativa]
Seq. No.
                  414067
                  uC-osflcyp151g09b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q5882722
BLAST score
                  630
                  9.0e-66
E value
Match length
                  170
% identity
                  65
NCBI Description
                  (AC008263) Contains similarity to gb Z95637
                  acyl-CoA:1-acylglycerol-3-phosphate acyltransferase from
                  Brassica napus. [Arabidopsis thaliana]
                  414068
Seq. No.
                  uC-osflcyp151g12b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3122858
BLAST score
                  722
                  1.0e-76
E value
Match length
                  166
                  83
% identity
NCBI Description
                  D-3-PHOSPHOGLYCERATE DEHYDROGENASE PRECURSOR (PGDH)
                  >gi_2189964_dbj_BAA20405_ (AB003280) Phosphoglycerate
                  dehydrogenase [Arabidopsis thaliana]
                  >gi_2804258_dbj_BAA24440_ (AB010407) phosphoglycerate
                  dehydrogenase [Arabidopsis thaliana]
Seq. No.
                  414069
Seq. ID
                  uC-osflcyp151h01b1
Method
                  BLASTX
NCBI GI
                  g4105721
BLAST score
                  447
E value
                  2.0e-44
Match length
                  138
% identity
NCBI Description
                  (AF050129) cell wall invertase Incwl; beta-fructosidase
                  [Zea mays]
                  414070
Seq. No.
Seq. ID
                  uC-osflcyp151h02b1
Method
                  BLASTX
```

q1255852

Seq. No.

Seq. ID

414075

uC-osflcyp151h10b1

```
BLAST score
                   166
E value
                   2.0e-11
                   97
Match length
                   37
% identity
NCBI Description
                  (U53339) simmilar to enoyl-CoA hydratases [Caenorhabditis
                  elegans]
                   414071
Seq. No.
                  uC-osflcyp151h04b1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g6016845
BLAST score
                  187
E value
                  1.0e-100
Match length
                  408
                   96
% identity
NCBI Description Oryza sativa genomic DNA, chromosome 1, clone:P0711E10
Seq. No.
                  414072
Seq. ID
                  uC-osflcyp151h06b1
Method
                  BLASTX
NCBI GI
                  g4314378
BLAST score
                  221
                  9.0e-18
E value
                  86
Match length
                  51
% identity
NCBI Description
                  (AC006232) putative lipase [Arabidopsis thaliana]
                  >gi 5306262 gb AAD41994.1 AC006233 5 (AC006233) putative
                  lipase [Arabidopsis thaliana]
                  414073
Seq. No.
                  uC-osflcyp151h08a1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2583133
BLAST score
                  177
E value
                  8.0e-13
Match length
                  41
% identity
                  83
NCBI Description (AC002387) unknown protein [Arabidopsis thaliana]
Seq. No.
                  414074
Seq. ID
                  uC-osflcyp151h10a1
Method
                  BLASTX
NCBI GI
                  g1362086
BLAST score
                  166
                  2.0e-11
E value
Match length
                  37
% identity
                  92
                  5\hbox{-methyltet} rahydropteroyltriglutamate--homocysteine
NCBI Description
                  S-methyltransferase (EC 2.1.1.14) - Madagascar periwinkle
                  >gi_2129919_pir__$65957
                  5-methyltetrahydropteroyltriglutamate--homocysteine
                  S-methyltransferase (EC 2.1.1.14) - Madagascar periwinkle
                  >gi_886471_emb_CAA58474_ (X83499) methionine synthase
                   [Catharanthus roseus]
```

BLASTX Method NCBI GI g1814403 714 BLAST score 1.0e-75 E value Match length 151 88 % identity (U84889) methionine synthase [Mesembryanthemum NCBI Description crystallinum] 414076 Seq. No. uC-osflcyp152a03b1 Seq. ID Method BLASTX g1762945 NCBI GI 412 BLAST score E value 3.0e-40 Match length 148 52 % identity (U66269) ORF; able to induce HR-like lesions [Nicotiana NCBI Description tabacum] 414077 Seq. No. uC-osflcyp152a05a1 Seq. ID Method BLASTX NCBI GI g3850821 356 BLAST score 1.0e-33 E value 94 Match length % identity 68 (Y18350) U2 snRNP auxiliary factor, large subunit NCBI Description [Nicotiana plumbaginifolia] 414078 Seq. No. uC-osflcyp152a06a1 Seq. ID BLASTX Method g283012 NCBI GI 299 BLAST score E value 4.0e-27 Match length 98 64 % identity ribulose-bisphosphate carboxylase (EC 4.1.1.39) large chain NCBI Description - rice chloroplast >gi_11955_emb_CAA28475_ (X04789) ribulose-1,5-bisphosphate carboxylase (AA 1 - 477) [Oryza sativa] 414079 Seq. No. uC-osflcyp152a08b1 Seq. ID Method BLASTX NCBI GI g4522004 BLAST score 436 5.0e-43E value Match length 165 % identity 56 NCBI Description (AC007069) putative histidine kinase, sensory transduction [Arabidopsis thaliana]

53971

414080

uC-osflcyp152a09a1

Seq. No. Seq. ID

```
Method
                  BLASTX
                  g1762945
NCBI GI
                  204
BLAST score
                  6.0e-16
E value
Match length
                  74
                  53
% identity
                  (U66269) ORF; able to induce HR-like lesions [Nicotiana
NCBI Description
                  tabacum]
                  414081
Seq. No.
                  uC-osflcyp152a09b1
Seq. ID
Method
                  BLASTX
                  g2984709
NCBI GI
BLAST score
                  464
                  3.0e-46
E value
Match length
                  88
                  99
% identity
                  (AF053468) DnaJ-related protein ZMDJ1 [Zea mays]
NCBI Description
                  414082
Seq. No.
                  uC-osflcyp152a11b1
Seq. ID
                  BLASTX
Method
NCBI GI
                  g132005
                  739
BLAST score
                  2.0e-78
E value
                  164
Match length
                  87
% identity
                  RIBULOSE BISPHOSPHATE CARBOXYLASE LARGE CHAIN PRECURSOR
NCBI Description
                   (RUBISCO LARGE SUBUNIT) >gi_68145_pir__RKRZL
                  ribulose-bisphosphate carboxylase (EC 4.1.1.39) large chain
                  precursor - rice chloroplast >gi_11992_emb_CAA34004_
                   (X15901) rbcL; RuBisCO large subunit [Oryza sativa]
                  >gi_344017_dbj_BAA00147_ (D00207) ribulose 1,5-bisphosphate
                   carboxylase large subunit [Oryza sativa]
                  >gi_226613_prf__1603356AK ribulose bisphosphate carboxylase
                   oxygenase L [Oryza sativa]
Seq. No.
                   414083
                   uC-osflcyp152b01b1
Seq. ID
                  BLASTX
Method
                  g2462760
NCBI GI
BLAST score
                   161
E value
                   9.0e-11
                   87
Match length
                   38
% identity
NCBI Description (AC002292) Hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   414084
Seq. ID
                   uC-osflcyp152b03b1
Method
                   BLASTX
NCBI GI
                   q3021270
BLAST score
                   174
E value
                   3.0e-12
Match length
                   110
                   38
% identity
NCBI Description
                   (AL022347) serine/threonine kinase-like protein
```

[Arabidopsis thaliana]

NCBI Description

414085 Seq. No. uC-osflcyp152b04a1 Seq. ID Method BLASTN q2331130 NCBI GI 205 BLAST score E value 1.0e-111 Match length 205 100 % identity Oryza sativa glycine-rich protein (OSGRP1) mRNA, complete NCBI Description 414086 Seq. No. Seq. ID uC-osflcyp152b04b1 Method BLASTX NCBI GI q4467157 BLAST score 323 E value 9.0e-30 Match length 134 51 % identity NCBI Description (AL035540) disease resistance response like protein [Arabidopsis thaliana] 414087 Seq. No. Seq. ID uC-osflcyp152b05a1 Method BLASTN NCBI GI g2773153 BLAST score 336 0.0e + 00E value Match length 360 99 % identity NCBI Description Oryza sativa abscisic acid- and stress-inducible protein (Asr1) mRNA, complete cds 414088 Seq. No. Seq. ID uC-osflcyp152b08b1 Method BLASTX NCBI GI q6094303 BLAST score 576 E value 2.0e-59 Match length 161 % identity 65 SELENOCYSTEINE METHYLTRANSFERASE (SECYS-METHYLTRANSFERASE) NCBI Description (SECYS-MT) >gi_4006848_emb_CAA10368_ (AJ131433) selenocysteine methyltransferase [Astragalus bisulcatus] Seq. No. 414089 Seq. ID uC-osflcyp152b10b1 Method BLASTX NCBI GI g2773154 BLAST score 309 E value 3.0e-28Match length 138 % identity 46

[Oryza sativa]

(AF039573) abscisic acid- and stress-inducible protein

Seq. ID

```
414090
Seq. No.
Seq. ID
                  uC-osflcyp152b12b1
Method
                  BLASTX
NCBI GI
                  q3201615
BLAST score
                   332
                  8.0e-31
E value
Match length
                  82
                   70
% identity
NCBI Description
                  (AC004669) unknown protein [Arabidopsis thaliana]
                   414091
Seq. No.
                  uC-osflcyp152c01a1
Seq. ID
Method
                  BLASTN
NCBI GI
                  q455499
BLAST score
                  46
E value
                  1.0e-16
Match length
                  58
                  95
% identity
NCBI Description Rice mRNA for ubiquitin-conjugating enzyme, partial
                  sequence
Seq. No.
                  414092
                  uC-osflcyp152c03b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4539383
BLAST score
                  155
E value
                  4.0e-10
                  83
Match length
                  39
% identity
NCBI Description
                  (AL035526) putative protein (fragment) [Arabidopsis
                  thaliana]
Seq. No.
                  414093
Seq. ID
                  uC-osflcyp152c05a1
Method
                  BLASTX
NCBI GI
                  g3128228
BLAST score
                  291
E value
                  4.0e-26
Match length
                  65
% identity
                  83
NCBI Description
                  (AC004077) putative ribosomal protein L18A [Arabidopsis
                  thaliana] >gi_3337376 (AC004481) putative ribosomal protein
                  L18A [Arabidopsis thaliana]
Seq. No.
                  414094
Seq. ID
                  uC-osflcyp152c05b1
Method
                  BLASTX
NCBI GI
                  g2501555
BLAST score
                  335
E value
                  4.0e-31
Match length
                  110
% identity
                  63
NCBI Description
                  POSSIBLE APOSPORY-ASSOCIATED PROTEIN C >gi 549984 (U13148)
                  possible apospory-associated protein [Pennisetum ciliare]
Seq. No.
                  414095
```

uC-osflcyp152c06a1

Method

BLASTX

```
Method
                  BLASTX
NCBI GI
                  g5917747
BLAST score
                  168
                  1.0e-11
E value
                  48
Match length
                  77
% identity
NCBI Description
                  (AF181492) elongation factor-1 alpha 3 [Lilium longiflorum]
Seq. No.
                  414096
                  uC-osflcyp152c06b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2979544
BLAST score
                  229
E value
                  1.0e-18
                  99
Match length
% identity
                  46
NCBI Description
                  (AC003680) putative cytochrome P-450 [Arabidopsis thaliana]
Seq. No.
                  414097
                  uC-osflcyp152c07a1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1203832
BLAST score
                  548
E value
                  2.0e-56
Match length
                  131
                  80
% identity
NCBI Description
                  (U46003) beta-D-glucan exohydrolase, isoenzyme ExoII
                   [Hordeum vulgare] >gi 1588407 prf 2208395A beta-D-glucan
                  exohydrolase [Hordeum vulgare]
                  414098
Seq. No.
                  uC-osflcyp152c07b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g131772
BLAST score
                  566
                  3.0e-58
E value
                  141
Match length
% identity
                  83
NCBI Description
                  40S RIBOSOMAL PROTEIN S14 (CLONE MCH1)
                  >gi 82723_pir A30097 ribosomal protein S14 (clone MCH1) -
                  maize
                  414099
Seq. No.
                  uC-osflcyp152c10b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3128228
BLAST score
                  768
E value
                  6.0e-82
Match length
                  161
                  89
% identity
NCBI Description
                  (AC004077) putative ribosomal protein L18A [Arabidopsis
                  thaliana] >gi_3337376 (AC004481) putative ribosomal protein
                  L18A [Arabidopsis thaliana]
                  414100
Seq. No.
                  uC-osflcyp152c11b1
Seq. ID
```

NCBI GI g2662343 839 BLAST score 3.0e-90 E value 168 Match length 96 % identity (D63581) EF-1 alpha [Oryza sativa] NCBI Description Seq. No. 414101 uC-osflcyp152c12a1 Seq. ID BLASTN Method NCBI GI g5734616 260 BLAST score 1.0e-144 E value 393 Match length 91 % identity NCBI Description Oryza sativa genomic DNA, chromosome 6, clone:P0538C01 Seq. No. 414102 uC-osflcyp152c12b1 Seq. ID Method BLASTX g2293480 NCBI GI BLAST score 281 3.0e-25 E value 65 Match length 86 % identity (AF011331) glycine-rich protein [Oryza sativa] NCBI Description

Seq. No. 414103

uC-osflcyp152d01b1 Seq. ID

Method BLASTN NCBI GI q3859567 BLAST score 320 E value 1.0e-180 Match length 446

97 % identity

NCBI Description Oryza sativa clone FIL1 unknown mRNA

Seq. No. 414104

uC-osflcyp152d02a1 Seq. ID

Method BLASTX NCBI GI q131283 BLAST score 285 2.0e-25 E value Match length 80 72 % identity

PHOTOSYSTEM II 44 KD REACTION CENTER PROTEIN (P6 PROTEIN) NCBI Description

(CP43) >gi_72710_pir__F2RZ44 photosystem II chlorophyll

a-binding protein psbC - rice chloroplast

>gi_11965_emb_CAA34014_ (X15901) PSII 43kDa protein [Oryza

sativa]

414105 Seq. No.

Seq. ID uC-osflcyp152d02b1

Method BLASTX NCBI GI g3461848 BLAST score 793 E value 7.0e-85

183 Match length 87 % identity (AC005315) putative ATPase [Arabidopsis thaliana] NCBI Description 414106 Seq. No. uC-osflcyp152d03a1 Seq. ID Method BLASTN NCBI GI g11957 36 BLAST score 5.0e-11 E value 76 Match length % identity 87 Rice complete chloroplast genome NCBI Description Seq. No. 414107 uC-osflcyp152d03b1 Seq. ID Method BLASTX NCBI GI q2104681 BLAST score 205 7.0e-16 E value 63 Match length 68 % identity (X97907) transcription factor [Vicia faba] NCBI Description 414108 Seq. No. uC-osflcyp152d04b1 Seq. ID Method BLASTX NCBI GI g1752734 BLAST score 658 5.0e-69 E value 170 Match length 69 % identity (D78510) beta-glucan-elicitor receptor [Glycine max] NCBI Description 414109 Seq. No. uC-osflcyp152d06b1 Seq. ID Method BLASTX NCBI GI g5081779 BLAST score 717 E value 6.0e-76182 Match length 76 % identity (AF150630) cellulose synthase [Gossypium hirsutum] NCBI Description 414110 Seq. No. uC-osflcyp152d07b1 Seq. ID Method BLASTX NCBI GI g131283 BLAST score 596 E value 6.0e-62 137 Match length % identity 83 NCBI Description PHOTOSYSTEM II 44 KD REACTION CENTER PROTEIN (P6 PROTEIN) (CP43) >gi_72710_pir__F2RZ44 photosystem II chlorophyll a-binding \overline{p} rotein $ps\overline{bC}$ - rice chloroplast >gi 11965 emb CAA34014 (X15901) PSII 43kDa protein [Oryza satīva]

Method

BLASTX

414111 Seq. No. uC-osflcyp152d08a1 Seq. ID Method BLASTN g11957 NCBI GI 269 BLAST score E value 1.0e-150 334 Match length 94 % identity Rice complete chloroplast genome NCBI Description Seq. No. 414112 uC-osflcyp152d08b1 Seg. ID Method BLASTX g1354849 NCBI GI BLAST score 398 2.0e-38 E value Match length 158 49 % identity (U57350) epoxide hydrolase [Nicotiana tabacum] NCBI Description Seq. No. 414113 Seq. ID uC-osflcyp152d09b1 Method BLASTX NCBI GI g1203832 BLAST score 707 8.0e-75 E value Match length 163 % identity 83 (U46003) beta-D-glucan exohydrolase, isoenzyme ExoII NCBI Description [Hordeum vulgare] >gi_1588407_prf__2208395A beta-D-glucan exohydrolase [Hordeum vulgare] 414114 Seq. No. uC-osflcyp152d10a1 Seq. ID BLASTX Method NCBI GI g1752734 BLAST score 180 4.0e-13 E value 42 Match length 79 % identity (D78510) beta-glucan-elicitor receptor [Glycine max] NCBI Description 414115 Seq. No. uC-osflcyp152d10b1 Seq. ID BLASTX Method NCBI GI g2262117 BLAST score 291 E value 6.0e-26 Match length 180 % identity 42 (AC002343) auxin inducible protein isolog [Arabidopsis NCBI Description thaliana] 414116 Seq. No. uC-osflcyp152d11b1 Seq. ID

E value

2.0e-47

```
NCBI GI
                  g1703129
                  940
BLAST score
                  1.0e-102
E value
                  186
Match length
                  96
% identity
                  ACTIN 11 >gi_2129522_pir__S68109 actin 11 - Arabidopsis
NCBI Description
                  thaliana >gi_1002533 (U27981) actin-11 [Arabidopsis
                  thaliana]
                  414117
Seq. No.
                  uC-osflcyp152d12a1
Seq. ID
Method
                  BLASTX
                  g5081779
NCBI GI
BLAST score
                  249
                  2.0e-21
E value
Match length
                  54
                  85
% identity
                  (AF150630) cellulose synthase [Gossypium hirsutum]
NCBI Description
                  414118
Seq. No.
                  uC-osflcyp152d12b1
Seq. ID
Method
                  BLASTX
                  g4204232
NCBI GI
                  657
BLAST score
                  6.0e-69
E value
Match length
                  165
                  79
% identity
NCBI Description
                  (AF035378) MADS-box protein 1 [Lolium temulentum]
                  414119
Seq. No.
                  uC-osflcyp152e01a1
Seq. ID
                  BLASTN
Method
                  g2570508
NCBI GI
                  54
BLAST score
                  2.0e-21
E value
                  74
Match length
% identity
                  93
NCBI Description Oryza sativa transmembrane protein mRNA, complete cds
                   414120
Seq. No.
                  uC-osflcyp152e01b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3763916
BLAST score
                   562
E value
                   9.0e-58
                  159
Match length
% identity
                   69
NCBI Description
                  (AC004450) unknown protein [Arabidopsis thaliana]
                  >gi 4531439 gb AAD22124.1 AC006224 6 (AC006224) unknown
                  protein [Arabidopsis thaliana]
                   414121
Seq. No.
Seq. ID
                  uC-osflcyp152e02b1
Method
                  BLASTX
NCBI GI
                   g6056425
BLAST score
                   419
```

```
Match length
                  139
% identity
                  74
NCBI Description
                  (AC009525) Putative ribosomal protein L19 [Arabidopsis
                  thaliana]
                  414122
Seq. No.
Seq. ID
                  uC-osflcyp152e04b1
Method
                  BLASTX
NCBI GI
                  q3928543
BLAST score
                  160
                  1.0e-10
E value
Match length
                  145
% identity
                  30
                  (AB016819) UDP-glucose glucosyltransferase [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  414123
                  uC-osflcyp152e07a1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2696804
BLAST score
                  300
                  3.0e-27
E value
Match length
                  57
% identity
                  96
NCBI Description (AB009665) water channel protein [Oryza sativa]
Seq. No.
                  414124
Seq. ID
                  uC-osflcyp152e07b1
Method
                  BLASTX
NCBI GI
                  q2894534
BLAST score
                  809
E value
                  1.0e-86
Match length
                  171
% identity
                  92
NCBI Description (AJ224327) aquaporin [Oryza sativa]
Seq. No.
                  414125
                  uC-osflcyp152e08b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4262232
BLAST score
                  231
                  3.0e-19
E value
Match length
                  91
                  52
% identity
NCBI Description
                  (AC006200) putative ribosomal protein L7 [Arabidopsis
                  thaliana]
Seq. No.
                  414126
Seq. ID
                  uC-osflcyp152e09b1
Method
                  BLASTX
NCBI GI
                  g3859568
                  795
BLAST score
                  5.0e-85
E value
Match length
                  148
                  100
% identity
```

NCBI Description (AF098752) unknown [Oryza sativa]

```
Seq. No.
                  414127
Seq. ID
                  uC-osflcyp152e10a1
Method
                  BLASTX
NCBI GI
                  g2244906
BLAST score
                  167
                  1.0e-11
E value
                  96
Match length
% identity
                  42
                  (Z97339) indole-3-acetate beta-glucosyltransferase like
NCBI Description
                  protein [Arabidopsis thaliana]
                  414128
Seq. No.
Seq. ID
                  uC-osflcyp152e10b1
                  BLASTX
Method
                  q5733877
NCBI GI
BLAST score
                  414
E value
                  2.0e-40
                  142
Match length
% identity
                  58
NCBI Description (AC007932) F11A17.13 [Arabidopsis thaliana]
                  414129
Seq. No.
                  uC-osflcyp152f01b1
Seq. ID
Method
                  BLASTX
                  q2289010
NCBI GI
                  220
BLAST score
                  1.0e-17
E value
                  45
Match length
                  84
% identity
NCBI Description
                  (AC002335) FKBP type peptidyl-prolyl cis-trans isomerase
                  isolog [Arabidopsis thaliana]
Seq. No.
                   414130
Seq. ID
                   uC-osflcyp152f02a1
Method
                  BLASTN
NCBI GI
                   g1261857
BLAST score
                   286
                   1.0e-160
E value
Match length
                   361
% identity
                   95
NCBI Description Rice CatA gene for catalase, complete cds
                   414131
Seq. No.
                   uC-osflcyp152f02b1
Seq. ID
Method
                  BLASTX
NCBI GI
                   g2130069
                   863
BLAST score
                   5.0e-93
E value
Match length
                   181
% identity
                   88
                  catalase (EC 1.11.1.6) catA - rice
NCBI Description
                   >gi 1261858 dbj BAA06232 (D29966) catalase [Oryza sativa]
                   414132
Seq. No.
                  uC-osflcyp152f03b1
Seq. ID
Method
                   BLASTX
                   g2827666
NCBI GI
```

```
BLAST score
                  361
E value
                  3.0e - 34
Match length
                  81
% identity
                  79
NCBI Description
                  (AL021637) hypothetical protein [Arabidopsis thaliana]
                  414133
Seq. No.
Seq. ID
                  uC-osflcyp152f04b1
Method
                  BLASTX
                  g1084455
NCBI GI
BLAST score
                  774
                  1.0e-82
E value
Match length
                  159
                  92
% identity
                  peptidylprolyl isomerase (EC 5.2.1.8) Cyp2 - rice
NCBI Description
                  >gi 600767 (L29469) cyclophilin 2 [Oryza sativa]
Seq. No.
                  414134
Seq. ID
                  uC-osflcyp152f06a1
Method
                  BLASTN
NCBI GI
                  g21796
                  48
BLAST score
                  6.0e-18
E value
Match length
                  80
                  90
% identity
NCBI Description Wheat histone H3 gene
                  414135
Seq. No.
Seq. ID
                  uC-osflcyp152f08a1
Method
                  BLASTN
NCBI GI
                  q2331130
BLAST score
                  205
E value
                  1.0e-111
Match length
                  274
% identity
                  97
NCBI Description Oryza sativa glycine-rich protein (OSGRP1) mRNA, complete
Seq. No.
                  414136
                  uC-osflcyp152f08b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2293480
BLAST score
                  449
E value
                  9.0e-45
                  89
Match length
                  98
% identity
                 (AF011331) glycine-rich protein [Oryza sativa]
NCBI Description
Seq. No.
                  414137
                  uC-osflcyp152f09a1
Seq. ID
Method
                  BLASTX
                  g4006872
NCBI GI
BLAST score
                  196
                  4.0e-15
E value
                  58
Match length
                   67
% identity
                  (Z99707) methionyl aminopeptidase-like protein [Arabidopsis
NCBI Description
```

thaliana]

414138 Seq. No. uC-osflcyp152f09b1 Seq. ID Method BLASTX NCBI GI q4006872 BLAST score 328 E value 3.0e-32 110 Match length 66 % identity (Z99707) methionyl aminopeptidase-like protein [Arabidopsis NCBI Description thaliana] Seq. No. 414139 Seq. ID uC-osflcyp152f10a1 Method BLASTN NCBI GI q600766 70 BLAST score E value 4.0e-31 Match length 194 % identity NCBI Description Oryza sativa cyclophilin 2 (Cyp2) gene, complete cds 414140 Seq. No. Seq. ID uC-osflcyp152f10b1 Method BLASTX q551288 NCBI GI 809 BLAST score E value 1.0e-86 Match length 176 % identity 86 (Z33611) phosphoglycerate mutase [Zea mays] NCBI Description Seq. No. 414141 Seq. ID uC-osflcyp152f11b1 Method BLASTX NCBI GI g122085 BLAST score 546 E value 7.0e-56 Match length 127 % identity 87 NCBI Description HISTONE H3 >gi 81641 pir S06250 histone H3 - Arabidopsis thaliana >gi_82482_pir__S04099 histone H3 (variant H3R-21) - rice >gi_1362194_pir__S57626 histone H3 - maize >gi 20251 emb CAA31969 (X13678) histone H3 (AA 1-136) [Oryza sativa] >gi 20253 emb CAA31970 (X13680) histone H3 (AA 1-136) [Oryza sativa] >gi_168493 (M36658) histone H3 (H3C3) [Zea mays] >gi_168495 (M13378) histone H3 [Zea mays] >gi_168497 (M13379) histone H3 [Zea mays] >gi_168506 (M35388) histone H3 [Zea mays] >gi_169655 (M77493) histone H3 [Petroselinum crispum] >gi 169657 (M77494) histone H3 [Petroselinum crispum] >gi_169659 (M77495) histone H3 [Petroselinum crispum] >gi_387565 (M17130) histone H3 [Arabidopsis thaliana] >gi_387567 (M17131) histone H3 [Arabidopsis thaliana] >gi_886738_emb_CAA59111_ (X84377)

histone 3 [Zea mays] >gi_1040764 (M35 $\overline{3}$ 87) histone H3 [Arabidopsis thaliana] >gi_1314779 (U54827) histone H3

Histone H3 [Asparagus officinalis] >gi 1667592 (U77296) histone 3 [Oryza sativa] >gi_3249101 (AC003114) Match to histone H3 gene gb M17131 and gb M35387 from A. thaliana. ESTs gb H76511 gb $\overline{H}76255$, gb $AA7\overline{1}2452$, gb N65260 and gb T42306 come from this gene. [Arabidopsis thaliana] >gi 5295939 dbj BAA81840.1 (AB026295) ESTs $C74\overline{0}53 (E302\overline{7}4)$, $\overline{D}15300 (C042\overline{5})$, AU030134 (E50667) correspond to a region of the predicted gene.; Similar to Asparagus officinalis mRNA for Histone H3.(X82414) [Oryza sativa] >gi 5295940 dbj BAA81841.1 (AB026295) ESTs C74053(E30274), D15300(C0425), AU030134(E50667) correspond to a region of the predicted gene.; Similar to Asparagus officinalis mRNA for Histone H3.(X82414) [Oryza sativa] >gi 225459 prf 1303352A histone H3 [Helicoverpa zea] >gi 225839 prf__1314298B histone H3 [Arabidopsis thaliana]

Seq. No. 414142

Seq. ID uC-osflcyp152g01b1

Method BLASTX
NCBI GI g2653879
BLAST score 162
E value 7.0e-11
Match length 75
% identity 48

NCBI Description (AF026389) adenyl cyclase [Nicotiana tabacum]

Seq. No. 414143

Seq. ID uC-osflcyp152g02b1

Method BLASTX
NCBI GI g2499819
BLAST score 734
E value 5.0e-78
Match length 142
% identity 98

NCBI Description ASPARTIC PROTEINASE ORYZASIN 1 PRECURSOR

>gi_2130068_pir__S66516 aspartic proteinase 1 precursor rice >gi_1030715_dbj_BAA06876_ (D32165) aspartic protease
[Oryza sativa] >gi_1711289_dbj_BAA06875_ (D32144) aspartic
protease [Oryza sativa]

Seq. No. 414144

Seq. ID uC-osflcyp152g04b1

Method BLASTX
NCBI GI g4455210
BLAST score 531
E value 4.0e-54
Match length 178
% identity 58

NCBI Description (AL035440) putative aspartate-tRNA ligase [Arabidopsis

thaliana]

Seq. No. 414145

Seq. ID uC-osflcyp152g05b1

Method BLASTN NCBI GI g6002775 BLAST score 523 E value 0.0e+00 Match length 545 % identity 99

NCBI Description Oryza sativa hypothetical protein, fertilin alpha subunit,

membrane protein homolog, and Myb-related protein genes,

complete cds; and unknown gene

Seq. No. 414146

Seq. ID uC-osflcyp152g06b1

Method BLASTX
NCBI GI 9480618
BLAST score 182
E value 3.0e-13
Match length 156
% identity 37

NCBI Description ATAF1 protein - Arabidopsis thaliana (fragment)

>gi 1345506 emb CAA52771 (X74755) ATAF1 [Arabidopsis

thaliana]

Seq. No. 414147

Seq. ID uC-osflcyp152g07a1

Method BLASTN
NCBI GI g4105602
BLAST score 327
E value 0.0e+00
Match length 343
% identity 99

NCBI Description Oryza sativa metallothionein (MTe) gene, complete cds

Seq. No. 414148

Seq. ID uC-osflcyp152g07b1

Method BLASTN
NCBI GI 94097337
BLAST score 264
E value 1.0e-146
Match length 341
% identity 99

NCBI Description Oryza sativa metallothionein-like protein mRNA, complete

cds

Seq. No. 414149

Seq. ID uC-osflcyp152g08a1

Method BLASTN
NCBI GI g2331130
BLAST score 205
E value 1.0e-111
Match length 205
% identity 100

NCBI Description Oryza sativa glycine-rich protein (OSGRP1) mRNA, complete

cds

Seq. No. 414150

Seq. ID uC-osflcyp152g08b1

Method BLASTX
NCBI GI g2293480
BLAST score 449
E value 1.0e-44

BLAST score

E value

634

8.0e-68

Match length 89 % identity (AF011331) glycine-rich protein [Oryza sativa] NCBI Description 414151 Seq. No. Seq. ID uC-osflcyp152g09b1 Method BLASTX NCBI GI a4115916 155 BLAST score 3.0e-10 E value 50 Match length % identity 54 NCBI Description (AF118222) F3H7.9 gene product [Arabidopsis thaliana] >gi 4539441 emb CAB40029.1_ (AL049523) putative protein [Arabidopsis thaliana] Seq. No. 414152 uC-osflcyp152g11b1 Seq. ID Method BLASTN q2773153 NCBI GI BLAST score 493 0.0e + 00E value 493 Match length % identity 100 Oryza sativa abscisic acid- and stress-inducible protein NCBI Description (Asr1) mRNA, complete cds 414153 Seq. No. Seq. ID uC-osflcyp152h02b1 Method BLASTX NCBI GI q2570511 BLAST score 596 E value 1.0e-62 Match length 157 ♂ identity 78 (AF022738) chlorophyll a-b binding protein [Oryza sativa] NCBI Description Seq. No. 414154 Seq. ID uC-osflcyp152h03b1 Method BLASTX NCBI GI g5354158 BLAST score 390 1.0e-37 E value Match length 109 % identity 63 (AF149841) digalactosyldiacylglycerol synthase [Arabidopsis NCBI Description thaliana] >gi_5354160_gb_AAD42379.1_AF149842_1 (AF149842) digalactosyldiacylglycerol synthase [Arabidopsis thaliana] >gi_6041825_gb_AAF02140.1_AC009918_12 (AC009918) digalactosyldiacylglycerol synthase [Arabidopsis thaliana] Seq. No. 414155 uC-osflcyp152h04b1 Seq. ID Method BLASTX q4158221 NCBI GI

```
Match length
                   137
% identity
                   89
                  (Y18624) reversibly glycosylated polypeptide [Oryza sativa]
NCBI Description
                   414156
Seq. No.
                   uC-osflcyp152h05b1
Seq. ID
                   BLASTX
Method
NCBI GI
                   q2662343
BLAST score
                   886
                   9.0e-96
E value
                   172
Match length
                   100
% identity
NCBI Description (D63581) EF-1 alpha [Oryza sativa]
                   414157
Seq. No.
                   uC-osflcyp152h06b1
Seq. ID
Method
                   BLASTN
                   q3135542
NCBI GI
BLAST score
                   82
                   1.0e-38
E value
                   117
Match length
                   94
% identity
NCBI Description Oryza sativa aquaporin (PIP2a) mRNA, complete cds
                   414158
Seq. No.
Seq. ID
                   uC-osflcyp152h07a1
                   BLASTX
Method
                   q1477428
NCBI GI
BLAST score
                   271
E value
                   1.0e-23
Match length
                   60
                   88
% identity
NCBI Description (X99623) alpha-tubulin 1 [Hordeum vulgare]
Seq. No.
                   414159
                   uC-osflcyp152h07b1
Seq. ID
                   BLASTX
Method
NCBI GI
                   g135399
BLAST score
                   802
E value
                   6.0e-86
Match length
                   175
% identity
                   87
                   TUBULIN ALPHA-1 CHAIN >gi_100716_pir__S20758 tubulin
NCBI Description
                   alpha-1 chain - rice >gi_Z0379_emb_CAA77988_ (Z11931) alpha
                   1 tubulin [Oryza sativa] \rightarrow gi_1\overline{13}61\overline{2}4_emb_CA\overline{A}62918_ (X91808)
                   alfa-tubulin [Oryza sativa]
                   414160
Seq. No.
                   uC-osflcyp152h09b1
Seq. ID
Method
                   BLASTX
                   g1617197
NCBI GI
                   304
BLAST score
                   2.0e-27
E value
Match length
                   76
                   76
% identity
NCBI Description (Z72488) CP12 [Nicotiana tabacum]
```

```
414161
Seq. No.
Seq. ID
                  uC-osflcyp152h10a1
                  BLASTX
Method
NCBI GI
                  q2662343
BLAST score
                  593
                  2.0e-61
E value
Match length
                  116
                  97
% identity
NCBI Description (D63581) EF-1 alpha [Oryza sativa]
                  414162
Seq. No.
                  uC-osflcyp152h10b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q283008
                  880
BLAST score
                  5.0e-95
E value
                  179
Match length
                  94
% identity
NCBI Description
                  sucrose synthase (EC 2.4.1.13) - rice
                  >gi 20366 emb CAA46017_ (X64770) sucrose synthase [Oryza
                  sativa]
                  414163
Seq. No.
Seq. ID
                  uC-osflcyp152h11b1
Method
                  BLASTX
                  g4467159
NCBI GI
                  274
BLAST score
                  5.0e-24
E value
Match length
                  87
% identity
                  56
NCBI Description (AL035540) hypothetical protein [Arabidopsis thaliana]
                   414164
Seq. No.
Seq. ID
                  uC-osflcyp152h12a1
Method
                  BLASTX
NCBI GI
                  g3135543
BLAST score
                  553
                  7.0e-57
E value
Match length
                  106
% identity
                  99
NCBI Description (AF062393) aquaporin [Oryza sativa]
                   414165
Seq. No.
                  uC-osflcyp153a02a1
Seq. ID
Method
                  BLASTX
                  g4490292
NCBI GI
                   237
BLAST score
                   9.0e-20
E value
                  67
Match length
% identity
                   63
NCBI Description (AL035678) putative protein [Arabidopsis thaliana]
                   414166
Seq. No.
                  uC-osflcyp153a02b1
Seq. ID
Method
                  BLASTX
NCBI GI
                   q559713
                   562
BLAST score
```

```
E value
                  8.0e-58
Match length
                  158
% identity
                  67
                  (D38552) The half39 protein is related to cyclophilin.
NCBI Description
                  [Homo sapiens]
                  414167
Seq. No.
Seq. ID
                  uC-osflcyp153a04a1
Method
                  BLASTX
                  q6063549
NCBI GI
                  396
BLAST score
E value
                  1.0e-38
                  83
Match length
                  87
% identity
                  (AP000615) EST AU070346(S12172) corresponds to a region of
NCBI Description
                  the predicted gene.; similar to AMP-binding protein.
                  (X94625) [Oryza sativa]
                  414168
Seq. No.
Seq. ID
                  uC-osflcyp153a04b1
                  BLASTX
Method
                  g6063549
NCBI GI
                  484
BLAST score
                  9.0e-49
E value
                  133
Match length
                  77
% identity
                  (AP000615) EST AU070346(S12172) corresponds to a region of
NCBI Description
                  the predicted gene.; similar to AMP-binding protein.
                  (X94625) [Oryza sativa]
Seq. No.
                  414169
Seq. ID
                  uC-osflcyp153a05b1
Method
                  BLASTX
NCBI GI
                  q2293480
BLAST score
                  449
E value
                  1.0e-44
                  89
Match length
% identity
                  (AF011331) glycine-rich protein [Oryza sativa]
NCBI Description
                  414170
Seq. No.
Seq. ID
                  uC-osflcyp153a07a1
                  BLASTX
Method
NCBI GI
                  q122089
BLAST score
                  154
E value
                  3.0e-10
Match length
                  34
                  88
% identity
                  HISTONE H3, EMBRYONIC >gi 10258 emb CAA27582 (X03952)
NCBI Description
                  histone H3 (aa 1-136) [Strongylocentrotus purpuratus]
Seq. No.
                  414171
Seq. ID
                  uC-osflcyp153a07b1
Method
                  BLASTX
NCBI GI
                  q3169061
BLAST score
                  182
                  1.0e-13
E value
```

```
91
Match length
                  45
% identity
                  (AL023704) putative cyclophilin-related peptidyl prolyl
NCBI Description
                  cis-trans isomerase [Schizosaccharomyces pombe]
Seq. No.
                  414172
                  uC-osflcyp153a08b1
Seq. ID
                  BLASTX
Method
                  q2583108
NCBI GI
                  147
BLAST score
                  4.0e-09
E value
                  147
Match length
                  29
% identity
                  (AC002387) putative surface protein [Arabidopsis thaliana]
NCBI Description
                  414173
Seq. No.
Seq. ID
                  uC-osflcyp153a10b1
Method
                  BLASTX
NCBI GI
                  q3096949
BLAST score
                  526
                  1.0e-53
E value
                  139
Match length
                  71
% identity
                  (Y16328) putative cyclic nucleotide-regulated ion channel
NCBI Description
                  [Arabidopsis thaliana] >gi 3894399 (AF067798) cyclic
                  nucleotide-gated cation channel [Arabidopsis thaliana]
                  414174
Seq. No.
Seq. ID
                  uC-osflcyp153a11a1
Method
                  BLASTN
                  q1261857
NCBI GI
                  341
BLAST score
                  0.0e + 00
E value
                  376
Match length
% identity
                  98
NCBI Description Rice CatA gene for catalase, complete cds
Seq. No.
                  414175
Seq. ID
                  uC-osflcyp153a11b1
Method
                  BLASTX
NCBI GI
                  g2130069
BLAST score
                  706
E value
                  1.0e-74
Match length
                  139
% identity
                  95
                  catalase (EC 1.11.1.6) catA - rice
NCBI Description
                  >gi 1261858 dbj BAA06232 (D29966) catalase [Oryza sativa]
                  414176
Seq. No.
Seq. ID
                  uC-osflcyp153a12a1
Method
                  BLASTX
                  g1170937
NCBI GI
BLAST score
                  298
                  4.0e-27
E value
Match length
                  66
                  88
% identity
                  S-ADENOSYLMETHIONINE SYNTHETASE 1 (METHIONINE
NCBI Description
```

ADENOSYLTRANSFERASE 1) (ADOMET SYNTHETASE 1) >gi 450549 emb CAA81481 (Z26867) S-adenosyl methionine synthetase [Oryza sativa] Seq. No. 414177 uC-osflcyp153a12b1 Seq. ID BLASTX Method NCBI GI q1170937 BLAST score 870 6.0e-94 E value 167 Match length 98 % identity NCBI Description S-ADENOSYLMETHIONINE SYNTHETASE 1 (METHIONINE ADENOSYLTRANSFERASE 1) (ADOMET SYNTHETASE 1) >gi 450549 emb CAA81481 (Z26867) S-adenosyl methionine synthetase [Oryza sativa] 414178 Seq. No. Seq. ID uC-osflcyp153b01a1 BLASTX Method q744518 NCBI GI 163 BLAST score 4.0e-11 E value Match length 85 44 % identity NCBI Description FKBP-rapamycin-associated protein [Homo sapiens] 414179 Seq. No. Seq. ID uC-osflcyp153b01b1 Method BLASTX NCBI GI g3337356 BLAST score 763 E value 2.0e-81 Match length 165 % identity 87 (AC004481) putative protein transport protein SEC61 alpha NCBI Description subunit [Arabidopsis thaliana] Seq. No. 414180 uC-osflcyp153b02a1 Seq. ID Method BLASTX q1168536 NCBI GI 319 BLAST score 2.0e-29 E value 69 Match length 83 % identity

PHYTEPSIN PRECURSOR (ASPARTIC PROTEINASE) NCBI Description

>gi_100567_pir__S19697 aspartic proteinase (EC 3.4.23.-) precursor - barley >gi_18904_emb_CAA39602 (X56136)

aspartic proteinase [Hordeum vulgare]

414181 Seq. No.

uC-osflcyp153b02b1 Seq. ID

BLASTX Method g2642159 NCBI GI 482 BLAST score 2.0e-69 E value

Match length 154 % identity 85

NCBI Description (AC003000) putative mannose-1-phosphate guanyltransferase

[Arabidopsis thaliana] >gi_3598958 (AF076484) GDP-mannose pyrophosphorylase [Arabidopsis thaliana] >gi_4151925

(AF108660) CYT1 protein [Arabidopsis thaliana]

Seq. No. 414182

Seq. ID uC-osflcyp153b03b1

Method BLASTX
NCBI GI g122085
BLAST score 456
E value 7.0e-47
Match length 121
% identity 86

NCBI Description HISTONE H3 >gi_81641_pir__S06250 histone H3 - Arabidopsis thaliana >gi_82482_pir__S04099 histone H3 (variant H3R-21)

- rice >gi 1362194 pir S57626 histone H3 - maize >gi 20251 emb CAA31969 (X13678) histone H3 (AA 1-136) [Oryza sativa] >gi 20253 emb CAA31970 (X13680) histone H3 (AA 1-136) [Oryza sativa] >gi 168493 (M3658) histone H3 (H3C3) [Zea mays] >gi 168495 (M13378) histone H3 [Zea mays]

>gi_168497 (M13379) histone H3 [Zea mays] >gi_168506
(M35388) histone H3 [Zea mays] >gi_169655 (M77493) histone

H3 [Petroselinum crispum] >gi_169657 (M77494) histone H3 [Petroselinum crispum] >gi_169659 (M77495) histone H3 [Petroselinum crispum] >gi_387565 (M17130) histone H3 [Arabidopsis thaliana] >gi_387567 (M17131) histone H3 [Arabidopsis thaliana] >gi_886738 emb_CAA59111_ (X84377) histone 3 [Zea mays] >gi_1040764 (M35387) histone H3 [Arabidopsis thaliana] >gi_1314779 (U54827) histone H3

[Arabidopsis thailana] >gi_1314//9 (U54827) filstone H3 homolog [Brassica napus] >gi_1531754_emb_CAA57811_ (X82414) Histone H3 [Asparagus officinalis] >gi_1667592 (U77296) histone 3 [Oryza sativa] >gi_3249101 (AC003114) Match to histone H3 gene gb_M17131 and gb_M35387 from A. thaliana. ESTs gb_H76511 gb_H76255, gb_AA712452, gb_N65260 and gb_T42306 come from this gene. [Arabidopsis thaliana]

>gi 5295939 dbj BAA81840.1 (AB026295) ESTs

 $C74\overline{0}53(E302\overline{7}4)$, $\overline{D}15300(C042\overline{5})$, AU030134(E50667) correspond to a region of the predicted gene.; Similar to Asparagus officinalis mRNA for Histone H3.(X82414) [Oryza sativa]

>gi 5295940 dbj BAA81841.1 (AB026295) ESTs

C74053(E30274),D15300(C0425),AU030134(E50667) correspond to a region of the predicted gene.; Similar to Asparagus officinalis mRNA for Histone H3.(X82414) [Oryza sativa] >gi_225459_prf__1303352A histone H3 [Helicoverpa zea]

>gi_225839_prf__1314298B histone H3 [Arabidopsis thaliana]

Seq. No. 414183

Seq. ID uC-osflcyp153b07a1

Method BLASTX
NCBI GI g1835731
BLAST score 172
E value 2.0e-12
Match length 39
% identity 87

NCBI Description (U86018) photosystem II 10 kDa polypeptide [Oryza sativa]

Method

BLASTX

```
414184
Seq. No.
Seq. ID
                  uC-osflcyp153b08b1
Method
                  {\tt BLASTX}
NCBI GI
                  g4826572
BLAST score
                  393
                  5.0e-38
E value
                  113
Match length
                  65
% identity
NCBI Description (AJ238848) polygalacturonase [Phleum pratense]
                  414185
Seq. No.
Seq. ID
                  uC-osflcyp153b09a1
Method
                  BLASTX
NCBI GI
                  g2642159
BLAST score
                  218
                  1.0e-17
E value
                  55
Match length
                  73
% identity
                  (AC003000) putative mannose-1-phosphate guanyltransferase
NCBI Description
                   [Arabidopsis thaliana] >gi 3598958 (AF076484) GDP-mannose
                  pyrophosphorylase [Arabidopsis thaliana] >gi 4151925
                   (AF108660) CYT1 protein [Arabidopsis thaliana]
                  414186
Seq. No.
Seq. ID
                  uC-osflcyp153b09b1
Method
                  BLASTX
                  g4490292
NCBI GI
                  383
BLAST score
                  7.0e-37
E value
Match length
                  138
% identity
                  59
NCBI Description (AL035678) putative protein [Arabidopsis thaliana]
                  414187
Seq. No.
Seq. ID
                  uC-osflcyp153b12b1
Method
                  BLASTX
NCBI GI
                  g6091756
BLAST score
                  391
                  1.0e-37
E value
Match length
                  131
% identity
                  53
NCBI Description (AC009327) putative peroxidase [Arabidopsis thaliana]
Seq. No.
                  414188
Seq. ID
                  uC-osflcyp153c01a1
Method
                  BLASTX
NCBI GI
                  q1531674
BLAST score
                  566
E value
                  2.0e-58
Match length
                  130
% identity
NCBI Description (U68462) actin [Striga asiatica]
Seq. No.
                  414189
                  uC-osflcyp153c01b1
Seq. ID
```

q417154 NCBI GI BLAST score 772 2.0e-82 E value Match length 163 % identity 92 HEAT SHOCK PROTEIN 82 >gi_100685_pir_ S25541 heat shock NCBI Description protein 82 - rice (strain Taichung Native One) >gi_20256_emb_CAA77978_ (Z11920) heat shock protein 82 (HSP82) [Oryza sativa] Seq. No. 414190 Seq. ID uC-osflcyp153c02a1 Method BLASTN NCBI GI q20257 BLAST score 57 E value 3.0e-23 Match length 220 88 % identity NCBI Description O.sativa hsp82 gene for heat shock protein Seq. No. 414191 Seq. ID uC-osflcyp153c04a1 Method BLASTX NCBI GI q123613 BLAST score 214 3.0e-17 E value Match length 74 % identity 61 HEAT SHOCK COGNATE 70 KD PROTEIN 1 >gi_100222 pir__S14949 NCBI Description heat shock cognate protein 70 - tomato >gi 19256 emb CAA37970 (X54029) heat shock protein cognate 70 [Lycopersicon esculentum] Seq. No. 414192 Seq. ID uC-osflcyp153c04b1 BLASTX Method NCBI GI q123620 BLAST score 723 1.0e-76 E value 167 Match length 85 % identity NCBI Description HEAT SHOCK COGNATE 70 KD PROTEIN 2 >gi 100224 pir__S14950 heat shock cognate protein 70 - tomato >gi 19258 emb CAA37971 (X54030) heat shock protein cognate 70 [Lycopersicon esculentum] 414193 Seq. No. Seq. ID uC-osflcyp153c06a1 Method BLASTN

Method BLASTN
NCBI GI g3885881
BLAST score 348
E value 0.0e+00
Match length 392
% identity 97

NCBI Description Oryza sativa inorganic pyrophosphatase (IPP) mRNA, complete

cds

```
414194
Seq. No.
                  uC-osflcyp153c06b1
Seq. ID
Method
                  BLASTX
                  g3885882
NCBI GI
                  810
BLAST score
                  7.0e-87
E value
                  156
Match length
                  98
% identity
NCBI Description (AF093629) inorganic pyrophosphatase [Oryza sativa]
                  414195
Seq. No.
                  uC-osflcyp153c08a1
Seq. ID
                  BLASTN
Method
NCBI GI
                  g20257
                  122
BLAST score
                  2.0e-62
E value
                  180
Match length
                  92
% identity
NCBI Description O.sativa hsp82 gene for heat shock protein
                  414196
Seq. No.
                  uC-osflcyp153c08b1
Seq. ID
                  {\tt BLASTX}
Method
                  g972931
NCBI GI
                   332
BLAST score
                   6.0e-31
E value
                   110
Match length
                   67
% identity
NCBI Description (U18416) IAA14 [Arabidopsis thaliana]
                   414197
Seq. No.
                   uC-osflcyp153c09b1
Seq. ID
                   BLASTX
Method
                   g2499819
NCBI GI
                   198
BLAST score
                   3.0e-15
E value
                   87
Match length
% identity
                   51
                   ASPARTIC PROTEINASE ORYZASIN 1 PRECURSOR
NCBI Description
                   >gi_2130068_pir__S66516 aspartic proteinase 1 precursor -
                   rice >gi 1030715 dbj BAA06876_ (D32165) aspartic protease
                   [Oryza sativa] >gi_1711289_dbj_BAA06875_ (D32144) aspartic
                   protease [Oryza sativa]
                   414198
Seq. No.
                   uC-osflcyp153c11a1
Seq. ID
                   BLASTX
Method
NCBI GI
                   g4103324
                   647
BLAST score
                   7.0e-68
E value
                   142
Match length
% identity
                   (AF022716) GDP-mannose pyrophosphorylase [Solanum
NCBI Description
                   tuberosum]
                   414199
 Seq. No.
                   uC-osflcyp153d02a1
 Seq. ID
```

```
BLASTX
Method
                  g4531444
NCBI GI
BLAST score
                  167
E value
                  1.0e-11
Match length
                  77
% identity
                  52
NCBI Description (AC006224) putative protein kinase [Arabidopsis thaliana]
Seq. No.
                  414200
                  uC-osflcyp153d03b1
Seq. ID
                  BLASTX
Method
                  g1666234
NCBI GI
BLAST score
                  253
E value
                  8.0e-22
Match length
                  53
% identity
                  91
NCBI Description (U76193) actin [Pisum sativum] >gi 1724143 (U81049) actin
                  [Pisum sativum]
Seq. No.
                  414201
                  uC-osflcyp153d04a1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4006890
BLAST score
                  338
E value
                  1.0e-31
Match length
                  72
                  86
% identity
NCBI Description (Z99708) ubiquitin--protein ligase-like protein
                   [Arabidopsis thaliana]
                   414202
Seq. No.
                  uC-osflcyp153d04b1
Seq. ID
                  BLASTX
Method
                  g3668069
NCBI GI
BLAST score
                  216
                   3.0e-17
E value
                  104
Match length
                   46
% identity
NCBI Description (U28007) Pto kinase interactor 1 [Lycopersicon esculentum]
                   414203
Seq. No.
                   uC-osflcyp153d05a1
Seq. ID
                   BLASTN
Method
                   g450548
NCBI GI
BLAST score
                   232
                   1.0e-127
E value
                   280
Match length
                   96
% identity
NCBI Description O.sativa (pRSAM-1) gene for S-adenosyl methionine
                   synthetase
                   414204
Seq. No.
                   uC-osflcyp153d05b1
Seq. ID
                   BLASTX
Method
NCBI GI
                   q4454464
                   437
BLAST score
                   3.0e-43
E value
```

```
Match length
                  118
% identity
NCBI Description (AC006234) unknown protein [Arabidopsis thaliana]
                  414205
Seq. No.
Seq. ID
                  uC-osflcyp153d06b1
Method
                  BLASTX
                  q3451284
NCBI GI
                  391
BLAST score
E value
                  8.0e-38
Match length
                  141
% identity
                  48
NCBI Description (AJ001924) cinnamyl alcohol dehydrogenase [Picea abies]
                  414206
Seq. No.
                  uC-osflcyp153d09b1
Seq. ID
Method
                  BLASTX
                  q584825
NCBI GI
                  587
BLAST score
E value
                  9.0e-61
                  137
Match length
                  79
% identity
                  B2 PROTEIN >gi 322726 pir__S32124 B2 protein - carrot
NCBI Description
                  >gi_297889_emb_CAA51078_ (X72385) B2 protein [Daucus
                  carotal
                  414207
Seq. No.
Seq. ID
                  uC-osflcyp153d10b1
Method
                  BLASTX
NCBI GI
                  g1170937
                  678
BLAST score
E value
                  2.0e-71
Match length
                  128
% identity
                  100
                  S-ADENOSYLMETHIONINE SYNTHETASE 1 (METHIONINE
NCBI Description
                  ADENOSYLTRANSFERASE 1) (ADOMET SYNTHETASE 1)
                  >gi_450549_emb_CAA81481_ (Z26867) S-adenosyl methionine
                  synthetase [Oryza sativa]
                  414208
Seq. No.
Seq. ID
                  uC-osflcyp153d12a1
                  BLASTX
Method
NCBI GI
                  g3341490
BLAST score
                  271
                  7.0e-24
E value
                  58
Match length
                  88
% identity
                  (AJ007705) phospoenolpyruvate carboxylase [Triticum
NCBI Description
                  aestivum]
                   414209
Seq. No.
Seq. ID
                  uC-osflcyp153d12b1
                  BLASTX
Method
NCBI GI
                  g2266947
BLAST score
                   687
                   8.0e-73
E value
                   141
Match length
```

```
% identity
                  (AF008939) phosphoenolpyruvate carboxylase 1 [Gossypium
NCBI Description
                  hirsutum]
                  414210
Seq. No.
                  uC-osflcyp153e02a1
Seq. ID
                  BLASTN
Method
                  g2331130
NCBI GI
BLAST score
                  245
                  1.0e-135
E value
                  253
Match length
                  99
% identity
NCBI Description Oryza sativa glycine-rich protein (OSGRP1) mRNA, complete
                  cds
                  414211
Seq. No.
                  uC-osflcyp153e02b1
Seq. ID
                  BLASTX
Method
                  q2293480
NCBI GI
BLAST score
                  426
                  6.0e-42
E value
                  88
Match length
                   94
% identity
NCBI Description (AF011331) glycine-rich protein [Oryza sativa]
                   414212
Seq. No.
                  uC-osflcyp153e03b1
Seq. ID
Method
                  BLASTX
                   g2506826
NCBI GI
                   343
BLAST score
                   4.0e-32
E value
                   97
Match length
                   71
% identity
NCBI Description NONSPECIFIC LIPID-TRANSFER PROTEIN 1 PRECURSOR (LTP 1)
                   (PAPI) >gi_1619604_emb_CAA69949.1_ (Y08691) lipid transfer
                   protein [Oryza satīva] >gi 1667590 (U77295) lipid transfer
                   protein [Oryza sativa]
                   414213
Seq. No.
                   uC-osflcyp153e04b1
Seq. ID
                   BLASTX
Method
                   g5714762
NCBI GI
                   400
BLAST score
                   8.0e-45
E value
                   99
Match length
                   94
% identity
                  (AF173881) serine/threonine protein phosphatase PP2A-4
NCBI Description
                   catalytic subunit [Oryza sativa subsp. indica]
                   414214
Seq. No.
                   uC-osflcyp153e05a1
Seq. ID
                   BLASTX
Method
                   g3915826
NCBI GI
                   210
BLAST score
                   8.0e-17
E value
                   45
Match length
                   93
 % identity
```



```
NCBI Description 60S RIBOSOMAL PROTEIN L5
                   414215
Seq. No.
Seq. ID
                   uC-osflcyp153e07b1
Method
                   BLASTX
NCBI GI
                   g3123745
BLAST score
                   271
                   1.0e-23
E value
Match length
                   131
% identity
                   47
                   (AB013447) aluminum-induced [Brassica napus]
NCBI Description
                   414216
Seq. No.
                   uC-osflcyp153e08a1
Seq. ID
Method
                   BLASTX
                   g5803256
NCBI GI
BLAST score
                   368
                   3.0e - 35
E value
Match length
                   69
                   100
% identity
                   (AP000399) ESTs C98280(C1391), D15843(C1391) correspond to a
NCBI Description
                   region of the predicted gene; similar to OsENOD93a gene for
                   early nodulin (AB018375) [Oryza sativa]
Seq. No.
                   414217
                   uC-osflcyp153e08b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   a5803256
BLAST score
                   436
E value
                   5.0e-43
Match length
                   112
% identity
                   (AP000399) ESTs C98280(C1391), D15843(C1391) correspond to a
NCBI Description
                   region of the predicted gene; similar to OsENOD93a gene for
                   early nodulin (AB018375) [Oryza sativa]
Seq. No.
                   414218
Seq. ID
                   uC-osflcyp153e09b1
Method
                   BLASTX
NCBI GI
                   q417103
BLAST score
                   478
E value
                   3.0e-51
Match length
                   134
% identity
                   HISTONE H3.2, MINOR >gi_282871_pir__S24346 histone
NCBI Description
                   H3.3-like protein - Arabidopsis thaliana
                   >gi_16324_emb_CAA42957_ (X60429) histone H3.3 like protein
[Arabidopsis thaliana] >gi_404825_emb_CAA42958_ (X60429)
                   histone H3.3 like protein [Arabidopsis thaliana] >gi_488563
                    (U09458) histone H3.2 [Medicago sativa] >gi 488567 (U09460)
```

histone H3.3 like protein [Arabidopsis thaliana] >gi_488563 (U09458) histone H3.2 [Medicago sativa] >gi_488567 (U09460) histone H3.2 [Medicago sativa] >gi_488569 (U09461) histone H3.2 [Medicago sativa] >gi_488575 (U09464) histone H3.2 [Medicago sativa] >gi_488577 (U09465) histone H3.2 [Medicago sativa] >gi_510911 emb_CAA56153 (X79714) histone H3 [Lolium temulentum] >gi_1435157 emb_CAA58445 (X83422) histone H3 variant H3.3 [Lycopersicon esculentum]

>gi_2558944 (AF024716) histone 3 [Gossypium hirsutum]

NCBI GI

BLAST score



>gi_3273350_dbj_BAA31218_ (AB015760) histone H3 [Nicotiana
tabacum] >gi_3885890 (AF093633) histone H3 [Oryza sativa]
>gi_4038469_gb_AAC97380_ (AF109910) histone H3 [Porteresia
coarctata] >gi_4490754_emb_CAB38916.1_ (AL035708) histone
H3.3 [Arabidopsis thaliana] >gi_4490755_emb_CAB38917.1_
(AL035708) Histon H3 [Arabidopsis thaliana]
>gi_6006364_dbj_BAA84794.1_ (AP000559) EST D15300(C0425)
corresponds to a region of the predicted gene.; Similar to
histone H3 (AB015760) [Oryza sativa]

```
414219
Seq. No.
Seq. ID
                   uC-osflcyp153e10b1
Method
                   BLASTX
NCBI GI
                   q542157
BLAST score
                   501
E value
                   9.0e-51
                   129
Match length
                   78
% identity
NCBI Description ribosomal 5S RNA-binding protein - Rice
Seq. No.
                   414220
Seq. ID
                   uC-osflcyp153e12b1
Method
                   BLASTX
NCBI GI
                   q4217999
BLAST score
                   597
                   7.0e-62
E value
Match length
                   144
                   78
% identity
NCBI Description
                  (AC006135) putative ubiquitin--protein ligase
                   (ubiquitin-conjugating enzyme) [Arabidopsis thaliana]
                   414221
Seq. No.
Seq. ID
                   uC-osflcyp153f01b1
Method
                   {\tt BLASTX}
NCBI GI
                   g228403
BLAST score
                   584
E value
                   2.0e-60
Match length
                   133
% identity
                   83
NCBI Description glycolate oxidase [Lens culinaris]
Seq. No.
                   414222
Seq. ID
                   uC-osflcyp153f03b1
Method
                   BLASTX
NCBI GI
                   g1848225
                   292
BLAST score
E value
                   4.0e-26
Match length
                   63
% identity
                  (U88090) nonspecific lipid transfer protein [Hordeum
NCBI Description
                   vulgare]
Seq. No.
                   414223
Seq. ID
                   uC-osflcyp153f08a1
Method
                   BLASTX
```

q1848225

NCBI Description

```
E value
                   3.0e-10
Match length
                   34
% identity
                   76
NCBI Description
                   (U88090) nonspecific lipid transfer protein [Hordeum
                   vulgare]
Seq. No.
                   414224
Seq. ID
                   uC-osflcyp153f08b1
Method
                   BLASTX
NCBI GI
                   g6094328
BLAST score
                   390
E value
                   1.0e-37
Match length
                   80
% identity
                   89
NCBI Description
                  SPERMIDINE SYNTHASE 1 (PUTRESCINE AMINOPROPYLTRANSFERASE 1)
                   (SPDSY 1) >gi_2821955_dbj_BAA24533 (AB006690) spermidine
                   synthase 1 [Hyoscyamus niger]
Seq. No.
                   414225
Seq. ID
                   uC-osflcyp153f09b1
Method
                   BLASTX
NCBI GI
                   q3643603
BLAST score
                   413
E value
                   2.0e-40
Match length
                   163
% identity
                   52
NCBI Description (AC005395) unknown protein [Arabidopsis thaliana]
Seq. No.
                   414226
Seq. ID
                   uC-osflcyp153f10a1
Method
                   BLASTX
NCBI GI
                   g3885892
BLAST score
                   374
E value
                   8.0e-36
Match length
                   75
                   97
% identity
NCBI Description (AF093634) photosystem-1 F subunit precursor [Oryza sativa]
Seq. No.
                   414227
Seq. ID
                   uC-osflcyp153f12b1
Method
                   BLASTX
NCBI GI
                   g6091756
BLAST score
                   430
E value
                   2.0e-42
Match length
                  139
                   56
% identity
NCBI Description
                  (AC009327) putative peroxidase [Arabidopsis thaliana]
Seq. No.
                   414228
Seq. ID
                  uC-osflcyp153g01b1
Method
                  BLASTX
NCBI GI
                  g3318615
BLAST score
                  417
E value
                  7.0e-47
Match length
                  114
% identity
```

54001

(AB016065) mitochondrial phosphate transporter [Oryza

```
sativa]
Seq. No.
                    414229
Seq. ID
                    uC-osflcyp153g03b1
Method
                    BLASTX
NCBI GI
                    g3914422
BLAST score
                    460
E value
                    5.0e-46
Match length
                    88
                    94
% identity
NCBI Description PROFILIN >gi_2154728_emb_CAA69669_ (Y08389) profilin 2 [Cynodon dactylon] >gi_2154730_emb_CAA69670_ (Y08390)
                   profilin 1 [Cynodon dactylon]
Seq. No.
                    414230
Seq. ID
                   uC-osflcyp153g04a1
Method
                   BLASTX
NCBI GI
                    g1168537
BLAST score
                   149
E value
                    1.0e-21
Match length
                   59
% identity
                    90
NCBI Description ASPARTIC PROTEINASE PRECURSOR >gi_82458_pir__JS0732
                   aspartic proteinase (EC 3.4.23.-) - rice
                    >gi_218143_dbj_BAA02242_ (D12777) aspartic proteinase
                    [Oryza sativa]
Seq. No.
                    414231
Seq. ID
                   uC-osflcyp153g04b1
Method
                   BLASTX
NCBI GI
                   g2662343
BLAST score
                   736
E value
                    3.0e-78
Match length
                   143
% identity
                    99
NCBI Description (D63581) EF-1 alpha [Oryza sativa]
Seq. No.
                    414232
Seq. ID
                   uC-osflcyp153g05b1
Method
                   BLASTX
NCBI GI
                   g3860245
BLAST score
                   610
E value
                   2.0e-63
Match length
                   164
% identity
                   70
NCBI Description
                  (AC005824) putative argonaute protein [Arabidopsis
                   thaliana]
Seq. No.
                   414233
```

Seq. ID uC-osflcyp153g06b1

BLASTX Method NCBI GI g1698548 BLAST score 308 E value 5.0e-28 Match length 164

% identity 43

NCBI Description (U58971) calmodulin-binding protein [Nicotiana tabacum]

% identity

```
Seq. No.
                   414234
Seq. ID
                   uC-osflcyp153q10b1
Method
                   BLASTX
NCBI GI
                   q3183991
BLAST score
                   447
E value
                   3.0e-44
Match length
                   166
% identity
NCBI Description
                  (AJ005173) P69F protein [Lycopersicon esculentum]
                   414235
Seq. No.
                   uC-osflcyp153g12a1
Seq. ID
Method
                   BLASTX
NCBI GI
                   q120668
BLAST score
                   374
E value
                   8.0e-36
Match length
                   78
                   91
% identity
NCBI Description
                   GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC
                   >gi_82399_pir__A24159 glyceraldehyde-3-phosphate
dehydrogenase (EC 1.2.1.12), cytosolic - barley (fragment)
                   >gi 167044 (M36650) glyceraldehyde-3-phosphate
                   dehydrogenase [Hordeum vulgare] >gi_225347_prf__1301218A
                   dehydrogenase, glyceraldehydephosphate [Hordeum vulgare var.
                   distichum]
Seq. No.
                   414236
Seq. ID
                   uC-osflcyp153g12b1
Method
                   BLASTX
NCBI GI
                   g3885892
BLAST score
                   242
E value
                   3.0e-20
Match length
                   113
% identity
NCBI Description (AF093634) photosystem-1 F subunit precursor [Oryza sativa]
                   414237
Seq. No.
Seq. ID
                   uC-osflcyp153h01b1
Method
                   BLASTX
NCBI GI
                   g2190547
BLAST score
                   419
E value
                   5.0e-41
Match length
                   145
                   54
% identity
NCBI Description
                   (AC001229) ESTs
                   gb T43256,gb 46316,gb N64930,gb AA395255,gb AA404382 come
                   from this gene. [Arabidopsis thaliana]
                   414238
Seq. No.
Seq. ID
                   uC-osflcyp153h02b1
Method
                   BLASTX
NCBI GI
                   g477280
BLAST score
                   473
E value
                   1.0e-60
Match length
                   152
                   78
```

```
NCBI Description mitochondrial processing peptidase (EC 3.4.99.41) 55K
                  protein precursor - potato >gi_410633_bbs_136740 cytochrome
                  c reductase-processing peptidase subunit \overline{I}, MPP subunit I,
                  P55 [potatoes, var. Marfona, tuber, Peptide Mitochondrial,
                  534 aa]
                  414239
Seq. No.
                  uC-osflcyp153h03a1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g5803242
BLAST score
                  240
                  1.0e-132
E value
                  325
Match length
                  99
% identity
NCBI Description Oryza sativa genomic DNA, chromosome 6, clone:P0535G04
                  414240
Seq. No.
                  uC-osflcyp153h03b1
Seq. ID
Method
                  BLASTX
                  g4579913
NCBI GI
BLAST score
                  171
                  9.0e-24
E value
                  134
Match length
                  52
% identity
                  (AB023423) sulfate transporter [Arabidopsis thaliana]
NCBI Description
                  414241
Seq. No.
                  uC-osflcyp153h04b1
Seq. ID
                  BLASTX
Method
NCBI GI
                  q2952328
BLAST score
                  742
E value
                  7.0e-79
Match length
                  143
                   99
% identity
                  (AF049889) 1-aminocyclopropane-1-carboxylate oxidase [Oryza
NCBI Description
                   sativa]
                   414242
Seq. No.
                  uC-osflcyp153h06b1
Seq. ID
Method
                  BLASTX
NCBI GI
                   g2462834
BLAST score
                   174
                   2.0e-12
E value
Match length
                   115
% identity
NCBI Description (AF000657) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   414243
Seq. ID
                   uC-osflcyp153h07a1
Method
                   BLASTN
NCBI GI
                   g2331130
BLAST score
                   43
E value
                   5.0e-15
                   71
Match length
% identity
                   90
                  Oryza sativa glycine-rich protein (OSGRP1) mRNA, complete
NCBI Description
```

cds

NCBI GI

BLAST score

414244 Seq. No. uC-osflcyp153h07b1 Seq. ID Method BLASTX g2293480 NCBI GI 424 BLAST score 9.0e-42 E value 85 Match length 96 % identity NCBI Description (AF011331) glycine-rich protein [Oryza sativa] 414245 Seq. No. uC-osflcyp153h08b1 Seq. ID Method BLASTX g4678950 NCBI GI 339 BLAST score 3.0e-40E value 137 Match length 68 % identity (AL049711) putative protein [Arabidopsis thaliana] NCBI Description Seq. No. 414246 uC-osflcyp153h10a1 Seq. ID Method BLASTX NCBI GI g5902359 BLAST score 388 E value 2.0e-37 Match length 88 84 % identity (AC009322) Heat-shock protein [Arabidopsis thaliana] NCBI Description Seq. No. 414247 uC-osflcyp153h10b1 Seq. ID Method BLASTX NCBI GI q3212868 BLAST score 307 E value 6.0e-28 117 Match length % identity 54 (AC004005) unknown protein [Arabidopsis thaliana] NCBI Description Seq. No. 414248 uC-osflcyp153h11a1 Seq. ID BLASTX Method NCBI GI g2952328 BLAST score 783 E value 9.0e-84 Match length 155 % identity 97 (AF049889) 1-aminocyclopropane-1-carboxylate oxidase [Oryza NCBI Description sativa] Seq. No. 414249 uC-osflcyp153h11b1 Seq. ID Method BLASTX

54005

g1168537

Seq. ID

```
4.0e-52
E value
Match length
                  124
                  82
% identity
NCBI Description
                  ASPARTIC PROTEINASE PRECURSOR >gi_82458_pir__JS0732
                  aspartic proteinase (EC 3.4.23.-) - rice
                  >gi_218143_dbj_BAA02242_ (D12777) aspartic proteinase
                   [Oryza sativa]
Seq. No.
                  414250
Seq. ID
                  uC-osflcyp154a02a1
Method
                  BLASTN
                  g394735
NCBI GI
BLAST score
                  419
                  0.0e + 00
E value
Match length
                  423
                  100
% identity
NCBI Description Rice lip19 mRNA for basic/leucine zipper protein
                  414251
Seq. No.
                  uC-osflcyp154a04a1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1170937
BLAST score
                  267
                  2.0e-23
E value
Match length
                  49
                   98
% identity
                 S-ADENOSYLMETHIONINE SYNTHETASE 1 (METHIONINE
NCBI Description
                  ADENOSYLTRANSFERASE 1) (ADOMET SYNTHETASE 1)
                  >gi_450549_{emb}_{CAA81481}_{(Z26867)} S-adenosyl methionine
                  synthetase [Oryza sativa]
                   414252
Seq. No.
                  uC-osflcyp154a04b1
Seq. ID
Method
                  BLASTX
NCBI GI
                   g1170937
BLAST score
                   762
E value
                   3.0e-81
Match length
                  145
% identity
                   99
                  S-ADENOSYLMETHIONINE SYNTHETASE 1 (METHIONINE
NCBI Description
                   ADENOSYLTRANSFERASE 1) (ADOMET SYNTHETASE 1)
                   >gi 450549 emb CAA81481 (Z26867) S-adenosyl methionine
                   synthetase [Oryza sativa]
Seq. No.
                   414253
Seq. ID
                   uC-osflcyp154a06a1
Method
                   BLASTX
NCBI GI
                   g4507711
BLAST score
                  144
                   7.0e-09
E value
                   48
Match length
% identity
                   60
                  tetratricopeptide repeat domain 1 >gi 1688074 (U46570)
NCBI Description
                   tetratricopeptide repeat protein [Homo sapiens]
Seq. No.
                   414254
```

54006

uC-osflcyp154a07a1

```
Method
                   BLASTX
NCBI GI
                   g4580455
BLAST score
                   178
                   8.0e-13
E value
Match length
                   58
% identity
                   69
NCBI Description (AC006081) unknown protein [Arabidopsis thaliana]
Seq. No.
                   414255
Seq. ID
                   uC-osflcyp154a08b1
Method
                   BLASTX
NCBI GI
                   g132105
BLAST score
                   528
E value
                   7.0e-54
Match length
                   139
% identity
                   72
NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
                   (RUBISCO SMALL SUBUNIT C) >gi_68094_pir__RKRZS9 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                   precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_
                   (D00643) small subunit of ribulose-1,5-bisphosphate
                   carboxylase (RuBPC) [Oryza sativa] >gi 2407283 (AF017364)
                   ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
                   sativa] >gi 226375 prf 1508256A ribulose bisphosphate
                   carboxylase S [Oryza sativa]
Seq. No.
                   414256
Seq. ID
                   uC-osflcyp154a09a1
Method
                   BLASTX
NCBI GI
                   g4249662
BLAST score
                   292
E value
                   3.0e-26
                   108
Match length
                   57
% identity
NCBI Description (AF089810) Altered Response to Gravity [Arabidopsis
                   thaliana]
                   414257
Seq. No.
Seq. ID
                   uC-osflcyp154a09b1
                   BLASTX
Method
NCBI GI
                   g4249662
BLAST score
                   772
E value
                   2.0e-82
Match length
                   176
% identity
                   84
NCBI Description
                  (AF089810) Altered Response to Gravity [Arabidopsis
                   thaliana]
Seq. No.
                   414258
Seq. ID
                   uC-osflcyp154a10b1
Method
                   BLASTX
NCBI GI
                   g6006892
BLAST score
                   561
E value
                   1.0e-57
Match length
                   126
% identity
                   83
NCBI Description (AC008153) unknown protein [Arabidopsis thaliana]
```

```
414259
Seq. No.
Seq. ID
                  uC-osflcyp154a11a1
Method
                  BLASTX
NCBI GI
                  g1929998
BLAST score
                  147
E value
                  2.0e-09
Match length
                  67
                  43
% identity
NCBI Description
                 (U77463) NADPH-dependent HC-toxin reductase [Hordeum
                  vulgare]
Seq. No.
                  414260
                  uC-osflcyp154a11b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2911358
BLAST score
                  483
E value
                  2.0e-48
Match length
                  144
                  67
% identity
NCBI Description (AF041043) NADPH HC toxin reductase [Zea mays]
Seq. No.
                  414261
Seq. ID
                  uC-osflcyp154b01a1
Method
                  BLASTX
NCBI GI
                  g2130069
                  200
BLAST score
E value
                  2.0e-15
                  39
Match length
                  97
% identity
NCBI Description catalase (EC 1.11.1.6) catA - rice
                  >gi_1261858_dbj_BAA06232_ (D29966) catalase [Oryza sativa]
Seq. No.
                  414262
Seq. ID
                  uC-osflcyp154b01b1
Method
                  BLASTX
NCBI GI
                  q66298
BLAST score
                  853
E value
                  6.0e-92
Match length
                  160
% identity
                  96
NCBI Description catalase (EC 1.11.1.6) - rice >gi 20192 emb CAA43814
                  (X61626) catalase [Oryza sativa]
Seq. No.
                  414263
Seq. ID
                  uC-osflcyp154b02a1
Method
                  BLASTX
NCBI GI
                  g4531444
BLAST score
                  245
E value
                  1.0e-20
Match length
                  109
% identity
                  54
NCBI Description (AC006224) putative protein kinase [Arabidopsis thaliana]
Seq. No.
                  414264
Seq. ID
                  uC-osflcyp154b03b1
Method
                  BLASTN
```

Match length

65

```
q968995
NCBI GI
BLAST score
                  40
                  3.0e-13
E value
                  56
Match length
                  93
% identity
                 Oryza sativa clone glyceraldehyde-3-phosphate dehydrogenase
NCBI Description
                  (Gpc) mRNA, complete cds
                  414265
Seq. No.
                  uC-osflcyp154b04a1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g5852164
BLAST score
                  166
E value
                  2.0e-11
                  77
Match length
                  39
% identity
                  (AJ249389) vacuolar ATPase subunit H [Manduca sexta]
NCBI Description
                   414266
Seq. No.
                  uC-osflcyp154b04b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4680661
BLAST score
                  275
                  4.0e-24
E value
                  179
Match length
                  32
% identity
NCBI Description
                  (AF132945) CGI-11 protein [Homo sapiens]
                  414267
Seq. No.
                  uC-osflcyp154b05a1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g5091496
BLAST score
                  53
E value
                  5.0e-21
Match length
                  142
                  93
% identity
NCBI Description
                  Oryza sativa genomic DNA, chromosome 6, clone P0680A03,
                  complete sequence
                   414268
Seq. No.
                  uC-osflcyp154b05b1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g5091496
                  57
BLAST score
E value
                   4.0e-23
Match length
                  174
                  89
% identity
NCBI Description
                  Oryza sativa genomic DNA, chromosome 6, clone P0680A03,
                  complete sequence
Seq. No.
                   414269
                  uC-osflcyp154b07a1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3264611
BLAST score
                  293
E value
                  2.0e-26
```

% identity

84

% identity NCBI Description (AF061511) seven in absentia homolog [Zea mays] Seq. No. 414270 uC-osflcyp154b08a1 Seq. ID BLASTX Method NCBI GI q2464901 159 BLAST score 1.0e-10 E value 48 Match length 60 % identity (Z99708) putative protein [Arabidopsis thaliana] NCBI Description Seq. No. 414271 Seq. ID uC-osflcyp154b08b1 Method BLASTX q2464901 NCBI GI BLAST score 516 2.0e-52 E value 133 Match length % identity 71 (Z99708) putative protein [Arabidopsis thaliana] NCBI Description Seq. No. 414272 uC-osflcyp154b10a1 Seq. ID Method BLASTX NCBI GI g671740 BLAST score 339 1.0e-31 E value Match length 65 98 % identity (X84730) ribulose-bisphosphate carboxylase [synthetic NCBI Description construct] 414273 Seq. No. uC-osflcyp154b10b1 Seq. ID Method BLASTX NCBI GI g132096 BLAST score 868 E value 1.0e-93 Match length 166 99 % identity NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN A PRECURSOR (RUBISCO SMALL SUBUNIT A) >gi_68095_pir__RKRZS6 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor (clone pOSSS2106) - rice >gi_218210_dbj_BAA00539_ (D00644) small subunit of ribulose-1,5-bisphosphate carboxylase (RuBPC) [Oryza sativa] Seq. No. 414274 uC-osflcyp154b11a1 Seq. ID Method BLASTN NCBI GI q4521189 BLAST score 41 E value 1.0e-13 Match length 113

BLAST score

216

```
NCBI Description Oryza sativa gene for Pib, complete cds
                  414275
Seq. No.
                  uC-osflcyp154b11b1
Seq. ID
Method
                  BLASTN
                  q4521189
NCBI GI
BLAST score
                  420
                  0.0e+00
E value
                  424
Match length
                  100
% identity
NCBI Description Oryza sativa gene for Pib, complete cds
                  414276
Seq. No.
                  uC-osflcyp154b12b1
Seq. ID
Method
                  BLASTX
                  g3901268
NCBI GI
BLAST score
                  271
                  1.0e-23
E value
Match length
                  147
                  37
% identity
                  (AF060173) SV2 related protein [Rattus norvegicus]
NCBI Description
Seq. No.
                  414277
                  uC-osflcyp154c01a1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3297808
BLAST score
                  247
E value
                  6.0e-21
                  85
Match length
                  53
% identity
                 (AL031032) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  414278
                  uC-osflcyp154c05b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2760839
                  369
BLAST score
E value
                  4.0e-35
Match length
                  132
                  54
% identity
NCBI Description (AC003105) putative receptor kinase [Arabidopsis thaliana]
                   414279
Seq. No.
                  uC-osflcyp154c06b1
Seq. ID
Method
                  BLASTX
                  g3258575
NCBI GI
BLAST score
                   494
E value
                  7.0e-50
Match length
                  133
% identity
NCBI Description (U89959) Hypothetical protein [Arabidopsis thaliana]
                   414280
Seq. No.
                  uC-osflcyp154c07b1
Seq. ID
Method
                  BLASTX
NCBI GI
                   g4584342
```

E value 3.0e-17
Match length 91
% identity 47
NCBI Description (AC0071

NCBI Description (AC007127) putative ubiquitin protein [Arabidopsis

thaliana]

Seq. No. 414281

Seq. ID uC-osflcyp154c10a1

Method BLASTX
NCBI GI g1304215
BLAST score 358
E value 6.0e-34
Match length 98
% identity 53

NCBI Description (D84392) precursor of rice 22 kDa protein of photosystem II

(PSII-S) [Oryza sativa]

Seq. No. 414282

Seq. ID uC-osflcyp154c11b1

Method BLASTX
NCBI GI g5731257
BLAST score 432
E value 1.0e-42
Match length 135
% identity 68

NCBI Description (AF165924) auxin-induced basic helix-loop-helix

transcription factor [Gossypium hirsutum]

Seq. No. 414283

Seq. ID uC-osflcyp154c12a1

Method BLASTX
NCBI GI g3023812
BLAST score 193
E value 1.0e-14
Match length 56
% identity 73

NCBI Description GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC

>gi_435046 (L26924) glyceraldehyde-phosphate dehydrogenase

[Ginkgo biloba]

Seq. No. 414284

Seq. ID uC-osflcyp154c12b1

Method BLASTX
NCBI GI g120669
BLAST score 462
E value 3.0e-46
Match length 113
% identity 80

NCBI Description GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC

>gi_66014_pir__DEJMG glyceraldehyde-3-phosphate
dehydrogenase (EC 1.2.1.12) - Magnolia liliiflora
>gi_19566_emb_CAA42905_ (X60347) glyceraldehyde
3-phosphate dehydrogenase [Magnolia liliiflora]

Seq. No. 414285

Seq. ID uC-osflcyp154d01a1

Method BLASTX

NCBI GI g2463584 BLAST score 307 7.0e-28 E value Match length 113 50 % identity NCBI Description (D38532) FBSB precursor [Ananas comosus] Seq. No. 414286 uC-osflcyp154d01b1 Seq. ID Method BLASTX NCBI GI g1323748 227 BLAST score E value 1.0e-18 Match length 102 % identity 49 (U32430) thiol protease [Triticum aestivum] NCBI Description Seq. No. 414287 uC-osflcyp154d03a1 Seq. ID Method BLASTX NCBI GI g1235664 BLAST score 323 8.0e-30 E value 88 Match length 76 % identity NCBI Description (U37936) novel calmodulin-like protein [Oryza sativa] >gi 3171148 (AF064456) calmodulin-like protein [Oryza sativa subsp. indica] Seq. No. 414288 uC-osflcyp154d03b1 Seq. ID Method BLASTX NCBI GI g1235664 BLAST score 605 E value 8.0e-63 Match length 150 % identity 55 NCBI Description (U37936) novel calmodulin-like protein [Oryza sativa] >gi 3171148 (AF064456) calmodulin-like protein [Oryza sativa subsp. indica] Seq. No. 414289 Seq. ID uC-osflcyp154d05a1 Method BLASTN NCBI GI g2196541 237 BLAST score E value 1.0e-130 Match length 460 % identity 93

NCBI Description Oryza sativa glycine-rich protein mRNA, complete cds

Seq. No. 414290

Seq. ID uC-osflcyp154d05b1

Method BLASTX
NCBI GI g2293480
BLAST score 444
E value 4.0e-44

Seq. No.

414296

Match length 93 % identity 94 NCBI Description (AF011331) glycine-rich protein [Oryza sativa] Seq. No. 414291 uC-osflcyp154d06a1 Seq. ID Method BLASTX NCBI GI g2130069 BLAST score 257 E value 5.0e-22 Match length 58 88 % identity NCBI Description catalase (EC 1.11.1.6) catA - rice >gi_1261858_dbj_BAA06232_ (D29966) catalase [Oryza sativa] 414292 Seq. No. Seq. ID uC-osflcyp154d06b1 Method BLASTX NCBI GI g2130069 BLAST score 694 E value 3.0e-73 Match length 159 % identity 81 NCBI Description catalase (EC 1.11.1.6) catA - rice >gi_1261858_dbj_BAA06232_ (D29966) catalase [Oryza sativa] Seq. No. 414293 Seq. ID uC-osflcyp154d08b1 Method BLASTX NCBI GI g5080827 BLAST score 392 E value 6.0e-38 Match length 109 71 % identity NCBI Description (AC007258) Hypothetical protein [Arabidopsis thaliana] Seq. No. 414294 Seq. ID uC-osflcyp154d09a1 Method BLASTX NCBI GI g1438883 BLAST score 162 E value 6.0e-11 Match length 60 % identity 48 NCBI Description (U43840) GmCK3p [Glycine max] Seq. No. 414295 Seq. ID uC-osflcyp154d09b1 Method BLASTX NCBI GI g1438883 BLAST score 162 E value 6.0e-11 Match length 60 % identity 48 NCBI Description (U43840) GmCK3p [Glycine max]

E value

1.0e-17

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uC-osflcyp154d10b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g6094303
BLAST score
                  557
E value
                  3.0e-57
Match length
                  157
                  66
% identity
NCBI Description
                  SELENOCYSTEINE METHYLTRANSFERASE (SECYS-METHYLTRANSFERASE)
                  (SECYS-MT) >gi 4006848 emb CAA10368 (AJ131433)
                  selenocysteine methyltransferase [Astragalus bisulcatus]
                  414297
Seq. No.
Seq. ID
                  uC-osflcyp154d11b1
Method
                  BLASTX
NCBI GI
                  g1706956
BLAST score
                  686
E value
                  2.0e-72
Match length
                  174
% identity
                  75
NCBI Description (U58283) cellulose synthase [Gossypium hirsutum]
Seq. No.
                  414298
Seq. ID
                  uC-osflcyp154d12a1
Method
                  BLASTX
NCBI GI
                  g3426041
BLAST score
                  213
E value
                  7.0e-17
Match length
                  62
% identity
                  58
NCBI Description (AC005168) unknown protein [Arabidopsis thaliana]
                  414299
Seq. No.
Seq. ID
                  uC-osflcyp154e01a1
Method
                  BLASTX
NCBI GI
                  q5823570
BLAST score
                  207
E value
                  2.0e-16
Match length
                  69
% identity
                  62
NCBI Description (AL049730) putative protein [Arabidopsis thaliana]
Seq. No.
                  414300
Seq. ID
                  uC-osflcyp154e03b1
Method
                  BLASTX
NCBI GI
                  g3510261
BLAST score
                  145
                  2.0e-09
E value
Match length
                  64
                  61
% identity
NCBI Description (AC005310) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  414301
Seq. ID
                  uC-osflcyp154e04a1
Method
                  BLASTX
NCBI GI
                  g2494165
BLAST score
                  220
```

Match length 54 % identity 76

NCBI Description DNA LIGASE (POLYDEOXYRIBONUCLEOTIDE SYNTHASE [ATP])

>gi_2129574_pir__S71278 DNA ligase - Arabidopsis thaliana >gi_1359495_emb_CAA66599_ (X97924) DNA ligase [Arabidopsis

thaliana]

Seq. No. 414302

Seq. ID uC-osflcyp154e04b1

Method BLASTX
NCBI GI g2494165
BLAST score 735
E value 5.0e-78
Match length 181
% identity 75

NCBI Description DNA LIGASE (POLYDEOXYRIBONUCLEOTIDE SYNTHASE [ATP])

>gi_2129574_pir__S71278 DNA ligase - Arabidopsis thaliana >gi_1359495_emb_CAA66599_ (X97924) DNA ligase [Arabidopsis

thaliana]

Seq. No. 414303

Seq. ID uC-osflcyp154e07b1

Method BLASTX
NCBI GI g3236247
BLAST score 444
E value 6.0e-44
Match length 175
% identity 50

NCBI Description (AC004684) SCARECROW-like protein [Arabidopsis thaliana]

Seq. No. 414304

Seq. ID uC-osflcyp154e08a1

Method BLASTX
NCBI GI g3169182
BLAST score 270
E value 1.0e-23
Match length 54
% identity 87

NCBI Description (AC004401) unknown protein [Arabidopsis thaliana]

Seq. No. 414305

Seq. ID uC-osflcyp154e08b1

Method BLASTX
NCBI GI g3860323
BLAST score 349
E value 5.0e-33
Match length 77
% identity 83

NCBI Description (AJ012688) hypothetical protein [Cicer arietinum]

Seq. No. 414306

Seq. ID uC-osflcyp154e09b1

Method BLASTX
NCBI GI g4558551
BLAST score 145
E value 6.0e-09
Match length 31

```
% identity
                  (AC007138) P-glycoprotein-like protein [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  414307
Seq. ID
                  uC-osflcyp154e11a1
Method
                  BLASTX
NCBI GI
                  q1084457
BLAST score
                  334
E value
                  4.0e-31
Match length
                  65
                  100
% identity
NCBI Description
                  elongation factor 1-beta - Rice >gi_432368_dbj_BAA04903_
                  (D23674) elongation factor 1 beta [Oryza sativa]
                  414308
Seq. No.
Seq. ID
                  uC-osflcyp154e11b1
Method
                  BLASTX
NCBI GI
                  q1084457
BLAST score
                  434
E value
                  7.0e-43
Match length
                  89
% identity
                  99
NCBI Description
                  elongation factor 1-beta - Rice >gi_432368_dbj_BAA04903_
                  (D23674) elongation factor 1 beta [Oryza sativa]
                  414309
Seq. No.
Seq. ID
                  uC-osflcyp154e12a1
Method
                  BLASTX
NCBI GI
                  g322854
BLAST score
                  334
E value
                  3.0e-31
Match length
                  77
% identity
                  88
NCBI Description
                  pollen-specific protein - rice >gi 20310 emb CAA78897
                  (Z16402) pollen specific gene [Oryza sativa]
Seq. No.
                  414310
Seq. ID
                  uC-osflcyp154e12b1
Method
                  BLASTX
NCBI GI
                  g322854
BLAST score
                  683
E value
                  5.0e-72
Match length
                  133
                  99
% identity
NCBI Description
                  pollen-specific protein - rice >gi 20310 emb CAA78897
                  (Z16402) pollen specific gene [Oryza sativa]
                  414311
Seq. No.
Seq. ID
                  uC-osflcyp154f01a1
Method
                  BLASTX
NCBI GI
                  g3334133
BLAST score
                  203
E value
                  4.0e-16
Match length
                  70
% identity
NCBI Description CYTOCHROME P450 89A2 (CYPLXXXIX) (ATH 6-1) >gi 1432145
```



(U61231) cytochrome P450 [Arabidopsis thaliana]

Seq. No. 414312

Seq. ID uC-osflcyp154f01b1

Method BLASTX
NCBI GI g3482918
BLAST score 645
E value 1.0e-67
Match length 137
% identity 91

NCBI Description (AC003970) Similar to ATP-citrate-lyase [Arabidopsis

thaliana]

Seq. No. 414313

Seq. ID uC-osflcyp154f02b1

Method BLASTX
NCBI GI g400803
BLAST score 547
E value 4.0e-56
Match length 125
% identity 83

NCBI Description 2,3-BISPHOSPHOGLYCERATE-INDEPENDENT PHOSPHOGLYCERATE MUTASE

(PHOSPHOGLYCEROMUTASE) (BPG-INDEPENDENT PGAM) (PGAM-I) >gi_283033_pir__A42807 phosphoglycerate mutase (EC 5.4.2.1), 2, 3-bisphosphoglycerate-independent - maize >gi_168588 (M80912) 2,3-bisphosphoglycerate-independent

phosphoglycerate mutase [Zea mays]

Seq. No. 414314

Seq. ID uC-osflcyp154f04b1

Method BLASTX
NCBI GI g3183094
BLAST score 432
E value 2.0e-42
Match length 96
% identity 84

NCBI Description ORNITHINE CARBAMOYLTRANSFERASE PRECURSOR (OTCASE)

(ORNITHINE TRANSCARBAMYLASE) >gi 971168 (U13684) ornithine

carbamoyltransferase [Pisum sativum]

Seq. No. 414315

Seq. ID uC-osflcyp154f05a1

Method BLASTX
NCBI GI g2198851
BLAST score 449
E value 1.0e-44
Match length 93
% identity 91

NCBI Description (AF007785) cystathionine gamma-synthase [Zea mays]

Seq. No. 414316

Seq. ID uC-osflcyp154f05b1

Method BLASTX
NCBI GI g2198851
BLAST score 634
E value 3.0e-66
Match length 127

% identity NCBI Description (AF007785) cystathionine gamma-synthase [Zea mays] Seq. No. 414317 Seq. ID uC-osflcyp154f06b1 Method BLASTX NCBI GI g6016075 BLAST score 261 E value 2.0e-26 Match length 96 % identity 68 GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC 2 NCBI Description >gi_312179_emb_CAA51676_ (X73151) glyceraldehyde 3-phosphate dehydrogenase (phosphorylating) [Zea mays] >gi_1184772 (U45855) cytosolic glyceroldehyde-3-phosphate
dehydrogenase GAPC2 [Zea mays] >gi_1185554 (U45858) glyceraldehyde-3-phosphate dehydrogenase [Zea mays] Seq. No. 414318 Seq. ID uC-osflcyp154f10b1 Method BLASTX NCBI GI g116054 BLAST score 671 1.0e-70 E value Match length 158 % identity 80 NCBI Description CALCIUM-DEPENDENT PROTEIN KINASE SK5 (CDPK) >gi_280393_pir__A43713 calcium-dependent protein kinase (EC 2.7.1.-) - soybean >gi 169931 (M64987) Glycine max calcium dependent protein kinase mRNA. [Glycine max] Seq. No. 414319 uC-osflcyp154f11b1 Seq. ID Method BLASTX NCBI GI g4895183 BLAST score 461 E value 5.0e-46Match length 150 58 % identity NCBI Description (AC007661) hypothetical protein [Arabidopsis thaliana] Seq. No. 414320 Seq. ID uC-osflcyp154f12a1 Method BLASTX NCBI GI g120668 BLAST score 514 E value 4.0e-52 109 Match length 91

% identity 91
NCBI Description GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC
>gi 82399 pir A24159 glyceraldehyde-3-phosphate

dehydrogenase (EC 1.2.1.12), cytosolic - barley (fragment)

>gi_167044 (M36650) glyceraldehyde-3-phosphate

dehydrogenase [Hordeum vulgare] >gi_225347_prf__1301218A dehydrogenase,glyceraldehydephosphate [Hordeum vulgare var.

distichum]

BLAST score

341

```
Seq. No.
                   414321
Seq. ID
                  uC-osflcyp154f12b1
Method
                  BLASTX
NCBI GI
                   g1184774
BLAST score
                  695
E value
                   2.0e-73
Match length
                  157
% identity
                   85
NCBI Description (U45856) cytosolic glyceroldehyde-3-phosphate dehydrogenase
                  GAPC3 [Zea mays]
Seq. No.
                   414322
Seq. ID
                  uC-osflcyp154q01b1
Method
                  BLASTX
NCBI GI
                  g2267139
BLAST score
                  178
E value
                   5.0e-13
Match length
                  40
% identity
                  80
NCBI Description (AF008910) ubiquitin-conjugating enzyme [Prunus armeniaca]
Seq. No.
                  414323
Seq. ID
                  uC-osflcyp154g02b1
Method
                  BLASTN
NCBI GI
                  q2773153
BLAST score
                  285
E value
                  1.0e-159
Match length
                  349
% identity
                  95
NCBI Description Oryza sativa abscisic acid- and stress-inducible protein
                   (Asr1) mRNA, complete cds
Seq. No.
                  414324
Seq. ID
                  uC-osflcyp154g03b1
Method
                  BLASTX
NCBI GI
                  g2832632
BLAST score
                  149
E value
                  1.0e-09
                  104
Match length
% identity
                  37
NCBI Description (AL021711) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  414325
Seq. ID
                  uC-osflcyp154g04b1
Method
                  BLASTX
NCBI GI
                  g3327204
BLAST score
                  279
                  1.0e-31
E value
Match length
                  132
% identity
                  58
NCBI Description (AB014595) KIAA0695 protein [Homo sapiens]
Seq. No.
                  414326
Seq. ID
                  uC-osflcyp154g05a1
Method
                  BLASTX
NCBI GI
                  g2499488
```

E value 8.0e-32 Match length 105 % identity 66 NCBI Description PYROPHOSPHATE--FRUCTOSE 6-PHOSPHATE 1-PHOSPHOTRANSFERASE ALPHA SUBUNIT (PFP) (6-PHOSPHOFRUCTOKINASE (PYROPHOSPHATE)) (PYROPHOSPHATE-DEPENDENT 6-PHOSPHOFRUCTOSE-1-KINASE) (PPI-PFK) >gi_483547_emb_CAA83682_ (Z32849) pyrophosphate-dependent phosphofructokinase alpha subunit [Ricinus communis] Seq. No. 414327 Seq. ID uC-osflcyp154g05b1 Method BLASTX NCBI GI q2499488 BLAST score 688 E value 1.0e-72 Match length 177 % identity 71 NCBI Description PYROPHOSPHATE--FRUCTOSE 6-PHOSPHATE 1-PHOSPHOTRANSFERASE ALPHA SUBUNIT (PFP) (6-PHOSPHOFRUCTOKINASE (PYROPHOSPHATE)) (PYROPHOSPHATE-DEPENDENT 6-PHOSPHOFRUCTOSE-1-KINASE) (PPI-PFK) >gi_483547_emb_CAA83682_ (Z32849) pyrophosphate-dependent phosphofructokinase alpha subunit [Ricinus communis] Seq. No. 414328 Seq. ID uC-osflcyp154q06b1 Method BLASTX NCBI GI g2833381 BLAST score 663 E value 2.0e-70 Match length 171 77 % identity NCBI Description GRANULE-BOUND GLYCOGEN (STARCH) SYNTHASE PRECURSOR >gi 1172159 (U44126) starch synthase [Ipomoea batatas] Seq. No. 414329 Seq. ID uC-osflcyp154q07a1 Method BLASTN NCBI GI g2773153 BLAST score 41 E value 9.0e-14 Match length 73 % identity 92 NCBI Description Oryza sativa abscisic acid- and stress-inducible protein (Asr1) mRNA, complete cds Seq. No. 414330 Seq. ID uC-osflcyp154g07b1

Method BLASTX NCBI GI g3935168 BLAST score 201 E value 1.0e-15 Match length 139 % identity

NCBI Description (AC004557) F17L21.11 [Arabidopsis thaliana]

Seq. ID

Method

```
Seq. No.
                   414331
Seq. ID
                   uC-osflcyp154g09a1
Method
                   BLASTX
NCBI GI
                   g3482918
BLAST score
                   449
E value
                   2.0e-44
Match length
                   96
% identity
                   89
NCBI Description
                  (AC003970) Similar to ATP-citrate-lyase [Arabidopsis
                   thaliana]
Seq. No.
                   414332
Seq. ID
                   uC-osflcyp154g09b1
Method
                   BLASTX
NCBI GI
                   q3024871
BLAST score
                   348
E value
                   8.0e-33
Match length
                   144
% identity
                   51
NCBI Description
                  HYPOTHETICAL 77.3 KD PROTEIN SLL0005
                   >gi_1001579_dbj_BAA10206_ (D64000) ABC1-like [Synechocystis
                   sp.]
Seq. No.
                   414333
Seq. ID
                   uC-osflcyp154g10b1
Method
                  BLASTX
NCBI GI
                   g1890575
BLAST score
                   518
E value
                   1.0e-52
Match length
                   106
% identity
                   90
NCBI Description
                  (X93174) xyloglucan endotransglycosylase (XET) [Hordeum
                   vulgare]
Seq. No.
                   414334
Seq. ID
                  uC-osflcyp154g12b1
Method
                  BLASTX
NCBI GI
                   q5080769
BLAST score
                  164
E value
                   3.0e-11
Match length
                  68
% identity
                   53
NCBI Description (AC007576) Unknown protein [Arabidopsis thaliana]
Seq. No.
                   414335
Seq. ID
                  uC-osflcyp154h01b1
Method
                  BLASTX
NCBI GI
                  g1350522
BLAST score
                  153
E value
                   6.0e-10
Match length
                  64
% identity
                   47
NCBI Description
                 (L47115) late embryogenesis abundant protein [Picea glauca]
Seq. No.
                  414336
```

54022

uC-osflcyp154h02b1

BLASTX

NCBI GI g6056421 BLAST score 277 E value 2.0e-24 Match length 116 % identity 49

NCBI Description (AC009525) Unknown protein [Arabidopsis thaliana]

Seq. No. 414337

Seq. ID uC-osflcyp154h03a1

Method BLASTX
NCBI GI g6056413
BLAST score 207
E value 3.0e-16
Match length 82
% identity 50

NCBI Description (AC009525) Unknown protein [Arabidopsis thaliana]

Seq. No. 414338

Seq. ID uC-osflcyp154h03b1

Method BLASTN
NCBI GI g4138731
BLAST score 39
E value 3.0e-12
Match length 194
% identity 56

NCBI Description Zea mays mRNA for proline-rich protein

Seq. No. 414339

Seq. ID uC-osflcyp154h04a1

Method BLASTX
NCBI GI g482311
BLAST score 233
E value 2.0e-19
Match length 48
% identity 96

NCBI Description photosystem II oxygen-evolving complex protein 1 - rice

(strain Nihonbare) >gi_739292 prf 2002393A oxygen-evolving

complex protein 1 [Oryza sativa]

Seq. No. 414340

Seq. ID uC-osflcyp154h04b1

Method BLASTX
NCBI GI g131388
BLAST score 547
E value 5.0e-56
Match length 164
% identity 69

NCBI Description OXYGEN-EVOLVING ENHANCER PROTEIN 1 PRECURSOR (OEE1) (33 KD

SUBUNIT OF OXYGEN EVOLVING SYSTEM OF PHOTOSYSTEM II) (33 KD

THYLAKOID MEMBRANE PROTEIN) >gi 100831 pir S16260

photosystem II oxygen-evolving complex protein 1 - common wheat x Sanduri wheat >gi_21844_emb_CAA40670_ (X57408) 33kDa oxygen evolving protein of photosystem II [Triticum

aestivum]

Seq. No. 414341

Seq. ID uC-osflcyp154h05b1

```
Method
                  BLASTX
NCBI GI
                  g5103837
BLAST score
                  343
E value
                  4.0e-32
Match length
                  100
                  67
% identity
NCBI Description
                  (AC007591) Simalar to gi 4377403 Polypeptide Deformylase
                  from Chlamydia pneumoniae genome gb_AE001687. [Arabidopsis
                  thaliana]
                  414342
Seq. No.
Seq. ID
                  uC-osflcyp154h06b1
Method
                  BLASTX
NCBI GI
                  g1652297
BLAST score
                  242
E value
                  3.0e-20
                  130
Match length
% identity
                  42
NCBI Description (D90904) hypothetical protein [Synechocystis sp.]
Seq. No.
                  414343
Seq. ID
                  uC-osflcyp154h08a1
Method
                  BLASTN
NCBI GI
                  q4138731
BLAST score
                  38
E value
                  9.0e-12
                  98
Match length
% identity
                  85
NCBI Description Zea mays mRNA for proline-rich protein
Seq. No.
                  414344
Seq. ID
                  uC-osflcyp154h09a1
Method
                  BLASTX
NCBI GI
                  g2267139
BLAST score
                  167
E value
                  1.0e-11
Match length
                  40
                  78
% identity
NCBI Description (AF008910) ubiquitin-conjugating enzyme [Prunus armeniaca]
Seq. No.
                  414345
Seq. ID
                  uC-osflcyp154h09b1
Method
                  BLASTX
NCBI GI
                  g3193292
BLAST score
                  402
E value
                  2.0e-41
Match length
                  157
% identity
                  54
NCBI Description
                 (AF069298) similar to ATPases associated with various
                  cellular activites (Pfam: AAA.hmm, score: 230.91)
                  [Arabidopsis thaliana]
```

Seq. No. 414346

Seq. ID uC-osflcyp154h10a1

Method BLASTX NCBI GI g1729971 BLAST score 454

Method

```
E value
                     3.0e-51
Match length
                    105
% identity
                    100
NCBI Description
                    TONOPLAST INTRINSIC PROTEIN, GAMMA (GAMMA TIP)
                    (AQUAPORIN-TIP) >gi_1076745_pir__S52004 gamma-Tip protein - rice >gi_473997_dbj_BAA05017_ (D25534) gamma-Tip [Oryza
                    sativa]
Seq. No.
                    414347
Seq. ID
                    uC-osflcyp154h10b1
Method
                    BLASTX
NCBI GI
                    q1729971
BLAST score
                    225
E value
                    8.0e-19
Match length
                    68
% identity
                    69
NCBI Description TONOPLAST INTRINSIC PROTEIN, GAMMA (GAMMA TIP)
                    (AQUAPORIN-TIP) >gi_1076745_pir__S52004 gamma-Tip protein - rice >gi_473997_dbj_BAA05017_ (D25534) gamma-Tip [Oryza
                    sativa]
Seq. No.
                    414348
Seq. ID
                    uC-osflcyp154h12b1
Method
                    BLASTX
NCBI GI
                    g627424
BLAST score
                    309
E value
                    4.0e-28
Match length
                    170
% identity
                    42
NCBI Description
                    dolichyl-diphosphooligosaccharide--protein glycotransferase
                    (EC 2.4.1.119) 50kD subunit - human >gi_2135018_pir__$66254
                    dolichyl-diphosphooligosaccharide--protein glycotransferase
                    (EC 2.4.1.119) 50K chain - human
Seq. No.
                    414349
Seq. ID
                    uC-osflcyp155a01b1
Method
                    BLASTX
NCBI GI
                    g6091726
BLAST score
                    172
E value
                    4.0e-12
Match length
                    84
% identity
NCBI Description (AC010797) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                    414350
Seq. ID
                    uC-osflcyp155a02b1
Method
                    BLASTX
NCBI GI
                    g4204300
BLAST score
                    285
E value
                    3.0e-25
Match length
                    116
% identity
NCBI Description
                   (AC003027) Unknown protein [Arabidopsis thaliana]
Seq. No.
                    414351
Seq. ID
```

54025

uC-osflcyp155a03b1

BLASTX

```
q6006867
NCBI GI
BLAST score
                    625
E value
                    4.0e-65
Match length
                   176
% identity
                   69
                  (AC009540) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   414352
Seq. ID
                   uC-osflcyp155a04b1
Method
                   BLASTX
NCBI GI
                   g1170937
BLAST score
                   837
E value
                   5.0e-90
Match length
                   162
% identity
                   99
NCBI Description
                   S-ADENOSYLMETHIONINE SYNTHETASE 1 (METHIONINE
                   ADENOSYLTRANSFERASE 1) (ADOMET SYNTHETASE 1)
                   >gi_450549 emb CAA81481 (Z26867) S-adenosyl methionine
                   synthetase [Oryza sativa]
Seq. No.
                   414353
Seq. ID
                   uC-osflcyp155a09b1
Method
                   BLASTX
NCBI GI
                   g129697
BLAST score
                   822
E value
                   3.0e-88
Match length
                   174
% identity
                   92
NCBI Description
                   PROLIFERATING CELL NUCLEAR ANTIGEN (PCNA) (CYCLIN)
                   >gi_100698_pir__S14415 proliferating cell nuclear antigen - rice >gi_20284_emb_CAA37979_ (X54046) proliferating cell
                   nuclear antigen [Oryza sativa]
Seq. No.
                   414354
Seq. ID
                   uC-osflcyp155a10b1
Method
                   BLASTX
NCBI GI
                   g1711036
BLAST score
                   491
E value
                   1.0e-49
Match length
                   133
% identity
NCBI Description
                   (U78952) hydroxyproline rich glycoprotein PsHRGP1 [Pisum
                   sativum]
Seq. No.
                   414355
Seq. ID
                   uC-osflcyp155b02b1
Method
                   BLASTX
NCBI GI
                   g3789952
BLAST score
                   824
E value
                   2.0e-88
```

Match length 171 % identity

NCBI Description (AF094775) chlorophyll a/b-binding protein presursor [Oryza

sativa]

Seq. No. 414356

Seq. ID uC-osflcyp155b03b1



Method BLASTX
NCBI GI g4895238
BLAST score 408
E value 1.0e-39
Match length 114
% identity 66

NCBI Description (AC007659) unknown protein [Arabidopsis thaliana]

Seq. No. 414357

Seq. ID uC-osflcyp155b05b1

Method BLASTX
NCBI GI g3582335
BLAST score 919
E value 1.0e-99
Match length 182
% identity 92

NCBI Description (AC005496) unknown protein [Arabidopsis thaliana]

Seq. No. 414358

Seq. ID uC-osflcyp155b06b1

Method BLASTX
NCBI GI g4455159
BLAST score 746
E value 2.0e-79
Match length 164
% identity 80

NCBI Description (AL021687) putative protein [Arabidopsis thaliana]

Seq. No. 414359

Seq. ID uC-osflcyp155b07b1

Method BLASTX
NCBI GI g124226
BLAST score 681
E value 1.0e-71
Match length 139
% identity 93

NCBI Description INITIATION FACTOR 5A-2 (EIF-5A) (EIF-4D)

>gi_100278_pir__S21059 translation initiation factor
eIF-5A.2 - curled-leaved tobacco >gi_19702_emb_CAA45104_
(X63542) eukaryotic initiation factor 5A (2) [Nicotiana

plumbaginifolia]

Seq. No. 414360

Seq. ID uC-osflcyp155b08b1

Method BLASTX
NCBI GI g1709846
BLAST score 503
E value 6.0e-51
Match length 139
% identity 42

NCBI Description PHOTOSYSTEM II 22 KD PROTEIN PRECURSOR >gi 706853 (U04336)

22 kDa component of photosystem II [Lycopersicon

esculentum]

Seq. No. 414361

Seq. ID uC-osflcyp155b09b1

Method BLASTX

```
g4960156
NCBI GI
                  295
BLAST score
                  2.0e-26
E value
                  104
Match length
                  55
% identity
                  (AF153284) putative progesterone-binding protein homolog
NCBI Description
                   [Arabidopsis thaliana]
                   414362
Seq. No.
                  uC-osflcyp155b11b1
Seq. ID
                  BLASTX
Method
                   g5903095
NCBI GI
                   504
BLAST score
                   4.0e-52
E value
                   174
Match length
                   65
% identity
                  (AC008017) Unknown protein [Arabidopsis thaliana]
NCBI Description
                   414363
Seq. No.
                   uC-osflcyp155b12b1
Seq. ID
                   BLASTX
Method
                   g3901268
NCBI GI
                   223
BLAST score
                   5.0e-18
E value
                   146
Match length
                   32
% identity
                  (AF060173) SV2 related protein [Rattus norvegicus]
NCBI Description
                   414364
Seq. No.
                   uC-osflcyp155c01b1
Seq. ID
                   BLASTX
Method
NCBI GI
                   g5031281
                   536
BLAST score
                   1.0e-54
E value
                   171
Match length
                   59
% identity
NCBI Description (AF139499) unknown [Prunus armeniaca]
                   414365
Seq. No.
                   uC-osflcyp155c03b1
Seq. ID
                   BLASTX
Method
NCBI GI
                   g3341443
                   257
BLAST score
                   5.0e-22
E value
                   120
Match length
 % identity
 NCBI Description (AJ223074) acid phosphatase [Glycine max]
 Seq. No.
                   414366
                   uC-osflcyp155c05b1
 Seq. ID
                   BLASTX
 Method
 NCBI GI
                   g1363051
                   270
 BLAST score
                   8.0e-24
 E value
                   114
 Match length
                    48
 % identity
 NCBI Description P58 protein - bovine >gi_468012 (U04631) PKR inhibitor P58
```

[Bos taurus] Seq. No. 414367 uC-osflcyp155c06b1 Seq. ID Method BLASTX NCBI GI g2832703 BLAST score 187 E value 9.0e-14Match length 66 58 % identity (AL021713) potassium channel protein KAT2 [Arabidopsis NCBI Description thaliana] 414368 Seq. No. Seq. ID uC-osflcyp155c07b1 BLASTX Method NCBI GI g4079811 BLAST score 181 4.0e-13 E value Match length 168 15 % identity NCBI Description (AF071173) Herc2 [Mus musculus] 414369 Seq. No. uC-osflcyp155c09b1 Seq. ID Method BLASTX q4415924 NCBI GI 237 BLAST score 1.0e-19 E value Match length 111 % identity 41 (AC006282) putative glucosyl transferase [Arabidopsis NCBI Description thaliana] Seq. No. 414370 Seq. ID uC-osflcyp155c10b1 Method BLASTX q5912299 NCBI GI 832 BLAST score 2.0e-89 E value Match length 169 % identity 98 NCBI Description (AJ133787) gigantea homologue [Oryza sativa] 414371 Seq. No. Seq. ID uC-osflcyp155c11b1 Method BLASTX NCBI GI g1370198 377 BLAST score 4.0e-36 E value Match length 113 71 % identity NCBI Description (Z73948) RAB8E [Lotus japonicus]

54029

414372

BLASTX

uC-osflcyp155c12b1

Seq. No. Seq. ID

Method

Method

NCBI GI

BLASTX

g2267006

```
q1171008
NCBI GI
                  457
BLAST score
E value
                  2.0e-45
                  120
Match length
% identity
                  66
                  POLLEN ALLERGEN PHL P 1 PRECURSOR (PHL P I)
NCBI Description
                  >gi 629812 pir__S44182 allergen Phl p I - common timothy
                  >gi 473360 emb CAA55390 (X78813) Phl p I allergen [Phleum
                  pratense]
                  414373
Seq. No.
                  uC-osflcyp155d01b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3608517
                  298
BLAST score
                  9.0e-27
E value
                  99
Match length
% identity
                  58
                  (AF090735) putative glycerol-3-phosphate acyltransferase
NCBI Description
                  [Cucurbita ficifolia]
Seq. No.
                  414374
                  uC-osflcyp155d02b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2865175
                  342
BLAST score
                  6.0e-32
E value
                  118
Match length
                  54
% identity
                  (AB010945) AtRer1A [Arabidopsis thaliana]
NCBI Description
                  >gi 4914434 emb CAB43637.1 (AL050351) AtRer1A [Arabidopsis
                  thaliana]
                  414375
Seq. No.
                  uC-osflcyp155d03b1
Seq. ID
                  BLASTX
Method
                  g6103623
NCBI GI
                  879
BLAST score
                  6.0e-95
E value
                  170
Match length
                  97
% identity
NCBI Description (AF172094) actin [Picea rubens]
                  414376
Seq. No.
Seq. ID
                  uC-osflcyp155d06b1
                  BLASTX
Method
                  q2624328
NCBI GI
BLAST score
                  508
                  1.0e-51
E value
                  113
Match length
                   88
% identity
NCBI Description (AJ002894) OsGRP2 [Oryza sativa]
                   414377
Seq. No.
Seq. ID
                  uC-osflcyp155d07b1
```

```
874
BLAST score
                  2.0e-94
E value
                  174
Match length
                  100
% identity
                  (AF006825) endosperm lumenal binding protein [Oryza sativa]
NCBI Description
                  414378
Seq. No.
                  uC-osflcyp155d08b1
Seq. ID
Method
                  BLASTX
                  q6041797
NCBI GI
BLAST score
                  347
E value
                  2.0e-32
                  143
Match length
                  47
% identity
NCBI Description (AC009755) unknown protein [Arabidopsis thaliana]
                  414379
Seq. No.
                  uC-osflcyp155d09b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q5007084
BLAST score
                   833
                   1.0e-89
E value
                  160
Match length
                   99
% identity
                  (AF155333) NADP-specific isocitrate dehydrogenase [Oryza
NCBI Description
                   sativa]
                   414380
Seq. No.
                   uC-osflcyp155d11b1
Seq. ID
                   BLASTX
Method
NCBI GI
                   q5679314
BLAST score
                   812
E value
                   4.0e-87
                   169
Match length
                   91
% identity
NCBI Description (AF164021) receptor kinase [Oryza sativa]
                   414381
Seq. No.
                   uC-osflcyp155e02b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g1353352
BLAST score
                   533
                   2.0e-54
E value
Match length
                   148
                   71
% identity
NCBI Description (U31975) alanine aminotransferase [Chlamydomonas
                   reinhardtii]
                   414382
Seq. No.
                   uC-osflcyp155e03b1
Seq. ID
                   BLASTX
Method
                   g3513744
NCBI GI
                   246
BLAST score
                   8.0e-21
E value
                   66
Match length
% identity
NCBI Description (AF080118) contains similarity to Medicago truncatula MtN3
```

(GB:Y08726) [Arabidopsis thaliana]

Seq. No. 414383 uC-osflcyp155e04b1 Seq. ID Method BLASTX NCBI GI g629561 BLAST score 242 E value 3.0e-20 Match length 153 % identity 35 SRG1 protein - Arabidopsis thaliana NCBI Description >gi_479047_emb_CAA55654_ (X79052) SRG1 [Arabidopsis
thaliana] >gi_5734767_gb_AAD50032.1_AC007651_27 (AC007651) SRG1 Protein [Arabidopsis thaliana] 414384 Seq. No. uC-osflcyp155e05b1 Seq. ID Method BLASTX NCBI GI g4836948 378 BLAST score E value 3.0e-36 Match length 82 % identity 90 (AC006085) Similar to human CGI-33 protein [Arabidopsis NCBI Description thaliana] 414385 Seq. No. Seq. ID uC-osflcyp155e07b1 Method BLASTN NCBI GI g5441876 BLAST score 37 4.0e-11 E value Match length 49 94 % identity NCBI Description Oryza sativa genomic DNA, chromosome 2, clone:P0437H03 (contig b) 414386 Seq. No. Seq. ID uC-osflcyp155e10b1 BLASTX Method NCBI GI g3928166 BLAST score 247 8.0e-21 E value 177 Match length % identity 31 NCBI Description (AJ010317) Sand [Fugu rubripes] 414387 Seq. No. uC-osflcyp155e11b1 Seq. ID BLASTXMethod NCBI GI g3928089 190 BLAST score 3.0e-14 E value 149 Match length

NCBI Description (AC005770) putative osr40 [Arabidopsis thaliana]

33

% identity

Seq. ID

```
414388
Seq. No.
Seq. ID
                  uC-osflcyp155e12b1
Method
                  BLASTX
NCBI GI
                  q2281089
BLAST score
                  344
                  3.0e-32
E value
                  79
Match length
                  82
% identity
                  (AC002333) Sm protein F isolog [Arabidopsis thaliana]
NCBI Description
                  414389
Seq. No.
                  uC-osflcyp155f01b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3551249
BLAST score
                  145
E value
                  7.0e-09
                  165
Match length
                  30
% identity
NCBI Description (AB012704) 184 [Daucus carota]
                  414390
Seq. No.
                  uC-osflcyp155f02b1
Seq. ID
Method
                  BLASTX
                  g1495366
NCBI GI
BLAST score
                  469
                  6.0e-47
E value
Match length
                  155
                  60
% identity
NCBI Description (Z69370) nitrite transporter [Cucumis sativus]
                  414391
Seq. No.
                  uC-osflcyp155f04b1
Seq. ID
                  BLASTX
Method
NCBI GI
                  q3885896
BLAST score
                  509
E value
                   1.0e-51
Match length
                  111
                   91
% identity
NCBI Description (AF093636) plastocyanin precursor [Oryza sativa]
Seq. No.
                   414392
                   uC-osflcyp155f05b1
Seq. ID
Method
                  BLASTX
NCBI GI
                   g400890
                   303
BLAST score
E value
                   2.0e-27
Match length
                   66
% identity
                   46
                  PHOTOSYSTEM II 22 KD PROTEIN PRECURSOR
NCBI Description
                   >gi_282837_pir__S26953 photosystem II 22K protein precursor
                   - spinach >qi 21307 emb CAA48557 (X68552) 22kD-protein of
                   PSII [Spinacia oleracea] >gi_260917_bbs_119338 (S49864)
                   photosystem II 22 kda polypeptide [spinach, Peptide, 274
                   aa] [Spinacia oleracea]
Seq. No.
                   414393
```

54033

uC-osflcyp155f07b1

BLASTX Method NCBI GI q2505865 519 BLAST score E value 7.0e-53145 Match length 25 % identity (Y12227) putative topoisomerase [Arabidopsis thaliana] NCBI Description 414394 Seq. No. uC-osflcyp155f09b1 Seq. ID Method BLASTX q5733874 NCBI GI 330 BLAST score 1.0e-30 E value Match length 165 % identity 42 (AC007932) F11A17.8 [Arabidopsis thaliana] NCBI Description 414395 Seq. No. uC-osflcyp155f10b1 Seq. ID Method BLASTX NCBI GI q4567271 BLAST score 192 E value 2.0e-14 161 Match length % identity 36 (AC006841) putative kinesin protein [Arabidopsis thaliana] NCBI Description 414396 Seq. No. Seq. ID uC-osflcyp155f12b1 Method BLASTX NCBI GI q3023713 BLAST score 739 2.0e-78 E value Match length 158 % identity 92 ENOLASE (2-PHOSPHOGLYCERATE DEHYDRATASE) NCBI Description (2-PHOSPHO-D-GLYCERATE HYDRO-LYASE) (OSE1) >gi_780372 (U09450) enolase [Oryza sativa] Seq. No. 414397 uC-osflcyp155g01b1 Seq. ID Method BLASTX g3776559 NCBI GI BLAST score 567 E value 6.0e-63

Match length 152 80 % identity

(ACO05388) Strong similarity to gene F14J9.26 gi_3482933 NCBI Description

cdc2 protein kinase homolog from A. thaliana BAC

gb_AC003970. ESTs gb_Z35332 and gb_F19907 come from this

gene. [Arabidopsis thaliana]

414398 Seq. No.

uC-osflcyp155g03b1 Seq. ID

Method BLASTX NCBI GI g2196878

```
BLAST score
                  1.0e-63
E value
                  147
Match length
                  73
% identity
                  (Y08292) NADH glutamate dehydrogenase [Nicotiana
NCBI Description
                  plumbaginifolia]
                  414399
Seq. No.
Seq. ID
                  uC-osflcyp155g04b1
Method
                  BLASTX
NCBI GI
                  g1710551
                  277
BLAST score
                  2.0e-24
E value
Match length
                  51
                  98
% identity
                  60S RIBOSOMAL PROTEIN L39 >qi 1177369 emb CAA64728.1
NCBI Description
                   (X95458) ribosomal protein L3\overline{9} [Zea mays]
                   414400
Seq. No.
                  uC-osflcyp155g06b1
Seq. ID
Method
                  BLASTX
NCBI GI
                   g2331131
BLAST score
                   198
E value
                   2.0e-22
Match length
                   86
% identity
                   73
NCBI Description (AF010579) glycine-rich protein [Oryza sativa]
                   414401
Seq. No.
                  uC-osflcyp155g07b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2293480
BLAST score
                   431
E value
                   2.0e-42
Match length
                   85
% identity
                   98
NCBI Description (AF011331) glycine-rich protein [Oryza sativa]
                   414402
Seq. No.
                   uC-osflcyp155g08b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g5902387
BLAST score
                   282
                   6.0e-25
E value
                   160
Match length
% identity
                   38
                  (AC009322) Similar to polygalacturonases [Arabidopsis
NCBI Description
                   thaliana]
                   414403
Seq. No.
Seq. ID
                   uC-osflcyp155g09b1
```

Method BLASTX
NCBI GI g4033424
BLAST score 701
E value 4.0e-74
Match length 154
% identity 84



SOLUBLE INORGANIC PYROPHOSPHATASE (PYROPHOSPHATE NCBI Description

PHOSPHO-HYDROLASE) (PPASE) >gi_2668746 (AF034947) inorganic

pyrophosphatase [Zea mays]

414404 Seq. No.

uC-osflcyp155g12b1 Seq. ID

Method BLASTX NCBI GI g5295980 BLAST score 678 3.0e-78E value Match length 152 98 % identity

NCBI Description (AB003323) MADS box-like protein [Oryza sativa]

414405 Seq. No.

Seq. ID uC-osflcyp155h02b1

Method BLASTX NCBI GI q4337177 BLAST score 610 E value 2.0e-63 Match length 164 71 % identity

(AC006416) Identical to gb_Y10557 g5bf gene from NCBI Description

Arabidopsis thaliana. ESTs gb_R30578, gb_R90475, gb_T22384, gb_T22425, gb_N64934 and gb_T46767 come from

this gene. [Arabidopsis thaliana]

414406 Seq. No.

uC-osflcyp155h03b1 Seq. ID

BLASTX Method NCBI GI q3913018 BLAST score 580 3.0e-64 E value Match length 143 % identity 95

FRUCTOSE-BISPHOSPHATE ALDOLASE, CHLOROPLAST PRECURSOR NCBI Description

(ALDP) >gi_218155_dbj_BAA02730_ (D13513) chloroplastic

aldolase [Oryza sativa]

414407 Seq. No.

uC-osflcyp155h04b1 Seq. ID

Method BLASTX NCBI GI g3687251 BLAST score 243 2.0e-20 E value Match length 89 % identity 58

NCBI Description (AC005169) unknown protein [Arabidopsis thaliana]

414408 Seq. No.

Seq. ID uC-osflcyp155h05b1

BLASTX Method NCBI GI g2493131 BLAST score 746 E value 2.0e-79 Match length 151 % identity 98



NCBI Description VACUOLAR ATP SYNTHASE SUBUNIT B ISOFORM 1 (V-ATPASE B SUBUNIT) >gi_167108 (L11862) vacuolar ATPase B subunit [Hordeum vulgare]

Seq. No. 414409

Seq. ID uC-osflcyp155h08b1

Method BLASTX
NCBI GI g6016151
BLAST score 633
E value 3.0e-81
Match length 166
% identity 92

NCBI Description IMMUNOGLOBULIN BINDING PROTEIN HOMOLOG 3 PRECURSOR (HEAT

SHOCK PROTEIN 70 HOMOLOG 3) >gi 1575130 (U58209) lumenal

binding protein cBiPe3 [Zea mays]

Seq. No. 414410

Seq. ID uC-osflcyp155h12b1

Method BLASTX
NCBI GI g2498726
BLAST score 240
E value 5.0e-20
Match length 165
% identity 38

NCBI Description DOLICHYL-DIPHOSPHOOLIGOSACCHARIDE--PROTEIN

GLYCOSYLTRANSFERASE 48 KD SUBUNIT PRECURSOR (OLIGOSACCHARYL TRANSFERASE 48 KD SUBUNIT) (DDOST 48 KD SUBUNIT) (OST5OP) >gi 1085153 pir__JC4132 oligosaccharyltransferase 50k chain

- fruit fly (Drosophila melanogaster) >gi 1019386_emb_CAA57525_ (X81999)

oligosaccharyltransferase subunit [Drosophila melanogaster]

Seq. No. 414411

Seq. ID uC-osflcyp156a01b1

Method BLASTX
NCBI GI g1805654
BLAST score 449
E value 1.0e-44
Match length 154
% identity 56

NCBI Description (X99972) calmodulin-stimulated calcium-ATPase [Brassica

oleracea]

Seq. No. 414412

Seq. ID uC-osflcyp156a02b1

Method BLASTX
NCBI GI g1173347
BLAST score 682
E value 7.0e-72
Match length 140
% identity 94

NCBI Description SEDOHEPTULOSE-1,7-BISPHOSPHATASE, CHLOROPLAST PRECURSOR

(SEDOHEPTULOSE-BISPHOSPHATASE) (SBPASE) (SED(1,7)P2ASE) >gi_100803_pir__S23452 sedoheptulose-bisphosphatase (EC 3.1.3.37) precursor - wheat >gi_14265_emb_CAA46507_ (X65540) sedoheptulose-1,7-bisphosphatase [Triticum

aestivum]

Method

BLASTX

```
Seq. No.
                   414413
Seq. ID
                  uC-osflcyp156a03b1
Method
                  BLASTX
NCBI GI
                  g4337178
                  191
BLAST score
E value
                   2.0e-14
Match length
                  56
% identity
                   70
NCBI Description
                  (AC006416) T31J12.5 [Arabidopsis thaliana]
Seq. No.
                   414414
Seq. ID
                  uC-osflcyp156a04a1
Method
                  BLASTN
NCBI GI
                  g5714761
BLAST score
                  55
E value
                   6.0e-22
Match length
                  130
% identity
                   58
NCBI Description
                  Oryza sativa subsp. indica serine/threonine protein
                  phosphatase PP2A-4 catalytic subunit (PP2A) gene, complete
Seq. No.
                   414415
Seq. ID
                  uC-osflcyp156a07b1
Method
                  BLASTX
NCBI GI
                  g1814403
BLAST score
                   648
E value
                   6.0e-68
Match length
                  152
% identity
                   84
                  (U84889) methionine synthase [Mesembryanthemum
NCBI Description
                  crystallinum]
Seq. No.
                   414416
Seq. ID
                  uC-osflcyp156a08b1
Method
                  BLASTX
NCBI GI
                  q4337178
BLAST score
                  534
E value
                  2.0e-54
                  122
Match length
% identity
                  81
NCBI Description (AC006416) T31J12.5 [Arabidopsis thaliana]
Seq. No.
                  414417
Seq. ID
                  uC-osflcyp156a10b1
Method
                  {\tt BLASTX}
NCBI GI
                  g5051780
BLAST score
                  187
E value
                  8.0e-31
Match length
                  106
                  62
% identity
NCBI Description
                  (AL078637) putative protein [Arabidopsis thaliana]
Seq. No.
                  414418
Seq. ID
                  uC-osflcyp156a11a1
```

q548770 NCBI GI BLAST score 180 E value 2.0e-13 35 Match length 100 % identity

NCBI Description 60S RIBOSOMAL PROTEIN L3 >gi 481228 pir S38359 ribosomal

protein L3 - rice >gi_303853_dbj_BAA02155_ (D12630)

ribosomal protein L3 [Oryza sativa]

414419 Seq. No.

Seq. ID uC-osflcyp156a11b1

Method BLASTX NCBI GI g548770 BLAST score 755 2.0e-80 E value Match length 145 99 % identity

NCBI Description 60S RIBOSOMAL PROTEIN L3 >gi 481228 pir S38359 ribosomal

protein L3 - rice >gi_303853_dbj_BAA02155_ (D12630)

ribosomal protein L3 [Oryza sativa]

414420 Seq. No.

Seq. ID uC-osflcyp156a12b1

Method BLASTX NCBI GI g399940 BLAST score 572 E value 4.0e-59 Match length 139 % identity 80

HEAT SHOCK 70 KD PROTEIN, MITOCHONDRIAL PRECURSOR NCBI Description

>gi_100004_pir__S25005 heat shock protein, 70K - kidney bean >gi_22636_emb_CAA47345_ (X66874) 70 kDa heat shock protein [Phaseolus vulgaris]

414421 Seq. No.

Seq. ID uC-osflcyp156b02b1

Method BLASTX NCBI GI g1431622 BLAST score 738 2.0e-78 E value Match length 158 % identity 87

NCBI Description (X99100) protein kinase [Trifolium repens]

Seq. No. 414422

Seq. ID uC-osflcyp156b03a1

Method BLASTX NCBI GI q5541704 BLAST score 151 E value 7.0e-10 Match length 42 % identity 71

NCBI Description (AL096860) 40S RIBOSOMAL PROTEIN S20 homolog [Arabidopsis

thaliana]

414423 Seq. No.

Seq. ID uC-osflcyp156b03b1

E value

6.0e-25

```
Method
                  BLASTX
NCBI GI
                  q5541704
BLAST score
                  472
E value
                  3.0e-47
Match length
                  103
                  87
% identity
NCBI Description
                  (AL096860) 40S RIBOSOMAL PROTEIN S20 homolog [Arabidopsis
                  thaliana]
                  414424
Seq. No.
Seq. ID
                  uC-osflcyp156b04a1
Method
                  BLASTX
NCBI GI
                  q4262152
BLAST score
                  393
E value
                   5.0e - 38
Match length
                  95
% identity
                  73
NCBI Description
                  (AC005275) putative frataxin-like protein [Arabidopsis
                  thaliana]
Seq. No.
                  414425
Seq. ID
                  uC-osflcyp156b04b1
Method
                  BLASTX
NCBI GI
                  q4262152
BLAST score
                  187
E value
                  7.0e-14
Match length
                  49
% identity
                   69
                  (AC005275) putative frataxin-like protein [Arabidopsis
NCBI Description
                  thaliana]
                   414426
Seq. No.
Seq. ID
                  uC-osflcyp156b07b1
Method
                  BLASTX
NCBI GI
                  q3176717
BLAST score
                  195
                  8.0e-15
E value
                  94
Match length
% identity
                   43
NCBI Description (AC002392) putative pectinesterase [Arabidopsis thaliana]
                   414427
Seq. No.
Seq. ID
                  uC-osflcyp156b09a1
Method
                  BLASTX
NCBI GI
                  g1261917
BLAST score
                  188
                   4.0e-14
E value
Match length
                  43
                  79
% identity
NCBI Description (X96979) lipid transfer protein 7a2b [Hordeum vulgare]
Seq. No.
                  414428
Seq. ID
                  uC-osflcyp156b09b1
Method
                  BLASTX
NCBI GI
                  q2618691
BLAST score
                  281
```





```
Match length
% identity
                  62
                  (AC002510) putative chloroplast envelope Ca2+-ATPase
NCBI Description
                   [Arabidopsis thaliana]
                  414429
Seq. No.
Seq. ID
                  uC-osflcyp156b10a1
Method
                  BLASTX
NCBI GI
                  g4262157
BLAST score
                  324
                  6.0e-30
E value
Match length
                  120
% identity
                  54
NCBI Description (AC005275) putative calmodulin [Arabidopsis thaliana]
Seq. No.
                  414430
                  uC-osflcyp156b10b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4262157
BLAST score
                  244
E value
                  1.0e-20
Match length
                  105
% identity
                  49
NCBI Description (AC005275) putative calmodulin [Arabidopsis thaliana]
Seq. No.
                  414431
Seq. ID
                  uC-osflcyp156b11b1
Method
                  BLASTX
NCBI GI
                  g6091756
BLAST score
                  180
E value
                  4.0e-25
Match length
                  113
% identity
                  53
NCBI Description (AC009327) putative peroxidase [Arabidopsis thaliana]
                  414432
Seq. No.
Seq. ID
                  uC-osflcyp156b12b1
Method
                  BLASTX
NCBI GI
                  g2244935
BLAST score
                  189
                  4.0e-14
E value
Match length
                  94
% identity
                  39
NCBI Description (Z97339) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  414433
Seq. ID
                  uC-osflcyp156c02b1
```

Method BLASTX NCBI GI g6091750 BLAST score 217 2.0e-17 E value Match length 153 % identity

NCBI Description (AC009992) unknown protein [Arabidopsis thaliana]

414434 Seq. No.

Seq. ID uC-osflcyp156c03b1

% identity

97

NCBI Description (AJ243961) 11332.8 [Oryza sativa]

```
BLASTX
Method
NCBI GI
                   g1915960
BLAST score
                   543
E value
                   1.0e-55
Match length
                   179
                   39
% identity
NCBI Description (Y07636) peptidylprolyl isomerase [Triticum aestivum]
Seq. No.
                   414435
Seq. ID
                   uC-osflcyp156c04a1
Method
                   BLASTX
NCBI GI
                   g2645999
BLAST score
                   293
E value
                   2.0e-26
Match length
                   67
                   85
% identity
                  (AF034631) chlorophyll a/b binding protein of LHCII type I
NCBI Description
                   precursor [Panax ginseng]
Seq. No.
                   414436
                   uC-osflcyp156c04b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   q320618
BLAST score
                   633
E value
                   4.0e-66
Match length
                   137
% identity
                   88
                   chlorophyll a/b-binding protein I precursor - rice
NCBI Description
                   >gi_218172_dbj_BAA00536_ (D00641) type I light-harvesting chlorophyll a/b-binding protein [Oryza sativa]
                   >gi 227611_prf_ 1707316A chlorophyll a/b binding protein 1
                   [Oryza sativa]
                   414437
Seq. No.
Seq. ID
                   uC-osflcyp156c06b1
Method
                   BLASTX
NCBI GI
                   g115772
BLAST score
                   246
                   6.0e-21
E value
Match length
                   69
                   81
% identity
NCBI Description CHLOROPHYLL A-B BINDING PROTEIN 1 PRECURSOR (LHCII TYPE I
                   CAB-1) (LHCP) >gi 82460 pir S03705 chlorophyll a/b-binding
                   protein 1R precursor - rice >gi 20178 emb CAA32108
                   (X13908) chlorophyll a/b-binding preprotein (AA -31 to 235)
                   [Oryza sativa]
                   414438
Seq. No.
Seq. ID
                   uC-osflcyp156c07a1
Method
                   BLASTX
NCBI GI
                   g5679844
BLAST score
                   473
E value
                   2.0e-47
Match length
                   88
```

414439 Seq. No. uC-osflcyp156c07b1 Seq. ID Method BLASTX g5852098 NCBI GI BLAST score 462 E value 1.0e-60 Match length 153 81 % identity NCBI Description (AL117264) zwh21.1 [Oryza sativa] Seq. No. 414440 Seq. ID uC-osflcyp156c08b1 Method BLASTX NCBI GI g5912299 BLAST score 832 2.0e-89 E value Match length 166 99 % identity NCBI Description (AJ133787) gigantea homologue [Oryza sativa] Seq. No. 414441 uC-osflcyp156c09b1 Seq. ID Method BLASTX NCBI GI g3309243 BLAST score 529 E value 4.0e-54 Match length 133 80 % identity (AF073507) aconitase-iron regulated protein 1 [Citrus NCBI Description limon] 414442 Seq. No. uC-osflcyp156c10a1 Seq. ID Method BLASTX NCBI GI g1084455 161 BLAST score 6.0e-11 E value 35 Match length % identity 94 NCBI Description peptidylprolyl isomerase (EC 5.2.1.8) Cyp2 - rice >gi_600767 (L29469) cyclophilin 2 [Oryza sativa] 414443 Seq. No. Seq. ID uC-osflcyp156c10b1 Method BLASTX q1084455 NCBI GI 374 BLAST score 8.0e-70 E value 133 Match length 99 % identity NCBI Description peptidylprolyl isomerase (EC 5.2.1.8) Cyp2 - rice >gi 600767 (L29469) cyclophilin 2 [Oryza sativa] 414444 Seq. No. Seq. ID uC-osflcyp156c11a1 Method BLASTX

54043

g115787

NCBI GI

BLAST score 432 1.0e-42E value 82 Match length 100 % identity CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I NCBI Description CAB-2) (LHCP) >gi_82461_pir__S03706 chlorophyll a/b-binding protein 2R precursor - rice >gi 20182 emb CAA32109 (X13909) chlorophyll a/b-binding preprotein (AA -28 to 235) [Oryza sativa] Seq. No. 414445 Seq. ID uC-osflcyp156c11b1 BLASTX Method NCBI GI g320618 BLAST score 380 6.0e-67 E value Match length 146 89 % identity chlorophyll a/b-binding protein I precursor - rice NCBI Description >gi_218172_dbj_BAA00536_ (D00641) type I light-harvesting chlorophyll a/b-binding protein [Oryza sativa] >gi 227611 prf 1707316A chlorophyll a/b binding protein 1 [Oryza sativa] 414446 Seq. No. Seq. ID uC-osflcyp156c12a1 Method BLASTX NCBI GI g1084455 350 BLAST score E value 6.0e-33 Match length 66 100 % identity NCBI Description peptidylprolyl isomerase (EC 5.2.1.8) Cyp2 - rice >gi 600767 (L29469) cyclophilin 2 [Oryza sativa] 414447 Seq. No. Seq. ID uC-osflcyp156c12b1 Method BLASTX NCBI GI g1084455 BLAST score 697 E value 1.0e-73

Match length 143 % identity 92

NCBI Description peptidylprolyl isomerase (EC 5.2.1.8) Cyp2 - rice >gi 600767 (L29469) cyclophilin 2 [Oryza sativa]

Seq. No. 414448

Seq. ID uC-osflcyp156d01b1

Method BLASTX NCBI GI g1742951 BLAST score 853 E value 6.0e-92 Match length 174 % identity 90

NCBI Description (Y09817) Ca2+-ATPase [Arabidopsis thaliana]

Seq. No. 414449

Seq. ID uC-osflcyp156d02b1 Method BLASTX NCBI GI q3236242 BLAST score 427 E value 5.0e-42 Match length 104 % identity NCBI Description (AC004684) putative ribosomal protein L36 [Arabidopsis thaliana] Seq. No. 414450 Seq. ID uC-osflcyp156d03a1 Method BLASTX NCBI GI g4531442 BLAST score 201 E value 2.0e-15 Match length 45 % identity 80 NCBI Description (AC006224) hypothetical protein [Arabidopsis thaliana] Seq. No. 414451 Seq. ID uC-osflcyp156d03b1 Method BLASTX NCBI GI g4531442 BLAST score 459 E value 1.0e-45 Match length 173 % identity 54 NCBI Description (AC006224) hypothetical protein [Arabidopsis thaliana] Seq. No. 414452 Seq. ID uC-osflcyp156d04a1 Method BLASTN NCBI GI q968995 BLAST score 67 E value 2.0e-29 Match length 127 % identity 88 NCBI Description Oryza sativa clone glyceraldehyde-3-phosphate dehydrogenase (Gpc) mRNA, complete cds 414453 Seq. No. Seq. ID uC-osflcyp156d04b1 Method BLASTN NCBI GI q2072554 BLAST score 310 E value 1.0e-174 Match length 390 % identity 95 NCBI Description Oryza sativa metallothionein-like protein mRNA, complete

Seq. No. 414454

Seq. ID uC-osflcyp156d05a1

Method BLASTX
NCBI GI g2914700
BLAST score 152

NCBI Description

```
6.0e-10
E value
Match length
                  76
% identity
                  45
NCBI Description
                  (AC003974) tRNA-processing protein SEN3-like [Arabidopsis
                  thaliana]
Seq. No.
                  414455
Seq. ID
                  uC-osflcyp156d05b1
Method
                  BLASTX
NCBI GI
                  g2914700
BLAST score
                  553
E value
                  9.0e-57
Match length
                  174
% identity
                  68
NCBI Description (AC003974) tRNA-processing protein SEN3-like [Arabidopsis
                  thaliana]
Seq. No.
                  414456
Seq. ID
                  uC-osflcyp156d07b1
Method
                  BLASTN
NCBI GI
                  g429007
BLAST score
                  38
E value
                  8.0e-12
Match length
                  78
                  87
% identity
NCBI Description Rice mRNA for Ca+2-ATPase (gene name SS304), partial cds
Seq. No.
                  414457
Seq. ID
                  uC-osflcyp156d08a1
Method
                  BLASTX
NCBI GI
                  g2267593
BLAST score
                  226
E value
                  2.0e-18
Match length
                  47
% identity
NCBI Description (AF009411) glycine-rich RNA-binding protein [Oryza sativa]
Seq. No.
                  414458
Seq. ID
                  uC-osflcyp156d08b1
Method
                  BLASTX
NCBI GI
                  q2293480
BLAST score
                  437
E value
                  3.0e-43
Match length
                  85
% identity
NCBI Description (AF011331) glycine-rich protein [Oryza sativa]
Seq. No.
                  414459
Seq. ID
                  uC-osflcyp156d09b1
Method
                  BLASTX
NCBI GI
                  g3548808
BLAST score
                  360
E value
                  4.0e-34
Match length
                  153
% identity
```

(AC005313) unknown protein [Arabidopsis thaliana]

Match length

156

```
Seq. No.
                   414460
Seq. ID
                   uC-osflcyp156d10a1
Method
                   BLASTX
NCBI GI
                   g3023816
BLAST score
                   164
E value
                   2.0e-11
Match length
                   35
% identity
                   86
                   GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC
NCBI Description
                   >gi 968996 (U31676) glyceraldehyde-3-phosphate
                   dehydrogenase [Oryza sativa]
Seq. No.
                   414461
Seq. ID
                   uC-osflcyp156d11a1
Method
                   BLASTX
NCBI GI
                   g6015059
BLAST score
                   440
E value
                   2.0e-43
Match length
                   87
                   100
% identity
NCBI Description ELONGATION FACTOR 1-ALPHA (EF-1-ALPHA) >gi 2996096
                   (AF030517) translation elongation factor-1 alpha; EF-1
                   alpha [Oryza sativa]
Seq. No.
                   414462
Seq. ID
                   uC-osflcyp156d11b1
Method
                   BLASTX
NCBI GI
                   g119150
BLAST score
                   935
E value
                   1.0e-101
Match length
                   177
                   99
% identity
NCBI Description ELONGATION FACTOR 1-ALPHA (EF-1-ALPHA)
                   >gi_82081_pir__S10507 translation elongation factor eEF-1 alpha chain - tomato >gi_19273_emb_CAA32618_ (X14449) EF
                   1-alpha (AA 1-448) [Lycopersicon esculentum]
                   >gi 295810 emb CAA37212 (X53043) elongation factor 1-alpha
                   [Lycopersicon esculentum]
                   414463
Seq. No.
Seq. ID
                   uC-osflcyp156e02a1
Method
                   BLASTN
NCBI GI
                   g1917018
BLAST score
                   73
                   1.0e-32
E value
Match length
                   125
% identity
                   90
NCBI Description Zea mays ribosomal protein S6 RPS6-1 (rps6-1) mRNA,
                   complete cds
Seq. No.
                   414464
Seq. ID
                   uC-osflcyp156e02b1
Method
                   BLASTX
NCBI GI
                   g1917019
BLAST score
                   634
                   3.0e-66
E value
```

Seq. No.

414470

```
% identity
NCBI Description (U92045) ribosomal protein S6 RPS6-1 [Zea mays]
                  414465
Seq. No.
                  uC-osflcyp156e06b1
Seq. ID
                  BLASTX
Method
NCBI GI
                  g4725948
BLAST score
                  233
E value
                  2.0e-19
Match length
                  53
                  81
% identity
NCBI Description (AL049730) pEARLI 1-like protein [Arabidopsis thaliana]
                  414466
Seq. No.
Seq. ID
                  uC-osflcyp156e10b1
Method
                  BLASTX
NCBI GI
                  g4097547
BLAST score
                  224
E value
                  3.0e-18
Match length
                  110
% identity
                  46
NCBI Description (U64906) ATFP3 [Arabidopsis thaliana]
                  414467
Seq. No.
Seq. ID
                  uC-osflcyp156e11b1
Method
                  BLASTX
NCBI GI
                  g4335756
BLAST score
                  348
E value
                  1.0e-32
Match length
                  136
                  50
% identity
NCBI Description (AC006284) putative ankyrin [Arabidopsis thaliana]
Seq. No.
                  414468
Seq. ID
                  uC-osflcyp156e12b1
                  BLASTX
Method
NCBI GI
                  g2072555
BLAST score
                  237
E value
                  1.0e-19
Match length
                  44
                  100
% identity
                  (AF001396) metallothionein-like protein [Oryza sativa]
NCBI Description
                  >gi_6103441 gb AAF03603.1 (AF147786) metallothionein-like
                  protein [Oryza sativa]
Seq. No.
                  414469
Seq. ID
                  uC-osflcyp156f03b1
Method
                  BLASTN
NCBI GI
                  g1737491
BLAST score
                  139
                  4.0e-72
E value
Match length
                  360
                  85
% identity
NCBI Description
                  Triticum aestivum poly(A)-binding protein (wheatpab) mRNA,
                  complete cds
```

```
Seq. ID
                   uC-osflcyp156f06b1
Method
                  BLASTX
NCBI GI
                   g100490
BLAST score
                  757
E value
                   1.0e-80
Match length
                   153
% identity
                   34
NCBI Description polyubiquitin - garden snapdragon (fragment)
                  >gi_16071 emb CAA48140 (X67957) ubiquitin [Antirrhinum
                  majus]
Seq. No.
                   414471
Seq. ID
                  uC-osflcyp156f07b1
Method
                  BLASTX
NCBI GI
                  q729135
BLAST score
                  277
E value
                  9.0e-25
Match length
                  87
% identity
                  66
NCBI Description CAFFEIC ACID 3-O-METHYLTRANSFERASE
                   (S-ADENOSYSL-L-METHIONINE: CAFFEIC ACID
                  3-O-METHYLTRANSFERASE) (COMT) >gi_283034_pir__$28612
                  catechol O-methyltransferase (EC 2.1.1.6) - maize
                  >qi 168532 (M73\bar{2}35) O-methyltransferase [Zea mays]
Seq. No.
                  414472
Seq. ID
                  uC-osflcyp156f08a1
Method
                  BLASTX
NCBI GI
                  q729944
BLAST score
                  229
E value
                  6.0e-19
Match length
                  54
% identity
                  74
NCBI Description
                  POLLEN ALLERGEN ZEA M 1 (ZEA M I) >gi 478272 pir JC1524
                  major allergen mI protein - maize >gi 293902 (L14271) Zea
                  mI [Zea mays]
Seq. No.
                  414473
Seq. ID
                  uC-osflcyp156f08b1
Method
                  BLASTX
NCBI GI
                  g1171008
BLAST score
                  460
E value
                  7.0e-46
Match length
                  120
% identity
                  66
NCBI Description
                  POLLEN ALLERGEN PHL P 1 PRECURSOR (PHL P I)
                  >gi 629812 pir S44182 allergen Phl p I - common timothy
                  >gi_473360_emb_CAA55390_ (X78813) Phl p I allergen [Phleum
                  pratense]
Seq. No.
                  414474
Seq. ID
                  uC-osflcyp156f09b1
Method
                  BLASTX
NCBI GI
                  g3021357
BLAST score
                  691
E value
                  6.0e-73
Match length
                  158
```

```
% identity
                  (AJ005082) UDP-galactose 4-epimerase [Cyamopsis
NCBI Description
                  tetragonoloba]
                  414475
Seq. No.
Seq. ID
                  uC-osflcyp156g01b1
Method
                  BLASTX
NCBI GI
                  g4455172
BLAST score
                  148
                  2.0e-12
E value
                  95
Match length
                  50
% identity
NCBI Description (AL035521) putative protein [Arabidopsis thaliana]
                  414476
Seq. No.
                  uC-osflcyp156g02b1
Seq. ID
                  BLASTX
Method
NCBI GI
                  g1370603
                  392
BLAST score
                  9.0e-43
E value
                  132
Match length
% identity
                  65
NCBI Description (X98245) annexin p35 [Zea mays]
Seq. No.
                  414477
                  uC-osflcyp156g05b1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g455499
BLAST score
                  50
                  6.0e-19
E value
                  58
Match length
                  97
% identity
NCBI Description Rice mRNA for ubiquitin-conjugating enzyme, partial
                  sequence
                  414478
Seq. No.
Seq. ID
                  uC-osflcyp156g06a1
Method
                  BLASTX
NCBI GI
                  g4158221
BLAST score
                  359
E value
                  4.0e-34
                  69
Match length
% identity
NCBI Description (Y18624) reversibly glycosylated polypeptide [Oryza sativa]
                  414479
Seq. No.
                  uC-osflcyp156g06b1
Seq. ID
                  BLASTX
Method
NCBI GI
                  g3646373
BLAST score
                  756
E value
                  2.0e-80
Match length
                  149
                   95
% identity
NCBI Description (AJ011078) RGP1 protein [Oryza sativa]
                   414480
Seq. No.
                  uC-osflcyp156g07b1
Seq. ID
```

BLASTX Method g2576363 NCBI GI BLAST score 315 6.0e-29 E value 107 Match length 53 % identity (U39783) amino acid transport protein [Arabidopsis NCBI Description thaliana] 414481 Seq. No. Seq. ID uC-osflcyp156g09b1 BLASTX Method NCBI GI q4581156 BLAST score 692 E value 5.0e-73 Match length 177 78 % identity NCBI Description (AC006919) putative pyruvate kinase [Arabidopsis thaliana] Seq. No. 414482 uC-osflcyp156g11b1 Seq. ID Method BLASTX NCBI GI q517500 BLAST score 331 1.0e-30 E value Match length 159 47 % identity (M87435) precursor of the oxygen evolving complex 17 kDa NCBI Description protein [Zea mays] >gi 444338 prf 1906386A photosystem II OE17 protein [Pisum sativum] 414483 Seq. No. uC-osflcyp156g12a1 Seq. ID Method BLASTX NCBI GI q464707 BLAST score 357 8.0e-34 E value 98 Match length 70 % identity NCBI Description 40S RIBOSOMAL PROTEIN S18 >gi 480908 pir S37496 ribosomal protein S18.A - Arabidopsis thaliana >gi 405613 emb CAA80684 (Z23165) ribosomal protein S18A [Arabidopsis thaliana] >gi_434343 emb_CAA82273_ (Z28701) S18 ribosomal protein [Arabidopsis thaliana] >qi 434345 emb CAA82274 (Z28702) S18 ribosomal protein [Arabidopsis thaliana] >gi_434906_emb_CAA82275_ (Z28962) S18 ribosomal protein [Arabidopsis thaliana] >gi 2505871 emb CAA72909 (Y12227) ribosomal protein S18A [Arabidopsis thaliana] >gi 3287678 (AC003979) Match to ribosomal S18 gene mRNA gb Z28701, DNA gb Z23165 from A. thaliana. ESTs gb_T21121, gb_Z17755, gb_ $\overline{R}64776$ and gb R30430 come from this gene. [Arabidopsis thaliana]

Seq. No. 414484

Seq. ID uC-osflcyp156g12b1

protein [Arabidopsis thaliana]

>gi 4538910 emb CAB39647.1 (AL049482) S18.A ribosomal

Method BLASTX NCBI GI g464707 BLAST score 645 E value 2.0e-67 152 Match length 78 % identity NCBI Description 40S RIBOSOMAL PROTEIN S18 >gi 480908 pir S37496 ribosomal protein S18.A - Arabidopsis thaliana >gi 405613 emb CAA80684 (Z23165) ribosomal protein S18A [Arabidopsis thaliana] >gi 434343 emb CAA82273 (Z28701) S18 ribosomal protein [Arabidopsis thaliana] >gi 434345 emb CAA82274 (Z28702) S18 ribosomal protein [Arabidopsis thaliana] >qi 434906 emb CAA82275 (Z28962) S18 ribosomal protein [Arabidopsis thaliana] >gi 2505871 emb CAA72909 (Y12227) ribosomal protein S18A [Arabidopsis thaliana] >gi 3287678 (AC003979) Match to ribosomal S18 gene mRNA gb_Z28701, DNA gb_Z23165 from A. thaliana. ESTs gb_T21121, gb_Z17755, gb_R64776 and gb R30430 come from this gene. [Arabidopsis thaliana] >gi 4538910 emb CAB39647.1 (AL049482) S18.A ribosomal protein [Arabidopsis thaliana] 414485 Seq. No. Seq. ID uC-osflcyp156h03b1

Method BLASTX
NCBI GI g3885329
BLAST score 349
E value 3.0e-33
Match length 88
% identity 76

NCBI Description (AC005623) alien-like protein [Arabidopsis thaliana]

Seq. No. 414486

Seq. ID uC-osflcyp156h05a1

Method BLASTN
NCBI GI g169662
BLAST score 39
E value 2.0e-12
Match length 75
% identity 88

NCBI Description Parsley S-adenosylhomocysteine hydrolase (SHH) mRNA,

complete cds

Seq. No. 414487

Seq. ID uC-osflcyp156h05b1

Method BLASTX
NCBI GI g2244750
BLAST score 726
E value 4.0e-77
Match length 151
% identity 91

NCBI Description (Z97335) adenosylhomocysteinase [Arabidopsis thaliana]

>gi_3088579_gb_AAC14714.1_ (AF059581)

S-adenosyl-L-homocysteine hydrolase [Arabidopsis thaliana]

Seq. No. 414488

Seq. ID uC-osflcyp156h06b1

```
BLASTX
Method
NCBI GI
                  q5823571
BLAST score
                  436
E value
                  5.0e-43
Match length
                  123
                  74
% identity
                  (AL049730) Ribosomal protein L7Ae-like [Arabidopsis
NCBI Description
                  thaliana]
                  414489
Seq. No.
                  uC-osflcyp156h08b1
Seq. ID
                  BLASTX
Method
NCBI GI
                  q3885329
                  771
BLAST score
E value
                  2.0e-82
Match length
                  163
                  90
% identity
NCBI Description (AC005623) alien-like protein [Arabidopsis thaliana]
Seq. No.
                  414490
                  uC-osflcyp156h09b1
Seq. ID
                  BLASTX
Method
NCBI GI
                  q4455172
BLAST score
                  510
                   9.0e-52
E value
Match length
                  138
                   71
% identity
NCBI Description (AL035521) putative protein [Arabidopsis thaliana]
Seq. No.
                   414491
                   uC-osflcyp156h10b1
Seq. ID
Method
                  BLASTX
                   g3168840
NCBI GI
                   290
BLAST score
                   7.0e-26
E value
Match length
                   66
                   83
% identity
NCBI Description (U88711) copper homeostasis factor [Arabidopsis thaliana]
                   414492
Seq. No.
                   uC-osflcyp156h11a1
Seq. ID
                   BLASTN
Method
                   g5441876
NCBI GI
                   117
BLAST score
E value
                   2.0e-59
Match length
                   151
                   19
% identity
NCBI Description Oryza sativa genomic DNA, chromosome 2, clone:P0437H03
                   (contig b)
```

Seq. No. 414493

Seq. ID uC-osflcyp157a03b1

Method BLASTX
NCBI GI g4688596
BLAST score 299
E value 3.0e-27
Match length 107

% identity (AJ005682) inositol 1,4,5-trisphosphate 5-phosphatase NCBI Description [Arabidopsis thaliana] 414494 Seq. No. Seq. ID uC-osflcyp157a04b1 Method BLASTX NCBI GI q1488647 BLAST score 589 5.0e-61 E value Match length 165 70 % identity (X99937) RNA helicase [Spinacia oleracea] NCBI Description 414495 Seq. No. uC-osflcyp157a05a1 Seq. ID Method BLASTX NCBI GI q3789942 BLAST score 304 E value 1.0e-27 65 Match length 19 % identity NCBI Description (AF093505) polyubiquitin [Saccharum hybrid cultivar H32-8560] Seq. No. 414496 uC-osflcyp157a05b1 Seq. ID Method BLASTX NCBI GI g82512 BLAST score 614 E value 5.0e-64 Match length 131 41 % identity NCBI Description ubiquitin precursor - rice (fragment) >gi 218189 dbj BAA02241 (D12776) poly-ubiquitin [Oryza sativa] 414497 Seq. No. uC-osflcyp157a06b1 Seq. ID Method BLASTX NCBI GI g1814403 BLAST score 564 E value 3.0e-58 Match length 116 90 % identity NCBI Description (U84889) methionine synthase [Mesembryanthemum crystallinum] 414498 Seq. No. Seq. ID uC-osflcyp157a08b1 Method BLASTN NCBI GI g5852170 BLAST score 524 E value 0.0e+00Match length 548 % identity 99 NCBI Description Oryza sativa indica(GLA4) genomic DNA, chromosome 4, BAC

Seq. No.

Seq. ID

414504

uC-osflcyp157b06b1

clone:t17804

414499 Seq. No. Seq. ID uC-osflcyp157b01a1 BLASTX Method NCBI GI g3337350 BLAST score 261 E value 1.0e-22 Match length 55 % identity 82 NCBI Description (AC004481) putative permease [Arabidopsis thaliana] 414500 Seq. No. Seq. ID uC-osflcyp157b03b1 Method BLASTX NCBI GI g2984709 BLAST score 375 E value 6.0e-38 96 Match length 79 % identity NCBI Description (AF053468) DnaJ-related protein ZMDJ1 [Zea mays] 414501 Seq. No. Seq. ID uC-osflcyp157b04b1 Method BLASTX NCBI GI q1171008 BLAST score 468 E value 6.0e-47Match length 126 65 % identity NCBI Description POLLEN ALLERGEN PHL P 1 PRECURSOR (PHL P I) >gi_629812_pir__S44182 allergen Phl p I - common timothy >gi 473360 emb CAA55390 (X78813) Phl p I allergen [Phleum pratense] 414502 Seq. No. Seq. ID uC-osflcyp157b05a1 Method BLASTX NCBI GI g1477428 BLAST score 406 2.0e-39 E value Match length 78 % identity NCBI Description (X99623) alpha-tubulin 1 [Hordeum vulgare] 414503 Seq. No. uC-osflcyp157b05b1 Seq. ID Method BLASTX NCBI GI g1477428 BLAST score 581 E value 4.0e-60 Match length 129 % identity NCBI Description (X99623) alpha-tubulin 1 [Hordeum vulgare]



```
BLASTX
Method
NCBI GI
                  g3341490
BLAST score
                  538
                  3.0e-55
E value
Match length
                  111
                  87
% identity
                  (AJ007705) phospoenolpyruvate carboxylase [Triticum
NCBI Description
                  aestivum]
                  414505
Seq. No.
Seq. ID
                  uC-osflcyp157b07b1
Method
                  BLASTX
NCBI GI
                  q4099408
BLAST score
                  519
                  6.0e-53
E value
Match length
                  114
% identity
                  84
                  (U86763) delta-type tonoplast intrinsic protein [Triticum
NCBI Description
                  aestivum]
Seq. No.
                  414506
Seq. ID
                  uC-osflcyp157b09a1
Method
                  BLASTX
NCBI GI
                  g2809245
BLAST score
                  324
E value
                  6.0e-30
Match length
                  77
% identity
                  81
NCBI Description (AC002560) F21B7.14 [Arabidopsis thaliana]
                  414507
Seq. No.
Seq. ID
                  uC-osflcyp157b09b1
```

Method BLASTX NCBI GI g2809245 BLAST score 368 E value 3.0e - 36106 Match length 75 % identity

NCBI Description (AC002560) F21B7.14 [Arabidopsis thaliana]

Seq. No. 414508

Seq. ID uC-osflcyp157b10b1

Method BLASTX g3775987 NCBI GI BLAST score 361 E value 3.0e-34Match length 158 35 % identity

NCBI Description (AJ010457) RNA helicase [Arabidopsis thaliana]

Seq. No. 414509

Seq. ID uC-osflcyp157b12a1

Method BLASTN NCBI GI g4126808 BLAST score 87

4.0e-41 E value Match length 114

Seq. ID

```
% identity
NCBI Description Oryza sativa mRNA for glyoxalase I, complete cds
                  414510
Seq. No.
Seq. ID
                  uC-osflcyp157b12b1
Method
                  BLASTX
NCBI GI
                  g4126809
BLAST score
                  896
                  6.0e-97
E value
                  167
Match length
                  58
% identity
NCBI Description (AB017042) glyoxalase I [Oryza sativa]
Seq. No.
                  414511
Seq. ID
                  uC-osflcyp157c02a1
Method
                  BLASTX
                  g2286153
NCBI GI
BLAST score
                  248
E value
                  4.0e-21
                  55
Match length
% identity
                  87
NCBI Description (AF007581) cytoplasmic malate dehydrogenase [Zea mays]
                  414512
Seq. No.
Seq. ID
                  uC-osflcyp157c02b1
                  BLASTX
Method
                  g2286153
NCBI GI
BLAST score
                  429
E value
                  2.0e-42
                  94
Match length
                  90
% identity
NCBI Description (AF007581) cytoplasmic malate dehydrogenase [Zea mays]
                  414513
Seq. No.
Seq. ID
                  uC-osflcyp157c03b1
                  BLASTX
Method
NCBI GI
                  q5803100
BLAST score
                  178
E value
                  9.0e-13
                  54
Match length
                  59
% identity
NCBI Description DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 18
                   (Myc-regulated) >gi 1498229 emb CAA67295 (X98743) RNA
                  helicase [Homo sapiens]
                  414514
Seq. No.
                  uC-osflcyp157c05a1
Seq. ID
Method`
                  BLASTX
NCBI GI
                  g4558547
BLAST score
                  184
                  2.0e-13
E value
                  59
Match length
% identity
NCBI Description (AC007138) hypothetical protein [Arabidopsis thaliana]
                  414515
Seq. No.
```

54057

uC-osflcyp157c05b1

```
BLASTX
Method
NCBI GI
                  g2735841
BLAST score
                  411
                  4.0e-40
E value
                  172
Match length
                  49
% identity
NCBI Description (AF010283) No definition line found [Sorghum bicolor]
Seq. No.
                  414516
                  uC-osflcyp157c06b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2911076
BLAST score
                  174
E value
                  2.0e-12
                  59
Match length
                  54
% identity
NCBI Description (AL021960) putative protein [Arabidopsis thaliana]
Seq. No.
                  414517
                  uC-osflcyp157c07a1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g6015059
                  340
BLAST score
                  8.0e-32
E value
Match length
                  66
                  100
% identity
NCBI Description ELONGATION FACTOR 1-ALPHA (EF-1-ALPHA) >gi 2996096
                   (AF030517) translation elongation factor-1 alpha; EF-1
                  alpha [Oryza sativa]
                   414518
Seq. No.
                  uC-osflcyp157c07b1
Seq. ID
                  BLASTX
Method
                  g2662343
NCBI GI
                  843
BLAST score
                  1.0e-90
E value
                  161
Match length
                  99
% identity
NCBI Description (D63581) EF-1 alpha [Oryza sativa]
Seq. No.
                   414519
Seq. ID
                  uC-osflcyp157c08b1
Method
                  BLASTN
NCBI GI
                  g19046
                  82
BLAST score
E value
                  5.0e-38
Match length
                  416
                  83
% identity
NCBI Description H.vulgare mRNA for seed protein B32E
                   414520
Seq. No.
                   uC-osflcyp157c09b1
Seq. ID
                   BLASTX
Method
NCBI GI
                   g3928090
BLAST score
                  272
                   8.0e-24
E value
```

54058

101

Match length

Method

BLASTX

% identity NCBI Description (AC005770) putative MTN3 protein [Arabidopsis thaliana] Seq. No. 414521 Seq. ID uC-osflcyp157c10b1 Method BLASTX NCBI GI g4539371 BLAST score 174 E value 3.0e-12 Match length 84 % identity 40 NCBI Description (AL049525) putative protein [Arabidopsis thaliana] Seq. No. 414522 Seq. ID uC-osflcyp157c11a1 Method BLASTX NCBI GI g3452497 BLAST score 353 E value 2.0e-33 Match length 83 % identity 82 NCBI Description (Y17796) ketol-acid reductoisomerase [Pisum sativum] Seq. No. 414523 Seq. ID uC-osflcyp157c11b1 Method BLASTX NCBI GI g3452497 BLAST score 589 E value 4.0e-61 Match length 139 % identity 81 NCBI Description (Y17796) ketol-acid reductoisomerase [Pisum sativum] 414524 Seq. No. Seq. ID uC-osflcyp157c12b1 Method BLASTX NCBI GI q5579092 BLAST score 397 E value 2.0e-38 153 Match length 53 % identity (AF100954) gibberellin 2-oxidase-like protein [Pisum NCBI Description sativum] Seq. No. 414525 Seq. ID uC-osflcyp157d01a1 Method BLASTX NCBI GI g485517 BLAST score 215 E value 3.0e-17 Match length 43 % identity 100 NCBI Description ADP, ATP carrier protein - rice Seq. No. 414526 uC-osflcyp157d01b1 Seq. ID

```
NCBI GI
                   q485517
BLAST score
                   666
E value
                   5.0e-70
Match length
                  131
                   100
% identity
NCBI Description ADP, ATP carrier protein - rice
Seq. No.
                   414527
Seq. ID
                  uC-osflcyp157d02b1
Method
                  BLASTX
NCBI GI
                  g2880043
BLAST score
                   332
E value
                   8.0e-31
Match length
                   108
% identity
                   60
                  (AC002340) putative 3-hydroxyisobutyryl-coenzyme A
NCBI Description
                  hydrolase [Arabidopsis thaliana]
Seq. No.
                   414528
                  uC-osflcyp157d03b1
Seq. ID
Method
                  BLASTX
NCBI GI
                   g461532
BLAST score
                   302
E value
                   4.0e-41
Match length
                   134
% identity
                   63
                  ADP-RIBOSYLATION FACTOR >gi 1362500 pir D49993
NCBI Description
                  ADP-ribosylation factor - Ajellomyces capsulata >gi 407693
                   (L25117) ADP-ribosylation factor [Histoplasma capsulatum]
Seq. No.
                   414529
Seq. ID
                   uC-osflcyp157d04b1
Method
                  BLASTX
NCBI GI
                   g2642165
BLAST score
                   232
E value
                   4.0e-19
                  174
Match length
                   34
% identity
NCBI Description (AC003000) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   414530
Seq. ID
                   uC-osflcyp157d05a1
Method
                  BLASTN
NCBI GI
                   g439585
BLAST score
                   101
E value
                   2.0e-49
                   203
Match length
                   88
% identity
NCBI Description Hordeum vulgare calreticulin (CRH1) mRNA, partial cds
Seq. No.
                   414531
                   uC-osflcyp157d05b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   q439588
BLAST score
                   809
                   8.0e-87
E value
```

160

Match length

```
% identity
                  (L27349) calreticulin [Hordeum vulgare]
NCBI Description
                  414532
Seq. No.
                  uC-osflcyp157d07a1
Seq. ID
                  BLASTN
Method
                  q4406131
NCBI GI
                  231
BLAST score
E value
                  1.0e-127
                  331
Match length
                  98
% identity
NCBI Description Oryza sativa MADS box protein (MADS16) mRNA, complete cds
                  414533
Seq. No.
                  uC-osflcyp157d07b1
Seq. ID
                  BLASTX
Method
                   g4406132
NCBI GI
                  730
BLAST score
                   1.0e-77
E value
Match length
                   140
                   99
% identity
NCBI Description (AF077760) MADS box protein [Oryza sativa]
                   414534
Seq. No.
                   uC-osflcyp157d08b1
Seq. ID
Method
                   BLASTX
                   q3618207
NCBI GI
                   273
BLAST score
                   6.0e-24
E value
Match length
                   110
% identity
                   45
NCBI Description (AL031579) conserved hypothetical protein
                   [Schizosaccharomyces pombe]
Seq. No.
                   414535
Seq. ID
                   uC-osflcyp157d11a1
Method
                   BLASTX
                   q5731756
NCBI GI
                   329
BLAST score
                   2.0e-30
E value
                   103
Match length
                   59
% identity
NCBI Description (AL109819) putative protein [Arabidopsis thaliana]
```

Seq. ID uC-osflcyp157d11b1

Method BLASTX
NCBI GI g5731756
BLAST score 392
E value 7.0e-38
Match length 127
% identity 61

NCBI Description (AL109819) putative protein [Arabidopsis thaliana]

Seq. No. 414537

Seq. ID uC-osflcyp157d12a1

Method BLASTX

Seq. ID Method

```
NCBI GI
                  q1362162
BLAST score
                  338
E value
                  1.0e-31
                  98
Match length
                  59
% identity
NCBI Description beta-glucosidase BGQ60 precursor - barley >gi 804656
                  (L41869) beta-glucosidase [Hordeum vulgare]
Seq. No.
                  414538
                  uC-osflcyp157d12b1
Seq. ID
                  BLASTX
Method
NCBI GI
                  q1362162
BLAST score
                  395
E value
                  3.0e-38
Match length
                  149
% identity
                  50
NCBI Description beta-glucosidase BGQ60 precursor - barley >gi 804656
                  (L41869) beta-glucosidase [Hordeum vulgare]
Seq. No.
                  414539
                  uC-osflcyp157e01b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3915866
BLAST score
                  256
E value
                  6.0e-22
Match length
                  60
% identity
                  78
                  GLUTAMINYL-TRNA SYNTHETASE (GLUTAMINE--TRNA LIGASE) (GLNRS)
NCBI Description
                  >gi 2995455_emb_CAA62901_ (X91787) tRNA-glutamine
                  synthetase [Lupinus luteus]
                  414540
Seq. No.
Seq. ID
                  uC-osflcyp157e03a1
Method
                  BLASTN
NCBI GI
                  g5803242
BLAST score
                  72
                  3.0e-32
E value
                  140
Match length
                  46
% identity
NCBI Description Oryza sativa genomic DNA, chromosome 6, clone:P0535G04
                  414541
Seq. No.
Seq. ID
                  uC-osflcyp157e04b1
Method
                  BLASTX
NCBI GI
                  q2501189
BLAST score
                  420
E value
                  3.0e-41
Match length
                  115
% identity
                  74
NCBI Description THIAMINE BIOSYNTHETIC ENZYME 1-1 PRECURSOR
                  >gi 2130146 pir S61419 thiamine biosynthetic enzyme thi1-1
                  - maize >gi 596078 (U17350) thiamine biosynthetic enzyme
                  [Zea mays]
Seq. No.
                  414542
```

54062

uC-osflcyp157e05b1

BLASTX

414547

```
NCBI GI
                  g2407281
BLAST score
                  793
                  6.0e-85
E value
Match length
                  150
% identity
NCBI Description (AF017363) ribulose 1,5-bisphosphate carboxylase small
                  subunit [Oryza sativa]
Seq. No.
                  414543
                  uC-osflcyp157e07a1
Seq. ID
Method
                  BLASTN
NCBI GI
                  q498737
BLAST score
                  35
                  6.0e-10
E value
Match length
                  111
% identity
NCBI Description H.vulgare (pMaW21) pseudo mRNA for beta-ketoacyl-ACP
                  synthase (partial)
Seq. No.
                  414544
                  uC-osflcyp157e07b1
Seq. ID
                  BLASTX
Method
NCBI GI
                  q3341677
BLAST score
                  389
                  1.0e-37
E value
Match length
                  144
% identity
                  47
NCBI Description (AC003672) putative glycosyl hydrolase [Arabidopsis
                  thaliana]
Seq. No.
                  414545
                  uC-osflcyp157e09a1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1729971
BLAST score
                  188
E value
                   3.0e-14
Match length
                  51
                   71
% identity
NCBI Description TONOPLAST INTRINSIC PROTEIN, GAMMA (GAMMA TIP)
                   (AQUAPORIN-TIP) >gi 1076745 pir S52004 gamma-Tip protein -
                   rice >gi 473997 dbj BAA05017 (D25534) gamma-Tip [Oryza
                   sativa]
                   414546
Seq. No.
                  uC-osflcyp157e09b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1729971
BLAST score
                  289
E value
                   3.0e-26
                  59
Match length
                   97
% identity
NCBI Description TONOPLAST INTRINSIC PROTEIN, GAMMA (GAMMA TIP)
                   (AQUAPORIN-TIP) >gi_1076745_pir__S52004 gamma-Tip protein -
                   rice >gi 473997_dbj_BAA05017_ (D25534) gamma-Tip [Oryza
                   sativa]
```

uC-osflcyp157e10b1 Seq. ID Method BLASTX NCBI GI g6093778 BLAST score 626 E value 3.0e-65

138

92 % identity PROTEASOME COMPONENT C3 (MACROPAIN SUBUNIT C3) NCBI Description (MULTICATALYTIC ENDOPEPTIDASE COMPLEX SUBUNIT C3)

20S proteasome subunit PAB1 [Arabidopsis thaliana]

>qi 4966368 gb AAD34699.1 AC006341_27 (AC006341) Identical

to gb Y13176 Arabidopsis Thaliana mRNA for proteasome

subunit prc3. ESTs gb H36972, gb T22551 and gb_T13800 come

from this gene

414548 Seq. No.

Match length

Seq. ID uC-osflcyp157e11a1

Method BLASTX NCBI GI q4454032 BLAST score 215 E value 4.0e-17 Match length 58 69 % identity

NCBI Description (AL035394) putative protein [Arabidopsis thaliana]

414549 Seq. No.

uC-osflcyp157e11b1 Seq. ID

Method BLASTX g4454032 NCBI GI 362 BLAST score 2.0e-36 E value 157 Match length % identity 52

NCBI Description (AL035394) putative protein [Arabidopsis thaliana]

414550 Seq. No.

Seq. ID uC-osflcyp157f02a1

BLASTN Method q4530610 NCBI GI 312 BLAST score 1.0e-175 E value Match length 444 % identity 98

Oryza sativa subsp. indica serine/threonine protein NCBI Description

phosphatase PP2A-2 catalytic subunit (Pp2A) gene, complete

cds

Seq. No. 414551

Seq. ID uC-osflcyp157f02b1

Method BLASTX q4530611 NCBI GI BLAST score 671 E value 1.0e-70 132 Match length % identity 96

```
NCBI Description (AF134552) serine/threonine protein phosphatase PP2A-2
                  catalytic subunit [Oryza sativa subsp. indica]
                  414552
Seq. No.
                  uC-osflcyp157f05b1
Seq. ID
                  {\tt BLASTX}
Method
NCBI GI
                  g710626
BLAST score
                  188
                  6.0e-14
E value
Match length
                  45
                  69
% identity
                  (D30719) ERD15 protein [Arabidopsis thaliana] >gi 3241941
NCBI Description
                  (AC004625) dehydration-induced protein ERD15 [Arabidopsis
                  thaliana] >gi 3894181 (AC005662) ERD15 protein [Arabidopsis
                  thaliana]
                  414553
Seq. No.
Seq. ID
                  uC-osflcyp157f06b1
Method
                  BLASTX
NCBI GI
                  g2286153
BLAST score
                  376
E value
                  3.0e-36
Match length
                  83
                  89
% identity
NCBI Description (AF007581) cytoplasmic malate dehydrogenase [Zea mays]
                  414554
Seq. No.
Seq. ID
                  uC-osflcyp157f08a1
Method
                  BLASTX
NCBI GI
                  g1815664
BLAST score
                  295
E value
                  1.0e-26
                  74
Match length
                  84
% identity
NCBI Description (U83671) low molecular mass heat shock protein Oshsp17.7
                  [Oryza sativa]
                  414555
Seq. No.
Seq. ID
                  uC-osflcyp157f08b1
                  BLASTX
Method
NCBI GI
                  g1815664
BLAST score
                  299
E value
                  3.0e-27
Match length
                  71
% identity
NCBI Description (U83671) low molecular mass heat shock protein Oshsp17.7
                  [Oryza sativa]
Seq. No.
                  414556
Seq. ID
                  uC-osflcyp157f09a1
Method
                  BLASTX
NCBI GI
                  g3915866
BLAST score
                  240
E value
                  4.0e-20
Match length
                  64
                  73
% identity
NCBI Description GLUTAMINYL-TRNA SYNTHETASE (GLUTAMINE--TRNA LIGASE) (GLNRS)
```





>gi_2995455_emb_CAA62901_ (X91787) tRNA-glutamine synthetase [Lupinus luteus]

Seq. No. 414557

Seq. ID uC-osflcyp157f09b1

Method BLASTX
NCBI GI g3915866
BLAST score 609
E value 2.0e-63
Match length 129
% identity 82

NCBI Description GLUTAMINYL-TRNA SYNTHETASE (GLUTAMINE--TRNA LIGASE) (GLNRS)

>gi_2995455_emb_CAA62901_ (X91787) tRNA-glutamine

synthetase [Lupinus luteus]

Seq. No. 414558

Seq. ID uC-osflcyp157f12a1

Method BLASTX
NCBI GI g3256035
BLAST score 194
E value 1.0e-14
Match length 85
% identity 41

NCBI Description (Y14274) putative serine/threonine protein kinase [Sorghum

bicolor]

Seq. No. 414559

Seq. ID uC-osflcyp157f12b1

Method BLASTX
NCBI GI g1777312
BLAST score 206
E value 4.0e-16
Match length 98
% identity 47

NCBI Description (D30622) novel serine/threonine protein kinase [Arabidopsis

thaliana]

Seq. No. 414560

Seq. ID uC-osflcyp157g04a1

Method BLASTX
NCBI GI g2055262
BLAST score 342
E value 7.0e-35
Match length 85
% identity 85

NCBI Description (AB003194) chitinase IIb [Oryza sativa]

Seq. No. 414561

Seq. ID uC-osflcyp157g04b1

Method BLASTX
NCBI GI g2570160
BLAST score 172
E value 3.0e-20
Match length 69
% identity 70

NCBI Description (D45181) chitinase [Chenopodium amaranticolor]

NCBI GI

```
414562
Seq. No.
Seq. ID
                  uC-osflcyp157g06b1
Method
                  BLASTN
NCBI GI
                  g1504051
BLAST score
                  40
                  6.0e-13
E value
Match length
                  48
% identity
                  96
                  Zea mays mRNA for Calcium-dependent protein kinase,
NCBI Description
                  complete cds
                  414563
Seq. No.
                  uC-osflcyp157g09b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4101703
BLAST score
                  289
                  7.0e-26
E value
Match length
                  126
% identity
                  45
NCBI Description (AF006078) glucose acyltransferase [Solanum berthaultii]
                  414564
Seq. No.
                  uC-osflcyp157g10a1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g2984708
BLAST score
                  48
E value
                  9.0e-18
                  80
Match length
                  90
% identity
                  Zea mays DnaJ-related protein ZMDJ1 (mdJ1) gene, complete
NCBI Description
                  cds >gi_5996689_gb_AR066473.1_AR066473 Sequence 2 from
                  patent US
                  414565
Seq. No.
Seq. ID
                  uC-osflcyp157g10b1
                  BLASTX
Method
NCBI GI
                  q2984709
BLAST score
                  798
E value
                  2.0e-85
                  173
Match length
                  88
% identity
NCBI Description (AF053468) DnaJ-related protein ZMDJ1 [Zea mays]
                  414566
Seq. No.
Seq. ID
                  uC-osflcyp157g11a1
                  BLASTX
Method
                  g515692
NCBI GI
                  228
BLAST score
E value
                  1.0e-18
Match length
                  43
                   100
% identity
NCBI Description (U12286) beta-tubulin [Glycine max]
                   414567
Seq. No.
Seq. ID
                   uC-osflcyp157g11b1
                   BLASTX
Method
```

54067

g1174600

```
685
BLAST score
                  4.0e-72
E value
Match length
                  129
% identity
                  100
                  TUBULIN BETA CHAIN >gi 493710 dbj BAA06382 (D30717)
NCBI Description
                  beta-tubulin [Oryza sativa]
                  414568
Seq. No.
Seq. ID
                  uC-osflcyp157h01b1
Method
                  BLASTX
NCBI GI
                  q4455270
BLAST score
                  165
                  3.0e-11
E value
Match length
                  98
% identity
                  35
NCBI Description (AL035527) putative protein [Arabidopsis thaliana]
                  414569
Seq. No.
                  uC-osflcyp157h02b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4688632
BLAST score
                  147
E value
                  1.0e-09
Match length
                  73
% identity
NCBI Description (AJ007449) trans-cinnamic 4-monooxygenase [Cicer arietinum]
Seq. No.
                  414570
                  uC-osflcyp157h07b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g6041814
BLAST score
                  151
                  1.0e-09
E value
Match length
                  36
% identity
                  69
NCBI Description (AC009918) hypothetical protein [Arabidopsis thaliana]
                   414571
Seq. No.
Seq. ID
                  uC-osflcyp158a01a1
                  BLASTX
Method
                  g3559814
NCBI GI
                  236
BLAST score
                   9.0e-20
E value
                  61
Match length
                  70
% identity
NCBI Description (Y15781) transketolase 1 [Capsicum annuum]
                   414572
Seq. No.
Seq. ID
                  uC-osflcyp158a01b1
                  BLASTX
Method
                  g2501356
NCBI GI
BLAST score
                  600
E value
                  2.0e-62
                  129
Match length
                   84
% identity
NCBI Description TRANSKETOLASE, CHLOROPLAST PRECURSOR (TK)
```

>qi 1658322 emb CAA90427 (Z50099) transketolase precursor

[Solanum tuberosum] 414573 Seq. No. Seq. ID uC-osflcyp158a02a1 Method BLASTX NCBI GI g2130069 BLAST score 200 E value 2.0e-15 39 Match length 97 % identity NCBI Description catalase (EC 1.11.1.6) catA - rice >gi_1261858_dbj_BAA06232_ (D29966) catalase [Oryza sativa] Seq. No. 414574 uC-osflcyp158a02b1 Seq. ID BLASTX Method NCBI GI g2130069 BLAST score 615 E value 3.0e-64 Match length 132 86 % identity NCBI Description catalase (EC 1.11.1.6) catA - rice >gi_1261858_dbj_BAA06232_ (D29966) catalase [Oryza sativa] Seq. No. 414575 uC-osflcyp158a03a1 Seq. ID BLASTN Method NCBI GI g2331130 BLAST score 206 1.0e-112 E value 246 Match length 96 % identity NCBI Description Oryza sativa glycine-rich protein (OSGRP1) mRNA, complete cds 414576 Seq. No. Seq. ID uC-osflcyp158a03b1 BLASTX Method g2293480 NCBI GI BLAST score 194 E value 4.0e-15 Match length 39 % identity NCBI Description (AF011331) glycine-rich protein [Oryza sativa] 414577 Seq. No. Seq. ID uC-osflcyp158a07b1 Method BLASTX NCBI GI g4835767 BLAST score 176 1.0e-12 E value 109 Match length % identity NCBI Description (AC007202) T8K14.16 [Arabidopsis thaliana]

54069

414578

uC-osflcyp158a08b1

Seq. No.

Seq. ID



Method BLASTX NCBI GI g2370253 BLAST score 348 9.0e-33 E value Match length 149 % identity 48 (Y13273) putative protein kinase [Lycopersicon esculentum] NCBI Description >gi 5669642 gb AAD46406.1 AF096250 1 (AF096250) ethylene-responsive protein kinase TCTR1 [Lycopersicon esculentum] 414579 Seq. No. uC-osflcyp158a09a1 Seq. ID Method BLASTX NCBI GI g6015065 BLAST score 390 E value 1.0e-37 Match length 82 % identity 90 ELONGATION FACTOR 2 (EF-2) >gi 2369714 emb CAB09900_ NCBI Description (Z97178) elongation factor 2 [Beta vulgaris] Seq. No. 414580 uC-osflcyp158a09b1 Seq. ID Method BLASTX NCBI GI q1841462 BLAST score 504 E value 2.0e-51 100 Match length % identity 96 NCBI Description (Y10991) Elongation factor 2 [Nicotiana tabacum] 414581 Seq. No. Seq. ID uC-osflcyp158a11b1 BLASTX Method NCBI GI q6016732 BLAST score 175 9.0e-13 E value 76 Match length % identity 49 (AC009325) hypothetical protein [Arabidopsis thaliana] NCBI Description >gi_6091719_gb_AAF03431.1 AC010797 7 (AC010797) hypothetical protein [Arabidopsis thaliana] Seq. No. 414582 Seq. ID uC-osflcyp158a12b1 Method BLASTX NCBI GI g2270994 BLAST score 187

E value 5.0e-14Match length 84 % identity

NCBI Description (AF004809) Ca+2-binding EF hand protein [Glycine max]

Seq. No. 414583

uC-osflcyp158b02b1 Seq. ID

Method BLASTX

Method

NCBI GI

BLAST score

BLASTX

595

g3819699

```
g3790100
NCBI GI
BLAST score
                  424
E value
                  3.0e-49
Match length
                  130
                  77
% identity
NCBI Description
                  (AF095520) pyrophosphate-dependent phosphofructokinase beta
                  subunit [Citrus X paradisi]
Seq. No.
                  414584
Seq. ID
                  uC-osflcyp158b03a1
Method
                  BLASTN
NCBI GI
                  g429005
BLAST score
                  105
E value
                  4.0e-52
Match length
                  145
                  95
% identity
NCBI Description Rice mRNA for ribosomal protein S25 (gene name SS289),
                  partial cds
Seq. No.
                  414585
Seq. ID
                  uC-osflcyp158b03b1
Method
                  BLASTX
NCBI GI
                  g1173187
BLAST score
                  525
E value
                  1.0e-53
Match length
                  104
                  94
% identity
                 40S RIBOSOMAL PROTEIN S23 (S12) >gi_1362041_pir__S56673
NCBI Description
                  ribosomal protein S23.e, cytosolic (clone RJ3) - garden
                  strawberry >gi_643074 (U19940) putative 40S ribosomal
                  protein s12 [Fragaria x ananassa]
Seq. No.
                  414586
Seq. ID
                  uC-osflcyp158b06b1
Method
                  BLASTX
NCBI GI
                  q3123745
                  230
BLAST score
E value
                  6.0e-19
                  75
Match length
                  60
% identity
NCBI Description (AB013447) aluminum-induced [Brassica napus]
Seq. No.
                  414587
Seq. ID
                  uC-osflcyp158b09b1
Method
                  BLASTN
NCBI GI
                  g5091597
BLAST score
                  108
                  1.0e-53
E value
                  148
Match length
                  93
% identity
NCBI Description Oryza sativa chromosome 1 BAC 10A19I, complete sequence
Seq. No.
                  414588
Seq. ID
                  uC-osflcyp158b11a1
```

```
9.0e-62
E value
Match length
                  145
                  80
% identity
                  (AJ009609) BnMAP4K alpha2 [Brassica napus]
NCBI Description
                  414589
Seq. No.
                  uC-osflcyp158b11b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3819699
BLAST score
                  158
                  1.0e-10
E value
Match length
                  110
% identity
                  36
NCBI Description (AJ009609) BnMAP4K alpha2 [Brassica napus]
                  414590
Seq. No.
                  uC-osflcyp158b12b1
Seq. ID
Method
                  BLASTN
                  q5803242
NCBI GI
BLAST score
                  35
                  5.0e-10
E value
                  39
Match length
                  97
% identity
NCBI Description Oryza sativa genomic DNA, chromosome 6, clone:P0535G04
                  414591
Seq. No.
                  uC-osflcyp158c02a1
Seq. ID
Method
                  BLASTN
                  q600766
NCBI GI
                  89
BLAST score
E value
                   3.0e-42
                  221
Match length
                   91
% identity
NCBI Description Oryza sativa cyclophilin 2 (Cyp2) gene, complete cds
Seq. No.
                   414592
Seq. ID
                   uC-osflcyp158c02b1
Method
                   BLASTX
NCBI GI
                   q1084455
BLAST score
                   648
E value
                   6.0e-68
Match length
                   133
% identity
                   91
                  peptidylprolyl isomerase (EC 5.2.1.8) Cyp2 - rice
NCBI Description
                  >gi_600767 (L29469) cyclophilin 2 [Oryza sativa]
Seq. No.
                   414593
                   uC-osflcyp158c03a1
Seq. ID
Method
                   BLASTN
NCBI GI
                   g1519250
BLAST score
                   276
E value
                   1.0e-154
                   284
Match length
                   99
% identity
NCBI Description Oryza sativa GF14-c protein mRNA, complete cds
Seq. No.
                   414594
```

E value

1.0e-19

uC-osflcyp158c03b1 Seq. ID BLASTX Method NCBI GI g1519251 BLAST score 525 8.0e-54 E value Match length 104 100 % identity NCBI Description (U65957) GF14-c protein [Oryza sativa] Seq. No. 414595 uC-osflcyp158c04a1 Seq. ID Method BLASTX NCBI GI q4581164 BLAST score 215 2.0e-17 E value 95 Match length % identity 45 NCBI Description (AC006220) putative polyprotein [Arabidopsis thaliana] Seq. No. 414596 uC-osflcyp158c04b1 Seq. ID Method BLASTX NCBI GI g2995405 BLAST score 238 E value 5.0e-20 Match length 126 37 % identity NCBI Description (Y12432) polyprotein [Ananas comosus] Seq. No. 414597 uC-osflcyp158c06b1 Seq. ID Method BLASTX NCBI GI g2062168 BLAST score 255 E value 6.0e-22 75 Match length % identity NCBI Description (AC001645) hypothetical protein [Arabidopsis thaliana] 414598 Seq. No. Seq. ID uC-osflcyp158c08b1 BLASTX Method g3023816 NCBI GI BLAST score 154 E value 1.0e-19 97 Match length 63 % identity NCBI Description GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC >qi 968996 (U31676) glyceraldehyde-3-phosphate dehydrogenase [Oryza sativa] 414599 Seq. No. uC-osflcyp158c09b1 Seq. ID Method BLASTX NCBI GI q4417283 236 BLAST score

```
Match length
                  114
% identity
                  38
NCBI Description (AC007019) putative cytochrome p450 [Arabidopsis thaliana]
Seq. No.
                  414600
                  uC-osflcyp158c10b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2498077
BLAST score
                  503
E value
                  4.0e-51
Match length
                  120
% identity
                  84
                  NUCLEOSIDE DIPHOSPHATE KINASE I (NDK I) (NDP KINASE I)
NCBI Description
                   (PP18) >gi 1777930 (U55019) nucleoside diphosphate kinase
                   [Saccharum officinarum]
                  414601
Seq. No.
                  uC-osflcyp158c11a1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g6041757
BLAST score
                  349
                  0.0e+00
E value
Match length
                  377
% identity
                  98
NCBI Description Genomic Sequence For Oryza sativa Clone 10P20, Lemont
                  Strain, Complete Sequence, complete sequence
Seq. No.
                  414602
                  uC-osflcyp158c11b1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g6041757
BLAST score
                  320
                  1.0e-180
E value
Match length
                  352
% identity
                  98
                  Genomic Sequence For Oryza sativa Clone 10P20, Lemont
NCBI Description
                  Strain, Complete Sequence, complete sequence
                   414603
Seq. No.
Seq. ID
                  uC-osflcyp158c12b1
Method
                  BLASTX
NCBI GI
                  g4218535
BLAST score
                  246
E value
                   2.0e-23
Match length
                  78
% identity
                   68
NCBI Description (AJ010829) GRAB1 protein [Triticum sp.]
                   414604
Seq. No.
Seq. ID
                  uC-osflcyp158d01a1
                  BLASTN
Method
NCBI GI
                  g2662340
BLAST score
                  202
E value
                  1.0e-110
Match length
                  259
% identity
                   96
NCBI Description Oryza sativa mRNA for EF-1 alpha, complete cds
```

% identity

414605 Seq. No. Seq. ID uC-osflcyp158d01b1 Method BLASTX NCBI GI g2662343 BLAST score 640 E value 5.0e-67 123 Match length 99 % identity NCBI Description (D63581) EF-1 alpha [Oryza sativa] 414606 Seq. No. Seq. ID uC-osflcyp158d06b1 Method BLASTX NCBI GI g2293480 BLAST score 425 E value 7.0e-4284 Match length 99 % identity NCBI Description (AF011331) glycine-rich protein [Oryza sativa] Seq. No. 414607 Seq. ID uC-osflcyp158d07a1 BLASTX Method NCBI GI q601871 BLAST score 400 E value 4.0e-79 152 Match length % identity 98 NCBI Description (L34039) manganese superoxide dismutase [Oryza sativa] 414608 Seq. No. Seq. ID uC-osflcyp158d07b1 Method BLASTX NCBI GI g1170937 BLAST score 621 E value 9.0e-65 Match length 120 % identity 98 NCBI Description S-ADENOSYLMETHIONINE SYNTHETASE 1 (METHIONINE ADENOSYLTRANSFERASE 1) (ADOMET SYNTHETASE 1) >gi_450549_emb_CAA81481_ (Z26867) S-adenosyl methionine synthetase [Oryza sativa] Seq. No. 414609 uC-osflcyp158d08a1 Seq. ID Method BLASTX q3695404 NCBI GI BLAST score 270 E value 1.0e-23 Match length 113

NCBI Description (AF096373) contains similarity to DnaJ domains (Pfam:

PF00226, E=5.8e-13) [Arabidopsis thaliana]

>gi_4538977_emb_CAB39765.1_ (AL049487) putative protein

[Arabidopsis thaliana]



```
414610
Seq. No.
Seq. ID
                  uC-osflcyp158d09b1
                  BLASTX
Method
NCBI GI
                  g112802
BLAST score
                  175
                  6.0e-13
E value
Match length
                  58
% identity
                  57
                  4-COUMARATE--COA LIGASE >gi 82454 pir JU0311
NCBI Description
                  4-coumarate--CoA ligase (EC 6.2.1.12) - rice
                  >qi 20161 emb CAA36850 (X52623) 4-coumarate-CoA ligase
                   [Oryza sativa]
                  414611
Seq. No.
                  uC-osflcyp158e01b1
Seq. ID
                  BLASTN
Method
                  g2739216
NCBI GI
                  77
BLAST score
                  3.0e-35
E value
                  85
Match length
                  98
% identity
NCBI Description Hordeum vulgare L41 ribosomal protein
                   414612
Seq. No.
                  uC-osflcyp158e06b1
Seq. ID
Method
                  BLASTX
                  g4006978
NCBI GI
BLAST score
                  191
E value
                   2.0e-14
Match length
                  90
                   41
% identity
NCBI Description (AJ131335) pollen allergen (group II) [Cynodon dactylon]
                   414613
Seq. No.
Seq. ID
                  uC-osflcyp158e08a1
Method
                  BLASTX
NCBI GI
                   g3789954
BLAST score
                   245
                   8.0e-21
E value
Match length
                   44
% identity
                   100
NCBI Description (AF094776) chlorophyll a/b-binding protein precursor [Oryza
                   sativa]
Seq. No.
                   414614
Seq. ID
                   uC-osflcyp158e08b1
Method
                   BLASTN
NCBI GI
                   q3789953
BLAST score
                   101
                   1.0e-49
E value
                   188
Match length
% identity
```

NCBI Description Oryza sativa chlorophyll a/b-binding protein precursor

(Cab26) mRNA, nuclear gene encoding chloroplast protein,

complete cds

Seq. No. 414615

```
uC-osflcyp158f02b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4006978
BLAST score
                  201
E value
                  1.0e-15
Match length
                  87
% identity
                 (AJ131335) pollen allergen (group II) [Cynodon dactylon]
NCBI Description
                  414616
Seq. No.
Seq. ID
                  uC-osflcyp158f03b1
                  BLASTX
Method
NCBI GI
                  q4803929
BLAST score
                  152
E value
                  8.0e-10
Match length
                  77
                  45
% identity
                  (AC006264) putative proline-rich protein [Arabidopsis
NCBI Description
                  thaliana]
                  414617
Seq. No.
Seq. ID
                  uC-osflcyp158f05b1
Method
                  BLASTX
NCBI GI
                  q4321401
BLAST score
                  338
E value
                  1.0e-31
Match length
                  91
                  33
% identity
NCBI Description (AF047353) LIM domain protein PLIM-2 [Helianthus annuus]
Seq. No.
                  414618
                  uC-osflcyp158f07b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g417154
BLAST score
                  614
E value
                   4.0e-64
Match length
                  131
                  92
% identity
NCBI Description HEAT SHOCK PROTEIN 82 >gi 100685 pir S25541 heat shock
                  protein 82 - rice (strain Taichung Native One)
                  >gi_20256_emb_CAA77978_ (Z11920) heat shock protein 82
                   (HSP82) [Oryza sativa]
                   414619
Seq. No.
Seq. ID
                  uC-osflcyp158f09a1
Method
                  BLASTX
NCBI GI
                  g3915052
BLAST score
                  353
E value
                   2.0e-33
                  77
Match length
                  81
% identity
NCBI Description SUCROSE SYNTHASE 1 (SUCROSE-UDP GLUCOSYLTRANSFERASE 1)
                   >gi 1255982 emb CAA65639.1 (X96938) sucrose-synthase 1
                   [Tulipa gesneriana]
Seq. No.
                   414620
Seq. ID
                   uC-osflcyp158f09b1
```

```
Method
                  BLASTX
NCBI GI
                  g3377802
                  773
BLAST score
                  1.0e-82
E value
                  160
Match length
                  86
% identity
                  (AF075597) Similar to sucrose synthase; T2H3.8 [Arabidopsis
NCBI Description
                  thaliana]
                  414621
Seq. No.
                  uC-osflcyp158f11a1
Seq. ID
                  {\tt BLASTX}
Method
NCBI GI
                  q3023947
                  202
BLAST score
                  1.0e-15
E value
                  80
Match length
                  53
% identity
NCBI Description PROBABLE HISTONE DEACETYLASE (RPD3 HOMOLOG) >gi 2665840
                   (AF035815) putative histone deacetylase RPD3 [Zea mays]
                  414622
Seq. No.
                  uC-osflcyp158f11b1
Seq. ID
                  BLASTX
Method
NCBI GI
                  g4467119
                   460
BLAST score
                   5.0e-46
E value
                  98
Match length
                   87
% identity
NCBI Description (AL035538) Histone deacetylase [Arabidopsis thaliana]
                   414623
Seq. No.
Seq. ID
                   uC-osflcyp158g01a1
                  BLASTX
Method
NCBI GI
                   q2623298
BLAST score
                  202
                   1.0e-15
E value
                   63
Match length
                   62
% identity
NCBI Description (AC002409) putative 4-alpha-glucanotransferase [Arabidopsis
                   thaliana]
                   414624
Seq. No.
Seq. ID
                   uC-osflcyp158g01b1
Method
                   BLASTX
                   q2623298
NCBI GI
                   433
BLAST score
E value
                   1.0e-42
Match length
                   142
% identity
NCBI Description (AC002409) putative 4-alpha-glucanotransferase [Arabidopsis
                   thaliana]
```

Seq. ID uC-osflcyp158g03a1

Method BLASTX NCBI GI q3370780 BLAST score 322

414631

```
5.0e-30
E value
Match length
                  58
                  100
% identity
NCBI Description (AB016497) chitinase [Oryza sativa]
                  414626
Seq. No.
Seq. ID
                  uC-osflcyp158g03b1
Method
                  BLASTX
NCBI GI
                  g629777
BLAST score
                  254
                  7.0e - 36
E value
                  98
Match length
                  76
% identity
NCBI Description chitinase (EC 3.2.1.14) - barley >gi_563487_emb_CAA55344_
                  (X78671) chitinase [Hordeum vulgare]
                  414627
Seq. No.
Seq. ID
                  uC-osflcyp158g08b1
Method
                  BLASTX
NCBI GI
                  g2191149
                  224
BLAST score
E value
                  2.0e-18
                  85
Match length
                  54
% identity
NCBI Description (AF007269) Similar to protein kinase [Arabidopsis thaliana]
                   414628
Seq. No.
Seq. ID
                  uC-osflcyp158g10b1
Method
                  BLASTX
NCBI GI
                  g4914452
                  328
BLAST score
                  1.0e-30
E value
Match length
                  115
                  58
% identity
NCBI Description (AL050398) putative protein [Arabidopsis thaliana]
                   414629
Seq. No.
Seq. ID
                  uC-osflcyp158g11b1
Method
                  BLASTX
NCBI GI
                  g5734470
                  176
BLAST score
E value
                   6.0e-13
Match length
                  95
% identity
NCBI Description (AL109832) hypothetical protein [Schizosaccharomyces pombe]
Seq. No.
                   414630
                  uC-osflcyp158h01a1
Seq. ID
Method
                  BLASTX
                  g4973264
NCBI GI
BLAST score
                  242
                  1.0e-20
E value
                  67
Match length
% identity
NCBI Description (AF144391) thioredoxin-like 5 [Arabidopsis thaliana]
```



```
uC-osflcyp158h02b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q5080776
BLAST score
                  539
E value
                  3.0e-55
Match length
                  129
                  77
% identity
NCBI Description
                  (AC007576) Similar to protein kinases [Arabidopsis
                  thaliana]
Seq. No.
                  414632
                  uC-osflcyp158h03b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q5816996
BLAST score
                  221
E value
                  5.0e-18
Match length
                  50
                  86
% identity
NCBI Description
                  (AL110123) ribosomal protein L32-like protein [Arabidopsis
                  thaliana]
                  414633
Seq. No.
Seq. ID
                  uC-osflcyp158h04b1
Method
                  BLASTX
NCBI GI
                  q1841462
BLAST score
                  246
                   7.0e-21
E value
Match length
                  123
                   53
% identity
NCBI Description (Y10991) Elongation factor 2 [Nicotiana tabacum]
                   414634
Seq. No.
Seq. ID
                  uC-osflcyp158h11a1
Method
                  BLASTN
NCBI GI
                   g20280
BLAST score
                   86
E value
                   1.0e-40
                  203
Match length
                   91
% identity
NCBI Description Rice gene for phenylalanine ammonia-lyase (EC 4.3.1.5)
Seq. No.
                   414635
                   uC-osflcyp158h11b1
Seq. ID
Method
                  BLASTX
NCBI GI
                   g129591
BLAST score
                   368
E value
                   3.0e-35
Match length
                  105
                   70
% identity
NCBI Description PHENYLALANINE AMMONIA-LYASE >gi_295824 emb CAA34226
                   (X16099) phenylalanine ammonia-Tyase [Oryza sativa]
```

Seq. ID uC-osflcyp159a02a1

Method BLASTN NCBI GI g5803242

BLAST score 50

```
E value
                  3.0e-19
                  87
Match length
                  92
% identity
NCBI Description Oryza sativa genomic DNA, chromosome 6, clone:P0535G04
                  414637
Seq. No.
Seq. ID
                  uC-osflcyp159a02b1
Method
                  BLASTX
NCBI GI
                  g5803266
BLAST score
                  733
                  6.0e-78
E value
Match length
                  141
                  99
% identity
                 (AP000399) ESTs AU078063(S15496), C97608(C60475),
NCBI Description
                  C28255(C60475) correspond to a region of the predicted
                  gene; similar to plastid transketolase 2 (Y15782) [Oryza
                  sativa]
Seq. No.
                  414638
Seq. ID
                  uC-osflcyp159a05a1
Method
                  BLASTX
NCBI GI
                  g129591
BLAST score
                  186
E value
                  9.0e-14
                  40
Match length
                  90
% identity
NCBI Description PHENYLALANINE AMMONIA-LYASE >gi_295824_emb_CAA34226
                  (X16099) phenylalanine ammonia-lyase [Oryza sativa]
                  414639
Seq. No.
Seq. ID
                  uC-osflcyp159a05b1
Method
                  BLASTX
                  g129591
NCBI GI
BLAST score
                  424
                  5.0e-42
E value
                  97
Match length
                  88
% identity
NCBI Description PHENYLALANINE AMMONIA-LYASE >gi 295824 emb CAA34226
                  (X16099) phenylalanine ammonia-lyase [Oryza sativa]
Seq. No.
                  414640
Seq. ID
                  uC-osflcyp159a08a1
Method
                  BLASTX
```

NCBI GI q1707019 BLAST score 252 E value 2.0e-21 Match length 165 % identity 37

NCBI Description (U78721) hypothetical protein [Arabidopsis thaliana]

Seq. No. 414641

uC-osflcyp159a08b1 Seq. ID

Method BLASTX NCBI GI g1707019 BLAST score 144 6.0e-09 E value Match length 58

```
% identity
NCBI Description (U78721) hypothetical protein [Arabidopsis thaliana]
                  414642
Seq. No.
                  uC-osflcyp159a10b1
Seq. ID
                  BLASTX
Method
NCBI GI
                  q3482919
BLAST score
                  152
E value
                  9.0e-10
Match length
                  106
                  36
% identity
NCBI Description (AC003970) Putative protein kinase [Arabidopsis thaliana]
Seq. No.
                  414643
                  uC-osflcyp159a11b1
Seq. ID
                  BLASTX
Method
NCBI GI
                  g283008
BLAST score
                  837
E value
                  4.0e-90
Match length
                  161
                  99
% identity
                  sucrose synthase (EC 2.4.1.13) - rice
NCBI Description
                  >gi 20366 emb CAA46017 (X64770) sucrose synthase [Oryza
                  sativa]
                  414644
Seq. No.
                  uC-osflcyp159b01a1
Seq. ID
                  BLASTX
Method
NCBI GI
                  g4586594
BLAST score
                  315
                  7.0e-29
E value
                  63
Match length
% identity
                  100
NCBI Description (AB025001) polyubiquitin [Cicer arietinum]
                  414645
Seq. No.
Seq. ID
                  uC-osflcyp159b01b1
Method
                  BLASTX
NCBI GI
                  g418854
BLAST score
                  703
                  2.0e-74
E value
Match length
                  142
% identity
                  18
NCBI Description ubiquitin precursor - parsley >gi_288112_emb_CAA45621_
                   (X64344) polyubiquitin [Petroselinum crispum]
                  >gi_288114_emb_CAA45622_ (X64345) polyubiquitin
                   [Petroselinum crispum]
Seq. No.
                  414646
                  uC-osflcyp159b02b1
Seq. ID
                  BLASTX
Method
NCBI GI
                  q5931653
BLAST score
                  318
E value
                  3.0e-29
Match length
                  147
                  47
% identity
```

NCBI Description (AJ011628) squamosa promoter binding protein-like 1

[Arabidopsis thaliana]

414647 Seq. No.

Seq. ID uC-osflcyp159b03b1

BLASTX Method NCBI GI g3913633 BLAST score 196 E value 4.0e-23 Match length 80 % identity 68

NCBI Description HYPOTHETICAL PROTEIN F8A5.25 >gi 2462742 (AC002292) Unknown

protein [Arabidopsis thaliana]

Seq. No. 414648

uC-osflcyp159b06b1 Seq. ID

Method BLASTX NCBI GI g3646373 BLAST score 383 E value 3.0e-3773 Match length 99 % identity

NCBI Description (AJ011078) RGP1 protein [Oryza sativa]

414649 Seq. No.

Seq. ID uC-osflcyp159b08b1

Method BLASTX NCBI GI g2618691 BLAST score 162 E value 6.0e-11 Match length 61

52 % identity

NCBI Description (AC002510) putative chloroplast envelope Ca2+-ATPase

[Arabidopsis thaliana]

Seq. No. 414650

Seq. ID uC-osflcyp159b09b1

Method BLASTX g4539435 NCBI GI BLAST score 522 4.0e-53 E value 156 Match length 56 % identity

NCBI Description (AL049523) putative protein [Arabidopsis thaliana]

Seq. No. 414651

Seq. ID uC-osflcyp159b12a1

BLASTN Method NCBI GI q398603 BLAST score 39 E value 2.0e-12 Match length 63 % identity 90

NCBI Description A.thaliana ATAF1 mRNA

Seq. No. 414652

Seq. ID uC-osflcyp159b12b1

Method BLASTX

```
q4218535
NCBI GI
BLAST score
                  404
                  2.0e-39
E value
                  94
Match length
                  74
% identity
NCBI Description (AJ010829) GRAB1 protein [Triticum sp.]
Seq. No.
                  414653
                  uC-osflcyp159c02b1
Seq. ID
                  BLASTX
Method
NCBI GI
                  q3402282
BLAST score
                  170
E value
                  6.0e-12
                  87
Match length
                  43
% identity
NCBI Description (AJ000997) proline-rich protein [Solanum tuberosum]
                  414654
Seq. No.
Seq. ID
                  uC-osflcyp159c05b1
Method
                  BLASTX
NCBI GI
                  g445612
BLAST score
                  479
E value
                  4.0e-48
Match length
                  121
                  76
% identity
NCBI Description ribosomal protein S19 [Solanum tuberosum]
                  414655
Seq. No.
                  uC-osflcyp159c09b1
Seq. ID
                  BLASTX
Method
NCBI GI
                  g4406809
BLAST score
                  147
                  3.0e-09
E value
Match length
                  70
                  39
% identity
NCBI Description (AC006201) unknown protein [Arabidopsis thaliana]
                  414656
Seq. No.
Seq. ID
                  uC-osflcyp159c10b1
Method
                  BLASTX
NCBI GI
                  g6009521
BLAST score
                  303
E value
                  1.0e-27
Match length
                  136
                  47
% identity
NCBI Description (AB021491) p100 co-activator [Mus musculus]
                  414657
Seq. No.
Seq. ID
                  uC-osflcyp159c11b1
                  BLASTX
Method
NCBI GI
                  q2605617
BLAST score
                  687
E value
                  2.0e-72
Match length
                  132
% identity
NCBI Description (D88617) OSMYB1 [Oryza sativa]
```



Seq. ID uC-osflcyp159c12a1

Method BLASTX
NCBI GI g417488
BLAST score 201
E value 2.0e-15
Match length 44
% identity 84

NCBI Description ALPHA-GLUCAN PHOSPHORYLASE, H ISOZYME (STARCH PHOSPHORYLASE

H) >gi_100452_pir__A40995 starch phosphorylase (EC 2.4.1.1)
H - potato >gi_169473 (M69038) alpha-glucan phosphorylase

type H isozyme [Solanum tuberosum]

Seq. No. 414659

Seq. ID uC-osflcyp159c12b1

Method BLASTX
NCBI GI g417488
BLAST score 476
E value 5.0e-48
Match length 111
% identity 84

NCBI Description ALPHA-GLUCAN PHOSPHORYLASE, H ISOZYME (STARCH PHOSPHORYLASE

H) >gi_100452_pir__A40995 starch phosphorylase (EC 2.4.1.1)
H - potato >gi_169473 (M69038) alpha-glucan phosphorylase

type H isozyme [Solanum tuberosum]

Seq. No. 414660

Seq. ID uC-osflcyp159d02a1

Method BLASTX
NCBI GI g5381253
BLAST score 234
E value 2.0e-19
Match length 63
% identity 70

NCBI Description (AB027752) peroxidase [Nicotiana tabacum]

Seq. No. 414661

Seq. ID uC-osflcyp159d03b1

Method BLASTX
NCBI GI g4588003
BLAST score 336
E value 2.0e-31
Match length 85
% identity 79

NCBI Description (AF085279) hypothetical EIF-2-Alpha [Arabidopsis thaliana]

Seq. No. 414662

Seq. ID uC-osflcyp159d04a1

Method BLASTX
NCBI GI g2500353
BLAST score 317
E value 3.0e-29
Match length 64
% identity 94

NCBI Description 60S RIBOSOMAL PROTEIN L10-3 (QM/R22) >gi 1293784 (U55048)

similar to human QM protein, a putative tumor supressor, and to maize ubiquinol-cytochrome C reductase complex

subunit VI requiring protein SC34 [Oryza sativa]

Seq. No. 414663 Seq. ID uC-osflcyp159d04b1 Method BLASTX NCBI GI g2500353 713 BLAST score E value 1.0e-75 137 Match length 97 % identity NCBI Description 60S RIBOSOMAL PROTEIN L10-3 (QM/R22) >gi 1293784 (U55048) similar to human QM protein, a putative tumor supressor, and to maize ubiquinol-cytochrome C reductase complex subunit VI requiring protein SC34 [Oryza sativa] 414664 Seq. No. Seq. ID uC-osflcyp159d06b1 Method BLASTX NCBI GI g4580389 BLAST score 344 E value 2.0e-32 Match length 123 57 % identity NCBI Description (AC007171) unknown protein [Arabidopsis thaliana] Seq. No. 414665 Seq. ID uC-osflcyp159d07a1 Method BLASTX NCBI GI g5262760 BLAST score 234 2.0e-19 E value Match length 51 % identity NCBI Description (AL080283) Beta-COP-like protein [Arabidopsis thaliana] Seq. No. 414666 Seq. ID uC-osflcyp159d07b1 Method BLASTX NCBI GI g5262759 BLAST score 654 E value 1.0e-68 Match length 148 % identity 84 NCBI Description (AL080283) putative protein [Arabidopsis thaliana] 414667 Seq. No. Seq. ID uC-osflcyp159d08a1 Method BLASTN NCBI GI g2267592 BLAST score 199 E value 1.0e-108 325 Match length % identity NCBI Description Oryza sativa glycine-rich RNA-binding protein mRNA,

Seq. No. 414668

complete cds

```
Seq. ID uC-osflcyp159d08b1
Method BLASTX
NCBI GI g2293480
BLAST score 451
```

% identity 100
NCBI Description (AF011331) glycine-rich protein [Oryza sativa]

Seq. No. 414669

E value

Match length

Seq. ID uC-osflcyp159d09b1

5.0e-45

88

Method BLASTX
NCBI GI g2213591
BLAST score 253
E value 1.0e-21
Match length 73
% identity 66

NCBI Description (AC000348) T7N9.11 [Arabidopsis thaliana]

Seq. No. 414670

Seq. ID uC-osflcyp159d10a1

Method BLASTX
NCBI GI g3269287
BLAST score 241
E value 3.0e-20
Match length 73
% identity 58

NCBI Description (AL030978) GH3 like protein [Arabidopsis thaliana]

Seq. No. 414671

Seq. ID uC-osflcyp159d10b1

Method BLASTX
NCBI GI g3269287
BLAST score 494
E value 5.0e-50
Match length 135
% identity 67

NCBI Description (AL030978) GH3 like protein [Arabidopsis thaliana]

Seq. No. 414672

Seq. ID uC-osflcyp159e01a1

Method BLASTX
NCBI GI g3980406
BLAST score 183
E value 2.0e-13
Match length 71
% identity 48

NCBI Description (AC004561) putative tropinone reductase [Arabidopsis

thaliana]

Seq. No. 414673

Seq. ID uC-osflcyp159e01b1

Method BLASTX
NCBI GI g3980400
BLAST score 197
E value 2.0e-15
Match length 65

```
% identity
                  (AC004561) putative tropinone reductase [Arabidopsis
NCBI Description
                  thaliana]
                  414674
Seq. No.
                  uC-osflcyp159e02a1
Seq. ID
Method
                  BLASTN
NCBI GI
                  q3859567
BLAST score
                  141
E value
                  3.0e-73
Match length
                  287
                  91
% identity
NCBI Description Oryza sativa clone FIL1 unknown mRNA
Seq. No.
                  414675
                  uC-osflcyp159e02b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3859568
BLAST score
                  629
E value
                  1.0e-65
Match length
                  119
                  99
% identity
NCBI Description (AF098752) unknown [Oryza sativa]
                  414676
Seq. No.
Seq. ID
                  uC-osflcyp159e03b1
Method
                  BLASTX
NCBI GI
                  q2501189
BLAST score
                  455
E value
                  2.0e-45
Match length
                  127
% identity
                  74
                  THIAMINE BIOSYNTHETIC ENZYME 1-1 PRECURSOR
NCBI Description
                  >gi_2130146_pir__S61419 thiamine biosynthetic enzyme thi1-1
                   - maize >gi 596078 (U17350) thiamine biosynthetic enzyme
                   [Zea mays]
                   414677
Seq. No.
                  uC-osflcyp159e04b1
Seq. ID
                  BLASTX
Method
NCBI GI
                  g5668667
                  852
BLAST score
E value
                  8.0e-92
                  164
Match length
% identity
                   98
NCBI Description (D63136) Beta-tubulin [Zinnia elegans]
                   414678
Seq. No.
Seq. ID
                  uC-osflcyp159e06b1
                  BLASTX
Method
                  g3080393
NCBI GI
BLAST score
                  422
E value
                  1.0e-41
                  122
Match length
% identity
                   66
NCBI Description
                  (AL022603) NADH dehydrogenase like protein [Arabidopsis
                   thaliana]
```

```
414679
Seq. No.
Seq. ID
                  uC-osflcyp159e07a1
Method
                  BLASTX
NCBI GI
                  g2961343
BLAST score
                  461
                  5.0e-46
E value
Match length
                  99
% identity
                  91
                  (AL022140) symbiosis-related like protein [Arabidopsis
NCBI Description
                  thaliana]
                  414680
Seq. No.
Seq. ID
                  uC-osflcyp159e07b1
Method
                  BLASTX
NCBI GI
                  g4581162
BLAST score
                  334
E value
                   4.0e-31
Match length
                  80
% identity
                  84
NCBI Description (AC006220) putative symbiosis-related protein [Arabidopsis
                  thaliana]
Seq. No.
                  414681
Seq. ID
                  uC-osflcyp159e08b1
Method
                  BLASTN
NCBI GI
                  q3885885
BLAST score
                  143
E value
                  2.0e-74
Match length
                  150
                  99
% identity
NCBI Description Oryza sativa Rieske Fe-S precursor protein (RISP) mRNA,
                  complete cds
Seq. No.
                   414682
                  uC-osflcyp159e09b1
Seq. ID
Method
                  BLASTN
NCBI GI
                  q454880
BLAST score
                  193
E value
                  1.0e-104
                  398
Match length
                  99
% identity
NCBI Description Rice mRNA for WSI724 protein induced by water stress,
                  complete cds
                  414683
Seq. No.
Seq. ID
                  uC-osflcyp159e10b1
Method
                  BLASTX
                  g854731
NCBI GI
BLAST score
                  748
                  1.0e-79
E value
Match length
                  156
% identity
NCBI Description (U19183) acetyl-coenzyme A carboxylase [Zea mays]
                   414684
Seq. No.
Seq. ID
                  uC-osflcyp159e11a1
```



Method BLASTX NCBI GI q4490705 BLAST score 317 E value 4.0e-29 Match length 76 79 % identity (AL035680) ribosomal protein L14-like protein [Arabidopsis NCBI Description thaliana] Seq. No. 414685 Seq. ID uC-osflcyp159e11b1 Method BLASTX NCBI GI q5762251 BLAST score 531 E value 3.0e-54 Match length 124 81 % identity NCBI Description (AB008846) Csf-1 [Cucumis sativus] Seq. No. 414686 Seq. ID uC-osflcyp159e12b1 Method BLASTX NCBI GI q2911044 BLAST score 189 E value 3.0e-14 Match length 107 % identity 39 NCBI Description (AL021961) putative protein [Arabidopsis thaliana] Seq. No. 414687 uC-osflcyp159f04b1 Seq. ID Method BLASTX NCBI GI q2632252 BLAST score 328 E value 1.0e-30 Match length 66 97 % identity NCBI Description (Y12464) serine/threonine kinase [Sorghum bicolor] Seq. No. 414688 Seq. ID uC-osflcyp159f07a1 BLASTX Method NCBI GI g1173218 BLAST score 306 7.0e-28 E value Match length 62 94 % identity 40S RIBOSOMAL PROTEIN S15A >gi 440824 (L27461) ribosomal NCBI Description

protein S15 [Arabidopsis thaliana] >gi 2150130 (AF001412) cytoplasmic ribosomal protein S15a [Arabidopsis thaliana]

414689 Seq. No.

Seq. ID uC-osflcyp159f12a1

BLASTN Method NCBI GI g5257255 BLAST score 224 E value 1.0e-123



Match length 263 % identity 97

NCBI Description Oryza sativa genomic DNA, chromosome 8, clone:P0026F07

Seq. No. 414690

Seq. ID uC-osflcyp159g01b1

Method BLASTX
NCBI GI g3482918
BLAST score 366
E value 6.0e-39
Match length 100
% identity 82

NCBI Description (AC003970) Similar to ATP-citrate-lyase [Arabidopsis

thaliana]

Seq. No. 414691

Seq. ID uC-osflcyp159g03b1

Method BLASTX
NCBI GI g1617206
BLAST score 174
E value 1.0e-12
Match length 48
% identity 71

NCBI Description (Z72489) CP12 [Pisum sativum]

Seq. No. 414692

Seq. ID uC-osflcyp159g06b1

Method BLASTX
NCBI GI g1707657
BLAST score 318
E value 3.0e-29
Match length 128
% identity 53

NCBI Description (Z71640) DnaJ homologue [Pisum sativum]

Seq. No. 414693

Seq. ID uC-osflcyp159g07a1

Method BLASTN
NCBI GI g2331130
BLAST score 206
E value 1.0e-112
Match length 206
% identity 100

NCBI Description Oryza sativa glycine-rich protein (OSGRP1) mRNA, complete

cds

Seq. No. 414694

Seq. ID uC-osflcyp159g07b1

Method BLASTX
NCBI GI g2293480
BLAST score 431
E value 1.0e-42
Match length 85
% identity 98

NCBI Description (AF011331) glycine-rich protein [Oryza sativa]

Seq. No. 414695

Seq. ID

uC-osflcyp159g08b1 Seq. ID BLASTX Method NCBI GI g2642213 BLAST score 312 1.0e-28 E value Match length 68 % identity 85 (AF030385) nitrate-induced NOI protein [Zea mays] NCBI Description >gi_2895781 (AF045033) nitrate-induced NOI protein [Zea mays] 414696 Seq. No. uC-osflcyp159g11b1 Seq. ID Method BLASTX NCBI GI g3319345 BLAST score 264 7.0e-23 E value Match length 160 % identity 38 NCBI Description (AF077407) contains similarity to maize transposon MuDR (GB:M76978) [Arabidopsis thaliana] Seq. No. 414697 uC-osflcyp159g12a1 Seq. ID Method BLASTX NCBI GI g2130069 194 BLAST score 9.0e-15 E value 39 Match length 95 % identity NCBI Description catalase (EC 1.11.1.6) catA - rice >gi_1261858_dbj_BAA06232_ (D29966) catalase [Oryza sativa] 414698 Seq. No. uC-osflcyp159g12b1 Seq. ID BLASTX Method NCBI GI g2130069 BLAST score 637 E value 8.0e-67 Match length 124 94 % identity NCBI Description catalase (EC 1.11.1.6) catA - rice >gi_1261858_dbj_BAA06232_ (D29966) catalase [Oryza sativa] Seq. No. 414699 Seq. ID uC-osflcyp159h02a1 Method BLASTN NCBI GI g2773153 BLAST score 209 E value 1.0e-114 Match length 257 95 % identity NCBI Description Oryza sativa abscisic acid- and stress-inducible protein (Asr1) mRNA, complete cds 414700 Seq. No.

54092

uC-osflcyp159h02b1

```
BLASTN
Method
NCBI GI
                  g2773153
BLAST score
                  169
                  5.0e-90
E value
                  356
Match length
% identity
                  88
                  Oryza sativa abscisic acid- and stress-inducible protein
NCBI Description
                  (Asr1) mRNA, complete cds
                  414701
Seq. No.
                  uC-osflcyp159h03b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4914332
BLAST score
                  299
E value
                  4.0e-27
Match length
                  113
                  57
% identity
NCBI Description (AC005489) F14N23.18 [Arabidopsis thaliana]
Seq. No.
                  414702
Seq. ID
                  uC-osflcyp159h04a1
Method
                  BLASTX
NCBI GI
                  g1352468
BLAST score
                  340
E value
                  6.0e-32
Match length
                  76
                  83
% identity
                  BETA-FRUCTOFURANOSIDASE 1 PRECURSOR (SUCROSE-6-PHOSPHATE
NCBI Description
                  HYDROLASE 1) (INVERTASE 1) >gi_1122439 (U16123) invertase
                  [Zea mays]
                   414703
Seq. No.
                  uC-osflcyp159h04b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1352468
BLAST score
                  609
                   2.0e-63
E value
Match length
                  128
% identity
                  88
                  BETA-FRUCTOFURANOSIDASE 1 PRECURSOR (SUCROSE-6-PHOSPHATE
NCBI Description
                   HYDROLASE 1) (INVERTASE 1) >gi_1122439 (U16123) invertase
                   [Zea mays]
                   414704
Seq. No.
                   uC-osflcyp159h05a1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1197587
                   313
BLAST score
                  1.0e-28
E value
                  63
Match length
                   100
% identity
NCBI Description (U46758) potassium channel beta subunit protein [Oryza
                   sativa]
                   414705
Seq. No.
Seq. ID
                   uC-osflcyp159h05b1
```

BLASTX

Method

```
q2832783
NCBI GI
BLAST score
                  532
                  2.0e-54
E value
Match length
                  115
% identity
                  86
NCBI Description (AJ225806) potassium channel beta subunit [Egeria densa]
Seq. No.
                  414706
Seq. ID
                  uC-osflcyp159h06b1
Method
                  BLASTX
NCBI GI
                  q1653767
BLAST score
                  164
                  3.0e-11
E value
Match length
                  53
                  58
% identity
NCBI Description (D90916) oligopeptidase A [Synechocystis sp.]
Seq. No.
                  414707
Seq. ID
                  uC-osflcyp159h07b1
Method
                  BLASTX
NCBI GI
                  g4432861
BLAST score
                  203
E value
                  5.0e-16
                  75
Match length
% identity
                  60
NCBI Description (AC006300) hypothetical protein [Arabidopsis thaliana]
                  414708
Seq. No.
                  uC-osflcyp159h09b1
Seq. ID
Method
                  BLASTX
                  g2266985
NCBI GI
BLAST score
                  460
                  7.0e-46
E value
                  127
Match length
% identity
                  69
NCBI Description (Y13943) METRS [Arabidopsis thaliana]
                  414709
Seq. No.
Seq. ID
                  uC-osflcyp159h10a1
                  BLASTX
Method
                  g4886756
NCBI GI
BLAST score
                  446
E value
                  3.0e-44
Match length
                  92
% identity
                  86
NCBI Description (AF088917) cellulose synthase catalytic subunit
                  [Arabidopsis thaliana]
                   414710
Seq. No.
Seq. ID
                  uC-osflcyp159h10b1
Method
                  BLASTX
NCBI GI
                  q4886756
                  490
BLAST score
E value
                  2.0e-49
Match length
                  119
% identity
NCBI Description (AF088917) cellulose synthase catalytic subunit
```

[Arabidopsis thaliana]

Seq. No. 414711 Seq. ID uC-osflcyp159h11b1 Method BLASTX NCBI GI g3337356 BLAST score 523 E value 3.0e-53Match length 109 % identity 94 NCBI Description (AC004481) putative protein transport protein SEC61 alpha subunit [Arabidopsis thaliana] Seq. No. 414712 Seq. ID uC-osflcyp159h12a1 Method BLASTN NCBI GI q450548 BLAST score 173 E value 1.0e-92 Match length 173 % identity 100 NCBI Description O.sativa (pRSAM-1) gene for S-adenosyl methionine synthetase Seq. No. 414713 Seq. ID uC-osflcyp159h12b1 Method BLASTX NCBI GI g1170937 BLAST score 667 E value 4.0e-70 Match length 129 98 % identity NCBI Description S-ADENOSYLMETHIONINE SYNTHETASE 1 (METHIONINE ADENOSYLTRANSFERASE 1) (ADOMET SYNTHETASE 1) >gi_450549_emb_CAA81481 (Z26867) S-adenosyl methionine synthetase [Oryza sativa] 414714 Seq. No. Seq. ID uC-osflcyp160a03a1 Method BLASTX NCBI GI g283000 BLAST score 406 2.0e-39 E value

Match length 79 % identity 97

NCBI Description 1,4-alpha-glucan branching enzyme (EC 2.4.1.18) I precursor - rice >gi_218151_dbj_BAA01855_ (D11082) branching enzyme-I

precursor [Oryza sativa]

>gi 4704818 gb AAD28284.1 AF136268 1 (AF136268)

starch-branching enzyme I [Oryza sativa subsp. japonica]

Seq. No. 414715

Seq. ID uC-osflcyp160a05a1

Method BLASTX NCBI GI q4689480 BLAST score 359 E value 4.0e-34

```
Match length
                  132
                  50
% identity
NCBI Description (AC007213) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  414716
Seq. ID
                  uC-osflcyp160a06a1
Method
                  BLASTN
NCBI GI
                  g5852170
BLAST score
                  68
E value
                  1.0e-29
Match length
                  120
% identity
                  46
                  Oryza sativa indica(GLA4) genomic DNA, chromosome 4, BAC
NCBI Description
                  clone:t17804
Seq. No.
                  414717
Seq. ID
                  uC-osflcyp160a10a1
Method
                  BLASTX
NCBI GI
                  g2072555
BLAST score
                  343
E value
                  4.0e-32
Match length
                  62
% identity
                  98
NCBI Description
                  (AF001396) metallothionein-like protein [Oryza sativa]
                  >gi_6103441_gb_AAF03603.1_ (AF147786) metallothionein-like
                  protein [Oryza sativa]
Seq. No.
                  414718
Seq. ID
                  uC-osflcyp160a11a1
Method
                  BLASTN
NCBI GI
                  g5852170
BLAST score
                  54
E value
                  2.0e-21
Match length
                  118
% identity
                  86
NCBI Description Oryza sativa indica(GLA4) genomic DNA, chromosome 4, BAC
                  clone:t17804
                  414719
Seq. No.
Seq. ID
                  uC-osflcyp160b01a1
Method
                  BLASTX
NCBI GI
                  g3157928
BLAST score
                  334
E value
                  4.0e-31
Match length
                  82
% identity
                  68
NCBI Description (AC002131) Similar to fumarylacetoacetate hydrolase,
                  gb L41670 from Emericella nidulans. [Arabidopsis thaliana]
Seq. No.
                  414720
Seq. ID
                  uC-osflcyp160b12a1
Method
                  BLASTX
NCBI GI
                  g5802606
BLAST score
                  146
E value
                  3.0e-09
Match length
                  43
% identity
                  65
```

```
NCBI Description (AF174486) methylenetetrahydrofolate reductase [Zea mays]
Seq. No.
                  414721
Seq. ID
                  uC-osflcyp160c01a1
Method
                  BLASTN
NCBI GI
                  g2984708
BLAST score
                  75
E value
                  8.0e-34
                  157
Match length
                  88
% identity
                  Zea mays DnaJ-related protein ZMDJ1 (mdJ1) gene, complete
NCBI Description
                  cds >gi 5996689 gb AR066473.1 AR066473 Sequence 2 from
                  patent US
Seq. No.
                  414722
Seq. ID
                  uC-osflcyp160c02a1
Method
                  BLASTX
NCBI GI
                  g136739
BLAST score
                  359
                  5.0e-34
E value
Match length
                  81
% identity
                  83
NCBI Description UTP--GLUCOSE-1-PHOSPHATE URIDYLYLTRANSFERASE (UDP-GLUCOSE
                  PYROPHOSPHORYLASE) (UDPGP) >gi 67061 pir XNPOU
                  UTP--glucose-1-phosphate uridylyltransferase (EC 2.7.7.9) -
                  potato >gi_218001_dbj_BAA00570_ (D00667) UDP-glucose
                  pyrophosphorylase precursor [Solanum tuberosum]
Seq. No.
                  414723
Seq. ID
                  uC-osflcyp160c03a1
Method
                  BLASTX
NCBI GI
                  g1136122
BLAST score
                  219
E value
                  3.0e-18
                  44
Match length
                  95
% identity
NCBI Description (X91807) alfa-tubulin [Oryza sativa]
Seq. No.
                  414724
Seq. ID
                  uC-osflcyp160c09a1
Method
                  BLASTX
NCBI GI
                  g3183991
BLAST score
                  279
E value
                  1.0e-24
Match length
                  137
% identity
                  45
NCBI Description (AJ005173) P69F protein [Lycopersicon esculentum]
Seq. No.
                  414725
Seq. ID
                  uC-osflcyp160c11a1
Method
                  BLASTN
NCBI GI
                  g3885887
BLAST score
                  448
E value
                  0.0e+00
Match length
                  452
                  100
% identity
NCBI Description Oryza sativa high mobility group protein (HMG) mRNA,
```

complete cds

Seq. No. 414726 Seq. ID uC-osflcyp160d01a1 Method BLASTX NCBI GI g3169182

BLAST score 258
E value 3.0e-22
Match length 54
% identity 85

NCBI Description (AC004401) unknown protein [Arabidopsis thaliana]

Seq. No. 414727

Seq. ID uC-osflcyp160d06a1

Method BLASTX
NCBI GI g2244787
BLAST score 221
E value 7.0e-18
Match length 71
% identity 61

NCBI Description (Z97335) hypothetical protein [Arabidopsis thaliana]

Seq. No. 414728

Seq. ID uC-osflcyp160d08a1

Method BLASTN
NCBI GI g2570514
BLAST score 317
E value 1.0e-178
Match length 369
% identity 96

NCBI Description Oryza sativa glycolate oxidase (GOX) mRNA, complete cds

Seq. No. 414729

Seq. ID uC-osflcyp160d09a1

Method BLASTX
NCBI GI 93790593
BLAST score 147
E value 3.0e-09
Match length 66
% identity 42

NCBI Description (AF079185) RING-H2 finger protein RHY1a [Arabidopsis

thaliana]

Seq. No. 414730

Seq. ID uC-osflcyp160e06a1

Method BLASTX
NCBI GI g5734618
BLAST score 175
E value 2.0e-12
Match length 108
% identity 36

NCBI Description (AP000391) Similar to Arabidopsis thaliana chromosome II

BAC F5H14 genomic sequence; unknown protein (AC006234)

[Oryza sativa]

Seq. No. 414731

Seq. ID uC-osflcyp160e08a1



Method BLASTN
NCBI GI g11957
BLAST score 463
E value 0.0e+00
Match length 495
% identity 98

NCBI Description Rice complete chloroplast genome

Seq. No. 414732

Seq. ID uC-osflcyp160f02a1

Method BLASTX
NCBI GI g2598575
BLAST score 300
E value 5.0e-27
Match length 121
% identity 48

NCBI Description (Y15293) MtN21 [Medicago truncatula]

Seq. No. 414733

Seq. ID uC-osflcyp160f03a1

Method BLASTX
NCBI GI g3885334
BLAST score 205
E value 5.0e-16
Match length 72
% identity 58

NCBI Description (AC005623) putative argonaute protein [Arabidopsis

thaliana]

Seq. No. 414734

Seq. ID uC-osflcyp160f10a1

Method BLASTX
NCBI GI g1076511
BLAST score 512
E value 6.0e-52
Match length 120
% identity 82

NCBI Description H+-transporting ATPase (EC 3.6.1.35) - kidney bean

>qi 758250 emb CAA59799 (X85804) H(+)-transporting ATPase

[Phaseolus vulgaris]

Seq. No. 414735

Seq. ID uC-osflcyp160f11a1

Method BLASTX
NCBI GI g2911280
BLAST score 338
E value 1.0e-31
Match length 80
% identity 76

NCBI Description (U73937) PK12 protein kinase [Nicotiana tabacum]

Seq. No. 414736

Seq. ID uC-osflcyp160g01a1

Method BLASTX
NCBI GI g4490297
BLAST score 337
E value 2.0e-31

Seq. No.

414742

```
126
Match length
% identity
NCBI Description (AL035678) putative protein [Arabidopsis thaliana]
                  414737
Seq. No.
Seq. ID
                  uC-osflcyp160g04a1
Method
                  BLASTX
NCBI GI
                  g4455244
BLAST score
                  334
E value
                  4.0e-31
Match length
                  143
                  45
% identity
NCBI Description (AL035523) MtN3-like protein [Arabidopsis thaliana]
Seq. No.
                  414738
Seq. ID
                  uC-osflcyp160g05a1
Method
                  BLASTX
NCBI GI
                  g2739382
BLAST score
                  257
E value
                  4.0e-22
Match length
                  123
                  47
% identity
                  (AC002505) myosin heavy chain-like protein [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  414739
Seq. ID
                  uC-osflcyp160h01a1
Method
                  BLASTN
NCBI GI
                  g1009209
BLAST score
                  66
E value
                  2.0e-29
                  70
Match length
                  99
% identity
NCBI Description Notothixos leiophyllus 18S ribosomal RNA gene, partial
                  sequence
                  414740
Seq. No.
Seq. ID
                  uC-osflcyp160h03a1
Method
                  BLASTX
NCBI GI
                  g3582335
BLAST score
                  483
E value
                  1.0e-48
Match length
                  104
                  82
% identity
NCBI Description (AC005496) unknown protein [Arabidopsis thaliana]
                  414741
Seq. No.
Seq. ID
                  uC-osflcyp160h04a1
Method
                  BLASTX
                  g3135543
NCBI GI
BLAST score
                  264
                  7.0e-23
E value
Match length
                  49
% identity
NCBI Description (AF062393) aquaporin [Oryza sativa]
```



uC-osflcyp160h05a1 Seq. ID BLASTX Method NCBI GI g2961176 BLAST score 378 E value 3.0e-36 92 Match length % identity NCBI Description (AF050674) ribosomal protein L27 precursor [Oryza sativa] Seq. No. 414743 Seq. ID uC-osflcyp160h06a1 Method BLASTX NCBI GI a5091520 BLAST score 267 E value 3.0e-23 57 Match length % identity 95 NCBI Description (AB023482) ESTs AU058081(E30812), AU058365(E50679), AU030138(E50679) correspond to a region of the predicted gene.; Similar to Spinacia oleracea mRNA for proteasome 37kD subunit.(X96974) [Oryza sativa] Seq. No. 414744 Seq. ID uC-osflcyp161a01b1 Method BLASTX NCBI GI g114332 BLAST score 157 E value 1.0e-10 Match length 34 % identity 97 NCBI Description PLASMA MEMBRANE ATPASE 1 (PROTON PUMP) >gi_482389_pir__A45506 H+-transporting ATPase (EC 3.6.1.35) LHAI - tomato >gi 170464 (M60166) H+-ATPase [Lycopersicon esculentum] >gi_228405_prf__1803518A H ATPase [Lycopersicon esculentum] Seq. No. 414745 Seq. ID uC-osflcyp161a07a1 Method BLASTX NCBI GI g3122858 BLAST score 338 E value 1.0e-31 85 Match length 78 % identity NCBI Description D-3-PHOSPHOGLYCERATE DEHYDROGENASE PRECURSOR (PGDH) >gi_2189964_dbj BAA20405 (AB003280) Phosphoglycerate dehydrogenase [Arabidopsis thaliana] >gi 2804258_dbj_BAA24440_ (AB010407) phosphoglycerate dehydrogenase [Arabidopsis thaliana]

Seq. No. 414746

Seq. ID uC-osflcyp161a07b1

Method BLASTX NCBI GI g2911042 BLAST score 366 E value 2.0e-35 Match length 86

Match length

95

% identity NCBI Description (AL021961) Phosphoglycerate dehydrogenase - like protein [Arabidopsis thaliana] Seq. No. 414747 Seq. ID uC-osflcyp161a08b1 Method BLASTX NCBI GI g2827709 316 BLAST score 2.0e-29 E value 91 Match length 65 % identity NCBI Description (AL021684) predicted protein [Arabidopsis thaliana] Seq. No. 414748 Seq. ID uC-osflcyp161a10b1 Method BLASTX NCBI GI g1076641 158 BLAST score E value 4.0e-11 Match length 43 % identity 67 tau-protein kinase (EC 2.7.1.135) homolog - common tobacco NCBI Description >gi 456356 emb CAA54803 (X77763) shaggy like protein kinase [Nicotiana tabacum] >gi 1094395 prf 2106142A Ser/Thr protein kinase [Nicotiana tabacum] Seq. No. 414749 Seq. ID uC-osflcyp161a11b1 Method BLASTX NCBI GI g6063548 323 BLAST score E value 4.0e-30 Match length 64 % identity 92 (AP000615) ESTs AU078175(C51476), AU068986(C51476) NCBI Description correspond to a region of the predicted gene.; similar to NADH dehydrogenase. (AC006532) [Oryza sativa] Seq. No. 414750 Seq. ID uC-osflcyp161b04b1 Method BLASTX NCBI GI g3334320 BLAST score 227 E value 1.0e-18 Match length 91 59 % identity NCBI Description 40S RIBOSOMAL PROTEIN SA (P40) >gi 2444420 (AF020553) ribosome-associated protein p40 [GTycine max] Seq. No. 414751 Seq. ID uC-osflcyp161b06b1 Method BLASTX NCBI GI g2662343 BLAST score 379 3.0e-42E value

% identity NCBI Description (D63581) EF-1 alpha [Oryza sativa] Seq. No. 414752 uC-osflcyp161b07a1 Seq. ID Method BLASTN NCBI GI g218209 BLAST score 190 E value 1.0e-102 270 Match length % identity 93 Oryza sativa mRNA for the small subunit of NCBI Description ribulose-1,5-bisphosphate carboxylase, complete cds, clone pOSSS2106 414753 Seq. No. Seq. ID uC-osflcyp161b07b1 Method BLASTX NCBI GI g2407281 BLAST score 212 E value 1.0e-27 Match length 84 % identity 82 NCBI Description (AF017363) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa] Seq. No. 414754 uC-osflcyp161b08a1 Seq. ID Method BLASTX NCBI GI g1881585 BLAST score 234 E value 2.0e-19 Match length 55 78 % identity NCBI Description (U72489) remorin [Solanum tuberosum] Seq. No. 414755 Seq. ID uC-osflcyp161b11b1 Method BLASTX NCBI GI g5732069 BLAST score 221 E value 1.0e-18 Match length 54 76 % identity NCBI Description (AF147263) contains similarity to Pfam family PF00036 - EF hand; score=11.7, E=0.66, N=1 [Arabidopsis thaliana] 414756 Seq. No. Seq. ID uC-osflcyp161c01b1 BLASTX Method NCBI GI g2245077 BLAST score 341 E value 4.0e-32 Match length 115 % identity

NCBI Description (Z97343) glucanase like protein [Arabidopsis thaliana]

```
Seq. No.
                  414757
Seq. ID
                  uC-osflcyp161c02b1
Method
                  BLASTX
NCBI GI
                  g133867
BLAST score
                  400
                  9.0e-40
E value
                  87
Match length
                  95
% identity
                  40S RIBOSOMAL PROTEIN S11 >gi_82722_pir__S16577 ribosomal
NCBI Description
                  protein S11 - maize >gi 22470 emb CAA39438 (X55967)
                  ribosomal protein S11 [Zea mays]
                  414758
Seq. No.
Seq. ID
                  uC-osflcyp161c03a1
Method
                  BLASTX
NCBI GI
                  g2499417
BLAST score
                  422
E value
                  2.0e-41
Match length
                  103
% identity
                  78
                  GLYCINE CLEAVAGE SYSTEM H PROTEIN PRECURSOR
NCBI Description
                  >gi_1085826_pir__S49248 H-protein - Flaveria anomala
                  >gi_547558_emb_CAA85761_ (Z37524) H-protein [Flaveria
                  anomalal
Seq. No.
                  414759
Seq. ID
                  uC-osflcyp161c03b1
Method
                  BLASTX
NCBI GI
                  g2570497
BLAST score
                  336
E value
                  8.0e-32
                  70
Match length
% identity
                  96
NCBI Description
                  (AF022731) H protein subunit of glycine decarboxylase
                   [Oryza sativa]
                  414760
Seq. No.
Seq. ID
                  uC-osflcyp161c04b1
Method
                  BLASTX
NCBI GI
                  g1709620
                  176
BLAST score
                  5.0e-13
E value
                  79
Match length
                  42
% identity
NCBI Description PROTEIN DISULFIDE ISOMERASE PRECURSOR (PDI) >gi 508975
                   (U11496) protein disulfide isomerase [Triticum aestivum]
                  >gi 1094851 prf 2106410A protein disulfide isomerase
                  [Triticum aestivum]
```

414761 Seq. No.

Seq. ID uC-osflcyp161c06b1

Method BLASTX NCBI GI g4646217 BLAST score 274 E value 2.0e-24 Match length 68 % identity 81



NCBI Description (AC007290) putative phosphoprotein phosphatase [Arabidopsis thaliana]

Seq. No. 414762

Seq. ID uC-osflcyp161c07a1

Method BLASTX
NCBI GI g115813
BLAST score 194
E value 8.0e-15
Match length 49
% identity 76

NCBI Description CHLOROPHYLL A-B BINDING PROTEIN 8 PRECURSOR (LHCI TYPE III

CAB-8) >gi_19182_emb_CAA33330_ (X15258) Type III

chlorophyll a/b-binding protein [Lycopersicon esculentum]

Seq. No. 414763

Seq. ID uC-osflcyp161c07b1

Method BLASTX
NCBI GI g82080
BLAST score 334
E value 3.0e-31
Match length 93
% identity 73

NCBI Description chlorophyll a/b-binding protein type III precursor - tomato

>gi_226872_prf__1609235A chlorophyll a/b binding protein

[Lycopersicon esculentum]

Seq. No. 414764

Seq. ID uC-osflcyp161c08b1

Method BLASTX
NCBI GI g3287696
BLAST score 250
E value 9.0e-22
Match length 71
% identity 69

NCBI Description (AC003979) Strong similarity to phosphoribosylanthranilate

transferase gb_D86180 from Pisum sativum. This ORF may be part of a larger gene that lies in the overlapping region.

[Arabidopsis thaliana]

Seq. No. 414765

Seq. ID uC-osflcyp161c10b1

Method BLASTX
NCBI GI g4185511
BLAST score 223
E value 2.0e-18
Match length 68
% identity 65

NCBI Description (AF102822) actin depolymerizing factor 4 [Arabidopsis

thaliana]

Seq. No. 414766

Seq. ID uC-osflcyp161d02a1

Method BLASTN
NCBI GI g3298473
BLAST score 303
E value 1.0e-170



Match length 332 % identity 97

NCBI Description Oryza sativa gene for ovpl, complete cds

Seq. No. 414767

Seq. ID uC-osflcyp161d02b1

Method BLASTX
NCBI GI g3298474
BLAST score 292
E value 6.0e-43
Match length 98
% identity 96

NCBI Description (AB012765) ovpl [Oryza sativa]

Seq. No. 414768

Seq. ID uC-osflcyp161d06b1

Method BLASTX
NCBI GI g1657621
BLAST score 423
E value 9.0e-42
Match length 118
% identity 69

NCBI Description (U72505) G6p [Arabidopsis thaliana] >gi_3068711 (AF049236)

putative acyl-coA dehydrogenase [Arabidopsis thaliana]
>gi_5478795_dbj_BAA82478.1_ (AB017643) Short-chain acyl CoA

oxidase [Arabidopsis thaliana]

Seq. No. 414769

Seq. ID uC-osflcyp161d07b1

Method BLASTX
NCBI GI g2267593
BLAST score 148
E value 8.0e-10
Match length 43
% identity 70

NCBI Description (AF009411) glycine-rich RNA-binding protein [Oryza sativa]

Seq. No. 414770

Seq. ID uC-osflcyp161d08b1

Method BLASTX
NCBI GI g2244839
BLAST score 232
E value 3.0e-19
Match length 92
% identity 42

NCBI Description (Z97337) hypothetical protein [Arabidopsis thaliana]

Seq. No. 414771

Seq. ID uC-osflcyp161d09b1

Method BLASTX
NCBI GI g3776005
BLAST score 641
E value 4.0e-67
Match length 144
% identity 85

NCBI Description (AJ010466) RNA helicase [Arabidopsis thaliana]

NCBI GI

BLAST score

q3688173

327

```
Seq. No.
                  414772
Seq. ID
                  uC-osflcyp161e02a1
Method
                  {\tt BLASTX}
NCBI GI
                  g4063821
BLAST score
                  184
E value
                  1.0e-13
Match length
                  38
                  95
% identity
NCBI Description (AB015204) plastidic ATP sulfurylase [Oryza sativa]
Seq. No.
                  414773
Seq. ID
                  uC-osflcyp161e02b1
Method
                  BLASTN
NCBI GI
                  q3986152
BLAST score
                  64
E value
                  4.0e-28
Match length
                  80
                  95
% identity
NCBI Description Oryza sativa gene for plastidic ATP sulfurylase, complete
                  cds
                  414774
Seq. No.
Seq. ID
                  uC-osflcyp161e03a1
Method
                  BLASTX
NCBI GI
                  g4138290
BLAST score
                  190
E value
                  2.0e-14
Match length
                  39
% identity
                  100
NCBI Description (AJ005841) thioredoxin M [Oryza sativa]
Seq. No.
                  414775
Seq. ID
                  uC-osflcyp161e03b1
Method
                  BLASTX
NCBI GI
                  g4138290
BLAST score
                  328
E value
                  1.0e-31
Match length
                  77
% identity
                  91
NCBI Description (AJ005841) thioredoxin M [Oryza sativa]
                  414776
Seq. No.
Seq. ID
                  uC-osflcyp161e06b1
Method
                  BLASTX
NCBI GI
                  q3641837
BLAST score
                  386
                  3.0e-37
E value
Match length
                  94
% identity
                  81
NCBI Description (AL023094) Nonclathrin coat protein gamma-like protein
                  [Arabidopsis thaliana]
Seq. No.
                  414777
Seq. ID
                  uC-osflcyp161e08b1
Method
                  BLASTX
```

NCBI GI

E value

BLAST score

Match length

g5257255

1.0e-16

46

105

```
E value
                  9.0e-47
Match length
                  137
% identity
                  63
NCBI Description
                 (AL031804) putative protein [Arabidopsis thaliana]
Seq. No.
                  414778
                  uC-osflcyp161e09a1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g4138289
BLAST score
                  191
E value
                  1.0e-103
                  211
Match length
% identity
                  98
NCBI Description Oryza sativa mRNA for thioredoxin M
Seq. No.
                  414779
Seq. ID
                  uC-osflcyp161f03b1
Method
                  BLASTX
NCBI GI
                  g1710663
BLAST score
                  157
E value
                  3.0e-20
Match length
                  75
                  71
% identity
NCBI Description PUTATIVE DNA-DIRECTED RNA POLYMERASE III 130 KD POLYPEPTIDE
                   (RNA POLYMERASE III SUBUNIT 2) >gi_1204209_emb_CAA93558
                   (Z69727) putative DNA-directed RNA polymerase III 130 kd
                  subunit [Schizosaccharomyces pombe]
Seq. No.
                   414780
Seq. ID
                  uC-osflcyp161f04b1
Method
                  BLASTX
NCBI GI
                  g2072555
BLAST score
                  237
E value
                  5.0e-20
Match length
                  44
% identity
                  100
                  (AF001396) metallothionein-like protein [Oryza sativa]
NCBI Description
                  >gi 6103441 gb AAF03603.1 (AF147786) metallothionein-like
                  protein [Oryza sativa]
                  414781
Seq. No.
Seq. ID
                  uC-osflcyp161f06b1
Method
                  BLASTX
NCBI GI
                  g4138583
BLAST score
                  213
E value
                  5.0e-17
                  102
Match length
                  50
% identity
NCBI Description (Y10821) plastidic ATP/ADP-transporter [Solanum tuberosum]
                   414782
Seq. No.
Seq. ID
                  uC-osflcyp161f07a1
Method
                  BLASTN
```

% identity NCBI Description Oryza sativa genomic DNA, chromosome 8, clone: P0026F07 414783 Seq. No. Seq. ID uC-osflcyp161f08b1 BLASTX Method NCBI GI g2129754 BLAST score 264 E value 6.0e-23Match length 60 87 % identity translation elongation factor Tu precursor - Arabidopsis NCBI Description thaliana >gi_1149571_emb_CAA61511_ (X89227) mitochondrial elongation factor Tu [Arabidopsis thaliana] 414784 Seq. No. Seq. ID uC-osflcyp161f09b1 Method BLASTX NCBI GI q5731756 BLAST score 382 E value 3.0e-38 Match length 112 73 % identity NCBI Description (AL109819) putative protein [Arabidopsis thaliana] 414785 Seq. No. uC-osflcyp161f10b1 Seq. ID Method BLASTX NCBI GI g320618 BLAST score 511 E value 5.0e-52 Match length 114 85 % identity NCBI Description chlorophyll a/b-binding protein I precursor - rice >gi_218172_dbj_BAA00536_ (D00641) type I light-harvesting chlorophyll a/b-binding protein [Oryza sativa] >gi 227611 prf 1707316A chlorophyll a/b binding protein 1 [Oryza sativa] 414786 Seq. No. Seq. ID uC-osflcyp161g04a1 Method BLASTN NCBI GI g1815680 BLAST score 164 E value 4.0e-87 Match length 272 % identity NCBI Description Oryza sativa expansin (Os-EXP4) mRNA, complete cds Seq. No. 414787 Seq. ID uC-osflcyp161g05b1

Method BLASTX g6093869 NCBI GI BLAST score 184 E value 3.0e-23 Match length 74 % identity 82

NCBI Description 60S RIBOSOMAL PROTEIN L13A >qi 2982259 (AF051212) probable 60s ribosomal protein L13a [Picea mariana] 414788 Seq. No. Seq. ID uC-osflcyp161g09b1 Method BLASTX NCBI GI g2493318 BLAST score 206 E value 3.0e-16 77 Match length 51 % identity NCBI Description BLUE COPPER PROTEIN PRECURSOR >gi 562779 emb CAA80963 (Z25471) blue copper protein [Pisum sativum] >gi 1098264 prf 2115352A blue Cu protein [Pisum sativum] 414789 Seq. No. Seq. ID uC-osflcyp161g11b1 Method BLASTX NCBI GI g5031281 BLAST score 260 E value 1.0e-22 Match length 60 78 % identity NCBI Description (AF139499) unknown [Prunus armeniaca] Seq. No. 414790 Seq. ID uC-osflcyp161h01a1 Method BLASTN NCBI GI g5257255 BLAST score 336

E value 0.0e+00Match length 360

% identity 99 NCBI Description Oryza sativa genomic DNA, chromosome 8, clone:P0026F07

Seq. No. 414791

Seq. ID uC-osflcyp161h01b1

Method BLASTN NCBI GI g5257255 BLAST score 147 E value 4.0e-77 235 Match length % identity 91

NCBI Description Oryza sativa genomic DNA, chromosome 8, clone:P0026F07

414792 Seq. No.

Seq. ID uC-osflcyp161h02b1

Method BLASTX NCBI GI g1732511 BLAST score 195 E value 5.0e-15 Match length 53 % identity 74

NCBI Description (U62742) Ran binding protein 1 homolog [Arabidopsis

thaliana]

Seq. No. 414793

Seq. No.

414798

```
Seq. ID
                  uC-osflcyp161h05a1
Method
                  BLASTX
NCBI GI
                  g4006890
BLAST score
                  429
E value
                  3.0e-42
Match length
                  100
% identity
                  76
NCBI Description (Z99708) ubiquitin--protein ligase-like protein
                  [Arabidopsis thaliana]
Seq. No.
                  414794
Seq. ID
                  uC-osflcyp161h05b1
Method
                  BLASTX
NCBI GI
                  q4217999
BLAST score
                  186
E value
                  2.0e-14
Match length
                  87
% identity
                  54
NCBI Description (AC006135) putative ubiquitin--protein ligase
                  (ubiquitin-conjugating enzyme) [Arabidopsis thaliana]
                  414795
Seq. No.
Seq. ID
                  uC-osflcyp161h08a1
Method
                  BLASTX
NCBI GI
                  g584706
BLAST score
                  291
E value
                  4.0e-26
Match length
                  59
% identity
                  98
NCBI Description ASPARTATE AMINOTRANSFERASE, CYTOPLASMIC (TRANSAMINASE A)
                  >gi_2130066_pir__JC5124 aspartate transaminase (EC
                  2.6.1.1), cytoplasmic - rice >gi_287298_dbj_BAA03504_
                  (D14673) aspartate aminotransferase [Oryza sativa]
Seq. No.
                  414796
Seq. ID
                  uC-osflcyp161h09b1
Method
                  BLASTN
NCBI GI
                  g167107
BLAST score
                  46
E value
                  2.0e-16
Match length
                  151
% identity
                  89
NCBI Description Hordeum vulgare vacuolar ATPase B subunit isoform mRNA,
                  complete cds
Seq. No.
                  414797
Seq. ID
                  uC-osflcyp161h10a1
Method
                  BLASTX
NCBI GI
                  q4006890
BLAST score
                  205
E value
                  6.0e-16
Match length
                  90
% identity
                  52
NCBI Description (Z99708) ubiquitin--protein ligase-like protein
                  [Arabidopsis thaliana]
```

```
Seq. ID
                   uC-osflcyp162a03b1
Method
                   BLASTX
NCBI GI
                   q3264767
BLAST score
                   269
E value
                   2.0e-23
Match length
                   69
                   72
% identity
NCBI Description (AF071893) AP2 domain containing protein [Prunus armeniaca]
Seq. No.
                   414799
Seq. ID
                   uC-osflcyp162a05b1
Method
                   BLASTX
NCBI GI
                   g2281449
BLAST score
                   200
E value
                   2.0e-15
Match length
                   58
% identity
                   69
NCBI Description (U90214) leucine zipper transcription factor TGA2.1
                    [Nicotiana tabacum]
Seq. No.
                   414800
Seq. ID
                   uC-osflcyp162a06b1
Method
                   BLASTX
NCBI GI
                   q729135
BLAST score
                   177
E value
                   7.0e-13
Match length
                   83
% identity
                   52
NCBI Description CAFFEIC ACID 3-0-METHYLTRANSFERASE
                    (S-ADENOSYSL-L-METHIONINE: CAFFEIC ACID
                   3-O-METHYLTRANSFERASE) (COMT) >gi_283034_pir__S28612 catechol O-methyltransferase (EC \overline{2.1.1.6}) - maize
                   >gi_168532 (M73235) O-methyltransferase [Zea mays]
Seq. No.
                   414801
Seq. ID
                   uC-osflcyp162a07a1
Method
                   BLASTX
NCBI GI
                   g4680179
BLAST score
                   413
E value
                   2.0e-40
Match length
                   106
% identity
                   81
NCBI Description (AF111709) polyprotein [Oryza sativa subsp. indica]
Seq. No.
                   414802
Seq. ID
                   uC-osflcyp162a10b1
Method
                   BLASTX
NCBI GI
                   q4510363
BLAST score
                   497
E value
                   3.0e-50
Match length
                   104
% identity
                   87
NCBI Description
                   (AC007017) putative DNA-binding protein [Arabidopsis
                   thaliana]
Seq. No.
                   414803
Seq. ID
                   uC-osflcyp162a11b1
```



Method BLASTX
NCBI GI g3695403
BLAST score 539
E value 3.0e-55
Match length 123
% identity 85

NCBI Description (AF096373) contains similarity to the pfkB family of carbohydrate kinases (Pfam: PF00294, E=1.6e-75)

[Arabidopsis thaliana] >gi_4538955_emb_CAB39779.1

(AL049488) fructokinase-like protein [Arabidopsis thaliana]

Seq. No. 414804

Seq. ID uC-osflcyp162b01b1

Method BLASTX
NCBI GI g1076724
BLAST score 457
E value 7.0e-46
Match length 100
% identity 82

NCBI Description LHCI-680, photosystem I antenna protein - barley

>gi_666054_emb_CAA59049_ (X84308) LHCI-680, photosystem I

antenna protein [Hordeum vulgare]

Seq. No. 414805

Seq. ID uC-osflcyp162b06a1

Method BLASTN
NCBI GI g3789947
BLAST score 62
E value 3.0e-26
Match length 134
% identity 87

NCBI Description Oryza sativa translation initiation factor 5A (eIF-5A)

mRNA, complete cds

Seq. No. 414806

Seq. ID uC-osflcyp162b08a1

Method BLASTX
NCBI GI g1351017
BLAST score 277
E value 2.0e-24
Match length 61
% identity 84

NCBI Description 40S RIBOSOMAL PROTEIN S9 (S4) >gi 629697 pir S45375

ribosomal protein S4 - common tobacco (fragment)

>gi_443960_emb_CAA78463_ (Z14085) RIBOSOMAL PROTEIN S4

[Nicotiana tabacum]

Seq. No. 414807

Seq. ID uC-osflcyp162b09b1

Method BLASTX
NCBI GI g1710780
BLAST score 481
E value 3.0e-48
Match length 153
% identity 63

NCBI Description 40S RIBOSOMAL PROTEIN S9 (S7) >gi_1321917_emb_CAA65433_

(X96613) cytoplasmic ribosomal protein S7 [Podospora

Seq. No.

Seq. ID

414813

uC-osflcyp162c04a1



anserina]

```
Seq. No.
                   414808
Seq. ID
                   uC-osflcyp162b11b1
Method
                   BLASTX
NCBI GI
                   q3789948
BLAST score
                   703
                   2.0e-74
E value
Match length
                   133
                   100
% identity
NCBI Description (AF094773) translation initiation factor 5A [Oryza sativa]
                   414809
Seq. No.
                   uC-osflcyp162b12b1
Seq. ID
Method
                   BLASTX
                   g2911067
NCBI GI
BLAST score
                   623
                   4.0e-65
E value
                   137
Match length
% identity
                  (AL021960) UV-damaged DNA-binding protein-like [Arabidopsis
NCBI Description
                   thaliana]
                   414810
Seq. No.
                   uC-osflcyp162c02a1
Seq. ID
Method
                   BLASTX
NCBI GI
                   q4417280
BLAST score
                   195
E value
                   9.0e-15
Match length
                   77
% identity
                   57
NCBI Description (AC007019) putative ATP synthase [Arabidopsis thaliana]
                   414811
Seq. No.
Seq. ID
                   uC-osflcyp162c03a1
Method
                   BLASTX
                   q1076724
NCBI GI
BLAST score
                   272
                   7.0e-24
E value
                   63
Match length
% identity
                   83
                   LHCI-680, photosystem I antenna protein - barley
NCBI Description
                   >gi_666054_emb_CAA59049_ (X84308) LHCI-680, photosystem I
antenna protein [Hordeum vulgare]
Seq. No.
                   414812
                   uC-osflcyp162c03b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   q1084358
BLAST score
                   377
E value
                   4.0e-36
                   139
Match length
% identity
                   56
NCBI Description ATP synthase - soybean
```

BLASTN Method NCBI GI q3850815 BLAST score 298 E value 1.0e-167 Match length 337 97 % identity NCBI Description Oryza sativa mRNA for U2 snRNP auxiliary factor, small subunit 35b Seq. No. 414814 uC-osflcyp162c06a1 Seq. ID Method BLASTX NCBI GI g1730560 BLAST score 151 E value 9.0e-10 Match length 32 % identity 88 ALPHA-GLUCAN PHOSPHORYLASE, H ISOZYME (STARCH PHOSPHORYLASE NCBI Description H) >gi_510932_emb_CAA84494_ (Z35117) alpha 1,4-glucan phosphorylase type H [Vicia faba] Seq. No. 414815 uC-osflcyp162c06b1 Seq. ID Method BLASTX NCBI GI q401140 BLAST score 839 E value 3.0e-90 Match length 158 % identity 100 NCBI Description SUCROSE SYNTHASE 2 (SUCROSE-UDP GLUCOSYLTRANSFERASE 2) >gi 20095 emb CAA41774 (X59046) sucrose-UDP glucosyltransferase (isoenzyme 2) [Oryza sativa] >qi 1587662 prf 2207194A sucrose synthase:ISOTYPE=2 [Oryza sativa] Seq. No. 414816 Seq. ID uC-osflcyp162c07b1 Method BLASTX NCBI GI q2880043 BLAST score 211 E value 1.0e-16 95 Match length % identity 46 NCBI Description (AC002340) putative 3-hydroxyisobutyryl-coenzyme A hydrolase [Arabidopsis thaliana]

Seq. No.

Seq. ID uC-osflcyp162c10b1

414817

Method BLASTX
NCBI GI g5263324
BLAST score 566
E value 2.0e-58
Match length 122
% identity 89

NCBI Description (AC007727) Identical to gb_Y13173 Arabidopsis thaliana mRNA for proteasome subunit. EST gb T76747 comes from this gene

Seq. ID

```
Seq. No.
                  414818
Seq. ID
                  uC-osflcyp162c11b1
Method
                  BLASTX
NCBI GI
                  g417488
BLAST score
                  514
E value
                  5.0e-61
Match length
                  169
% identity
                  73
NCBI Description ALPHA-GLUCAN PHOSPHORYLASE, H ISOZYME (STARCH PHOSPHORYLASE
                  H) >gi_100452_pir__A40995 starch phosphorylase (EC 2.4.1.1)
                  H - potato >gi 169473 (M69038) alpha-glucan phosphorylase
                  type H isozyme [Solanum tuberosum]
                  414819
Seq. No.
Seq. ID
                  uC-osflcyp162c12a1
Method
                  BLASTN
NCBI GI
                  g20094
BLAST score
                  442
E value
                  0.0e+00
Match length
                  450
% identity
                  100
NCBI Description O.sativa RSs2 gene for sucrose-UDP glucosyltransferase
                  (isozyme 2)
Seq. No.
                  414820
Seq. ID
                  uC-osflcyp162d01b1
Method
                  BLASTX
NCBI GI
                  g5915836
BLAST score
                  297
E value
                  8.0e-27
Match length
                  94
                  62
% identity
NCBI Description CYTOCHROME P450 71D7 >gi_1762144 (U48435) putative
                  cytochrome P450 [Solanum chacoense]
                  414821
Seq. No.
Seq. ID
                  uC-osflcyp162d04b1
Method
                  BLASTX
NCBI GI
                  g3786001
BLAST score
                  206
E value
                  1.0e-16
Match length
                  53
% identity
NCBI Description (AC005499) unknown protein [Arabidopsis thaliana]
Seq. No.
                  414822
Seq. ID
                  uC-osflcyp162d06a1
Method
                  BLASTX
NCBI GI
                  g4176424
BLAST score
                  205
                  4.0e-16
E value
Match length
                  44
% identity
NCBI Description (AB022674) ribosomal protein L12 [Oryza sativa]
Seq. No.
                  414823
```

54116

uC-osflcyp162d08b1



Method BLASTX
NCBI GI g3513727
BLAST score 580
E value 6.0e-60
Match length 167
% identity 65

NCBI Description (AF080118) contains similarity to TPR domains (Pfam: TPR.hmm: score: 11.15) and kinesin motor domains (Pfam: kinesin2.hmm, score: 17.49, 20.52 and 10.94) [Arabidopsis thaliana] >gi_4539358_emb_CAB40052.1_ (AL049525) putative

protein [Arabidopsis thaliana]

Seq. No. 414824

Seq. ID uC-osflcyp162d10b1

Method BLASTX
NCBI GI g126888
BLAST score 522
E value 2.0e-53
Match length 107
% identity 93

NCBI Description MALATE DEHYDROGENASE [NADP], CHLOROPLAST PRECURSOR (NADP-MDH) >gi_319840_pir__DEMZMC malate dehydrogenase

(NADP+) (EC 1.1.1.82) precursor, chloroplast - maize >gi_22368_emb_CAA34213_ (X16084) precursor protein (AA -57 to 375) [Zea mays] >gi_226766_prf__1604473A NADP malate

dehydrogenase [Zea mays]

Seq. No. 414825

Seq. ID uC-osflcyp162d11a1

Method BLASTN
NCBI GI g4176423
BLAST score 83
E value 7.0e-39
Match length 148
% identity 88

NCBI Description Oryza sativa rpl12-2 gene for chloroplast ribosomal protein

L12, complete cds

Seq. No. 414826

Seq. ID uC-osflcyp162d11b1

Method BLASTX
NCBI GI g4176424
BLAST score 170
E value 5.0e-12
Match length 35
% identity 100

NCBI Description (AB022674) ribosomal protein L12 [Oryza sativa]

Seq. No. 414827

Seq. ID uC-osflcyp162d12b1

Method BLASTX
NCBI GI g3850816
BLAST score 467
E value 1.0e-46
Match length 93
% identity 91

NCBI Description (Y18348) U2 snRNP auxiliary factor, small subunit [Oryza



sativa]

```
Seq. No.
                   414828
                  uC-osflcyp162e01b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2773154
BLAST score
                  280
E value
                   9.0e-25
Match length
                   124
% identity
                   48
                  (AF039573) abscisic acid- and stress-inducible protein
NCBI Description
                   [Oryza sativa]
Seq. No.
                   414829
Seq. ID
                  uC-osflcyp162e03b1
Method
                  BLASTX
NCBI GI
                  g3386614
BLAST score
                   251
E value
                   2.0e-21
Match length
                  55
                   38
% identity
NCBI Description (AC004665) putative transcription factor SF3 [Arabidopsis
                  thaliana]
Seq. No.
                   414830
Seq. ID
                  uC-osflcyp162e04b1
Method
                  BLASTX
NCBI GI
                  q2286153
BLAST score
                  571
E value
                   6.0e-59
Match length
                  121
% identity
                   94
NCBI Description (AF007581) cytoplasmic malate dehydrogenase [Zea mays]
Seq. No.
                   414831
Seq. ID
                  uC-osflcyp162e05a1
Method
                  BLASTX
NCBI GI
                   q1706328
BLAST score
                   216
E value
                   1.0e-17
Match length
                   44
                   95
% identity
NCBI Description PYRUVATE DECARBOXYLASE ISOZYME 2 (PDC) >gi 1009710 (U27350)
                  pyruvate decarboxylase 2 [Oryza sativa] >g\bar{i} 1777455
                   (U38199) pyruvate decarboxylase 2 [Oryza sativa]
                   414832
Seq. No.
Seq. ID
                  uC-osflcyp162e05b1
                  BLASTX
Method
                  g2827524
NCBI GI
BLAST score
                  507
E value
                  2.0e-51
Match length
                  136
% identity
                   68
```

Seq. No. 414833

NCBI Description (AL021633) predicted protein [Arabidopsis thaliana]

Seq. No.

Seq. ID

414838

uC-osflcyp162e12a1

```
uC-osflcyp162e06b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1323748
BLAST score
                  200
E value
                  2.0e-15
Match length
                  84
                  49
% identity
NCBI Description
                 (U32430) thiol protease [Triticum aestivum]
                  414834
Seq. No.
Seq. ID
                  uC-osflcyp162e08a1
Method
                  BLASTN
NCBI GI
                  q2182028
BLAST score
                  361
E value
                  0.0e + 00
Match length
                  385
% identity
                  98
NCBI Description Oryza sativa mRNA for shaggy-like kinase etha
                  414835
Seq. No.
                  uC-osflcyp162e09b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2182029
BLAST score
                  412
                  3.0e-40
E value
Match length
                  86
% identity
NCBI Description (Y13437) shaggy-like kinase etha (OSKetha) [Oryza sativa]
                  414836
Seq. No.
Seq. ID
                  uC-osflcyp162e10b1
Method
                  BLASTX
NCBI GI
                  g1706326
BLAST score
                  233
E value
                  2.0e-19
Match length
                  65
                  74
% identity
                  PYRUVATE DECARBOXYLASE ISOZYME 1 (PDC)
NCBI Description
                  >gi 2146786_pir__S65470 pyruvate decarboxylase (EC 4.1.1.1)
                   (clone PDC1) - Garden pea >gi_1177603_emb_CAA91444_
                   (Z66543) pyruvate decarboxylase [Pisum sativum]
                   414837
Seq. No.
Seq. ID
                  uC-osflcyp162e11b1
Method
                  BLASTX
NCBI GI
                  g3834307
BLAST score
                  320
E value
                  2.0e-29
Match length
                  116
                  55
% identity
                  (AC005679) Strong similarity to gene T10I14.120 gi_2832679
NCBI Description
                  putative protein from Arabidopsis thaliana BAC gb_AL021712.
                   ESTs gb_N65887 and gb_N65627 come from this gene.
                   [Arabidopsis thaliana]
```

BLAST score

E value

116

1.0e-58

```
BLASTX
Method
NCBI GI
                   q2342494
                   256
BLAST score
E value
                   4.0e-22
                   79
Match length
                   56
% identity
                  (D14058) bromelain [Ananas comosus]
NCBI Description
                   >gi_2463582_dbj_BAA22543_ (D38531) FB31 precursor (FB13
precursor) [Ananas comosus]
                   414839
Seq. No.
                   uC-osflcyp162e12b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g1408222
BLAST score
                   321
                   1.0e-29
E value
                   99
Match length
                   69
% identity
NCBI Description (U60764) pathogenesis-related protein [Sorghum bicolor]
Seq. No.
                   414840
                   uC-osflcyp162f02b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g1167836
                   350
BLAST score
E value
                   5.0e-33
Match length
                   91
                   64
% identity
                   (Z68893) protein with incomplete signal sequence [Holcus
NCBI Description
                   lanatus]
                   414841
Seq. No.
                   uC-osflcyp162f03a1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g5499713
BLAST score
                   533
                   2.0e-54
E value
                   127
Match length
                   76
% identity
NCBI Description (U78762) receptor-like kinase ARK1AS [Triticum aestivum]
                   414842
Seq. No.
                   uC-osflcyp162f03b1
Seq. ID
                   BLASTX
Method
NCBI GI
                   g2286153
BLAST score
                   372
                   8.0e-36
E value
                   78
Match length
% identity
NCBI Description (AF007581) cytoplasmic malate dehydrogenase [Zea mays]
                   414843
Seq. No.
Seq. ID
                   uC-osflcyp162f06a1
                   BLASTN
Method
NCBI GI
                   q460990
```

```
Match length
                  212
% identity
                  89
NCBI Description O.sativa (Arborio) Beta Tubulin mRNA, clone OSTB-16
Seq. No.
                  414844
Seq. ID
                  uC-osflcyp162f06b1
Method
                  BLASTX
NCBI GI
                  g2119278
                  581
BLAST score
                  6.0e-67
E value
                  158
Match length
                  89
% identity
NCBI Description tubulin beta-1 chain - rice
                  414845
Seq. No.
Seq. ID
                  uC-osflcyp162f07b1
Method
                  BLASTX
NCBI GI
                  g4115364
BLAST score
                  476
E value
                  1.0e-47
Match length
                  108
% identity
                  78
NCBI Description (AC005957) putative fatty acid elongase [Arabidopsis
                  thaliana]
                  414846
Seq. No.
Seq. ID
                  uC-osflcyp162f08a1
Method
                  BLASTX
NCBI GI
                  g2286153
BLAST score
                  213
E value
                  4.0e-17
                  43
Match length
                  93
% identity
NCBI Description (AF007581) cytoplasmic malate dehydrogenase [Zea mays]
                  414847
Seq. No.
Seq. ID
                  uC-osflcyp162f10a1
Method
                  BLASTX
NCBI GI
                  q678547
BLAST score
                  180
E value
                  4.0e-13
Match length
                  82
% identity
                  49
NCBI Description (L13654) peroxidase [Lycopersicon esculentum]
                  414848
Seq. No.
                  uC-osflcyp162f10b1
Seq. ID
                  BLASTX
Method
NCBI GI
                  g4204761
BLAST score
                  442
E value
                  9.0e-44
Match length
                  123
% identity
NCBI Description (U51192) peroxidase precursor [Glycine max]
Seq. No.
                  414849
Seq. ID
                  uC-osflcyp162f11a1
```

Method BLASTX
NCBI GI g548852
BLAST score 416
E value 8.0e-41
Match length 82
% identity 98

NCBI Description 40S RIBOSOMAL PROTEIN S21 >gi_481227_pir__S38357 ribosomal protein S21 - rice >gi_303839_dbj_BAA02158_ (D12633) 40S

subunit ribosomal protein [Oryza sativa]

Seq. No. 414850

Seq. ID uC-osflcyp162f11b1

Method BLASTX
NCBI GI g548852
BLAST score 418
E value 5.0e-41
Match length 82
% identity 98

NCBI Description 40S RIBOSOMAL PROTEIN S21 >gi_481227_pir__S38357 ribosomal

protein S21 - rice >gi_303839_dbj_BAA02158_ (D12633) 40S

subunit ribosomal protein [Oryza sativa]

Seq. No. 414851

Seq. ID uC-osflcyp162g01b1

Method BLASTX
NCBI GI g100638
BLAST score 300
E value 2.0e-27
Match length 78
% identity 65

NCBI Description pollen allergen Lol p I precursor (clone 5A) - perennial

ryegrass >gi 168316 (M57474) pollen allergen [Lolium

perenne]

Seq. No. 414852

Seq. ID uC-osflcyp162g02a1

Method BLASTX
NCBI GI g115787
BLAST score 329
E value 1.0e-30
Match length 63
% identity 100

NCBI Description CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I

CAB-2) (LHCP) >gi_82461_pir__S03706 chlorophyll a/b-binding

protein 2R precursor - rice >gi 20182 emb CAA32109

(X13909) chlorophyll a/b-binding preprotein (AA -28 to 235)

[Oryza sativa]

Seq. No. 414853

Seq. ID uC-osflcyp162g02b1

Method BLASTX
NCBI GI g320618
BLAST score 453
E value 3.0e-45
Match length 96
% identity 90

NCBI Description chlorophyll a/b-binding protein I precursor - rice

```
[Oryza sativa]
                   414854
Seq. No.
Seq. ID
                  uC-osflcyp162g03a1
Method
                  BLASTX
NCBI GI
                  g1362009
                  301
BLAST score
E value
                  3.0e-27
                  79
Match length
% identity
                   42
NCBI Description ubiquitin-like protein 7 - Arabidopsis thaliana
Seq. No.
                   414855
                  uC-osflcyp162g03b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1362009
BLAST score
                   435
E value
                   5.0e-43
Match length
                  110
% identity
                   49
NCBI Description ubiquitin-like protein 7 - Arabidopsis thaliana
Seq. No.
                  414856
Seq. ID
                  uC-osflcyp162g05b1
Method
                  BLASTX
NCBI GI
                   g283012
BLAST score
                  579
E value
                   1.0e-66
Match length
                  146
% identity
                  85
                  ribulose-bisphosphate carboxylase (EC 4.1.1.39) large chain
NCBI Description
                   - rice chloroplast >gi_11955_emb_CAA28475_ (X04789)
                  ribulose-1,5-bisphosphate carboxylase (AA 1 - 477) [Oryza
                  sativa]
Seq. No.
                   414857
Seq. ID
                  uC-osflcyp162g07b1
Method
                  BLASTX
NCBI GI
                  q4204376
BLAST score
                  171
E value
                   3.0e-12
Match length
                  41
% identity
NCBI Description (U62750) acidic ribosomal protein P2a-4 [Zea mays]
Seq. No.
                   414858
Seq. ID
                  uC-osflcyp162g08b1
Method
                  BLASTX
NCBI GI
                  g320618
BLAST score
                  338
E value
                  9.0e-32
Match length
                  75
% identity
                  89
NCBI Description chlorophyll a/b-binding protein I precursor - rice
```

>gi_218172_dbj_BAA00536_ (D00641) type I light-harvesting chlorophyll a/b-binding protein [Oryza sativa] >gi 227611 prf 1707316A chlorophyll a/b binding protein 1 >gi_218172_dbj_BAA00536_ (D00641) type I light-harvesting
chlorophyll a/b-binding protein [Oryza sativa]
>gi_227611_prf__1707316A chlorophyll a/b binding protein 1
[Oryza sativa]

Seq. No. 414859

Seq. ID uC-osflcyp162g09a1

Method BLASTX
NCBI GI g1170937
BLAST score 247
E value 5.0e-21
Match length 47
% identity 96

NCBI Description S-ADENOSYLMETHIONINE SYNTHETASE 1 (METHIONINE ADENOSYLTRANSFERASE 1) (ADOMET SYNTHETASE 1)

>gi_450549_emb_CAA81481_ (Z26867) S-adenosyl methionine

synthetase [Oryza sativa]

Seq. No. 414860

Seq. ID uC-osflcyp162g09b1

Method BLASTX
NCBI GI g1170937
BLAST score 383
E value 8.0e-37
Match length 92
% identity 80

NCBI Description S-ADENOSYLMETHIONINE SYNTHETASE 1 (METHIONINE

ADENOSYLTRANSFERASE 1) (ADOMET SYNTHETASE 1)

>gi 450549 emb CAA81481 (Z26867) S-adenosyl methionine

synthetase [Oryza sativa]

Seq. No. 414861

Seq. ID uC-osflcyp162g10a1

Method BLASTX
NCBI GI g283012
BLAST score 701
E value 4.0e-74
Match length 147
% identity 90

NCBI Description ribulose-bisphosphate carboxylase (EC 4.1.1.39) large chain

- rice chloroplast >gi_11955_emb_CAA28475_ (X04789) ribulose-1,5-bisphosphate carboxylase (AA 1 - 477) [Oryza

sativa]

Seq. No. 414862

Seq. ID uC-osflcyp162g12b1

Method BLASTX
NCBI GI g4539291
BLAST score 402
E value 5.0e-39
Match length 168
% identity 50

NCBI Description (AL049480) putative protein [Arabidopsis thaliana]

Seq. No. 414863

Seq. ID uC-osflcyp162h01b1

Method BLASTX

q4850408 NCBI GI 269 BLAST score E value 1.0e-23 82 Match length % identity 51 (AC007357) Contains PF 00097 Zinc finger (C3HC4) ring NCBI Description finger motif. [Arabidopsis thaliana] Seq. No. 414864 Seq. ID uC-osflcyp162h02a1 Method BLASTX NCBI GI g2696804 BLAST score 424 1.0e-41 E value 79 Match length 100 % identity NCBI Description (AB009665) water channel protein [Oryza sativa] 414865 Seq. No. Seq. ID uC-osflcyp162h02b1 Method BLASTX NCBI GI q2894534 BLAST score 785 E value 5.0e-84 Match length 158 % identity NCBI Description (AJ224327) aquaporin [Oryza sativa] 414866 Seq. No. uC-osflcyp162h04b1 Seq. ID Method BLASTX NCBI GI g5031281 BLAST score 373 E value 1.0e-35 Match length 124 % identity 60 NCBI Description (AF139499) unknown [Prunus armeniaca] 414867 Seq. No. Seq. ID uC-osflcyp162h05b1 Method BLASTX NCBI GI g4680211 375 BLAST score 4.0e-36 E value Match length 118 % identity 67 NCBI Description (AF114171) hypothetical protein [Sorghum bicolor] 414868 Seq. No. Seq. ID uC-osflcyp162h06b1 Method BLASTX NCBI GI g5915857 BLAST score 611 9.0e-64 E value Match length 123 % identity 92 NCBI Description CYTOCHROME P450 98A1 >gi_2766448 (AF029856) cytochrome P450

CYP98A1 [Sorghum bicolor]

414869 Seq. No. Seq. ID uC-osflcyp162h08b1 BLASTX Method NCBI GI g5302811 BLAST score 441 E value 1.0e-43 156 Match length % identity 60 (Z97342) putative serine protease-like protein [Arabidopsis NCBI Description thaliana] 414870 Seq. No. Seq. ID uC-osflcyp162h09a1 BLASTX Method NCBI GI g1076724 BLAST score 364 E value 1.0e-34 70 Match length 94 % identity NCBI Description LHCI-680, photosystem I antenna protein - barley >gi_666054_emb_CAA59049_ (X84308) LHCI-680, photosystem I
antenna protein [Hordeum vulgare] Seq. No. 414871 uC-osflcyp162h09b1 Seq. ID Method BLASTX NCBI GI g2306981 BLAST score 445 4.0e-44E value 84 Match length % identity 93 NCBI Description (AF010321) photosystem I antenna protein [Oryza sativa] 414872 Seq. No. Seq. ID uC-osflcyp162h11b1 BLASTX Method NCBI GI g1173027 BLAST score 441 1.0e-43 E value 123 Match length 71 % identity NCBI Description 60S RIBOSOMAL PROTEIN L31 >gi_915313 (U23784) ribosomal protein L31 [Nicotiana glutinosa] 414873 Seq. No. Seq. ID uC-osflcyp162h12a1 Method BLASTN NCBI GI g2331130 BLAST score 295 E value 1.0e-165 Match length 323 % identity

NCBI Description Oryza sativa glycine-rich protein (OSGRP1) mRNA, complete

```
Seq. No.
                  414874
Seq. ID
                  uC-osflcyp162h12b1
Method
                  BLASTX
NCBI GI
                  g2208988
BLAST score
                  402
E value
                  3.0e-39
Match length
                  93
% identity
                  81
NCBI Description (Y10117) signal recognition particle subunit 9 [Zea mays]
Seq. No.
                  414875
Seq. ID
                  uC-osflcyp168a01a1
Method
                  BLASTN
NCBI GI
                  g20280
BLAST score
                  303
E value
                  1.0e-170
Match length
                  355
                  97
% identity
NCBI Description Rice gene for phenylalanine ammonia-lyase (EC 4.3.1.5)
Seq. No.
                  414876
Seq. ID
                  uC-osflcyp168a01b1
Method
                  BLASTX
NCBI GI
                  g129591
BLAST score
                  546
E value
                  3.0e-56
Match length
                  114
                  96
% identity
NCBI Description PHENYLALANINE AMMONIA-LYASE >gi 295824 emb CAA34226
                  (X16099) phenylalanine ammonia-lyase [Oryza sativa]
Seq. No.
                  414877
Seq. ID
                  uC-osflcyp168a03a1
Method
                  BLASTN
NCBI GI
                  g416266
BLAST score
                  76
                  9.0e-35
E value
Match length
                  147
% identity
                  88
NCBI Description Rice mRNA for oxygen-evolving protein, partial sequence
Seq. No.
                  414878
Seq. ID
                  uC-osflcyp168a03b1
Method
                  BLASTX
                  q131388
NCBI GI
BLAST score
                  515
E value
                  2.0e-52
Match length
                  157
% identity
                  69
NCBI Description OXYGEN-EVOLVING ENHANCER PROTEIN 1 PRECURSOR (OEE1) (33 KD
                  SUBUNIT OF OXYGEN EVOLVING SYSTEM OF PHOTOSYSTEM II) (33 KD
                  THYLAKOID MEMBRANE PROTEIN) >gi_100831_pir__$16260
                  photosystem II oxygen-evolving complex protein 1 - common
                  wheat x Sanduri wheat >gi 21844 emb CAA40670 (X57408)
                  33kDa oxygen evolving protein of photosystem II [Triticum
```

aestivum]



Seq. No. 414879

Seq. ID uC-osflcyp168a07b1

Method BLASTX
NCBI GI g2914703
BLAST score 470
E value 4.0e-47
Match length 133
% identity 64

NCBI Description (AC003974) unknown protein [Arabidopsis thaliana]

Seq. No. 414880

Seq. ID uC-osflcyp168a08b1

Method BLASTX
NCBI GI g2911059
BLAST score 545
E value 6.0e-56
Match length 137
% identity 78

NCBI Description (AL021961) putative protein [Arabidopsis thaliana]

Seq. No. 414881

Seq. ID uC-osflcyp168a10b1

Method BLASTX
NCBI GI g2668744
BLAST score 473
E value 1.0e-47
Match length 90
% identity 94

NCBI Description (AF034946) ubiquitin conjugating enzyme [Zea mays]

Seq. No. 414882

Seq. ID uC-osflcyp168a11a1

Method BLASTX
NCBI GI g2191138
BLAST score 280
E value 6.0e-25
Match length 62
% identity 84

NCBI Description (AF007269) A_IG002N01.18 gene product [Arabidopsis

thaliana]

Seq. No. 414883

Seq. ID uC-osflcyp168b01b1

Method BLASTX
NCBI GI g671740
BLAST score 617
E value 3.0e-64
Match length 115
% identity 98

NCBI Description (X84730) ribulose-bisphosphate carboxylase [synthetic

construct]

Seq. No. 414884

Seq. ID uC-osflcyp168b02b1

Method BLASTX NCBI GI g1173073 BLAST score 278

E value

1.0e-11

1.0e-24 E value Match length 109 56 % identity 60S ACIDIC RIBOSOMAL PROTEIN P2 >gi 1076787 pir S54179 NCBI Description acidic ribosomal protein 60S - maize >gi 2130117 pir S65781 acidic ribosomal protein P2 - maize >gi 790508 emb CAA60251 (X86553) 60S acidic ribosomal protein [Zea mays] Seq. No. 414885 Seq. ID uC-osflcyp168b03a1 Method BLASTX NCBI GI q3080424 BLAST score 246 9.0e-21 E value Match length 60 % identity 85 (AL022604) NAD+ dependent isocitrate dehydrogenase subunit NCBI Description 1 [Arabidopsis thaliana] Seq. No. 414886 Seq. ID uC-osflcyp168b03b1 Method BLASTX NCBI GI g3790188 BLAST score 325 E value 3.0e-30 82 Match length 77 % identity NCBI Description (Y14431) NAD-dependent isocitrate dehydrogenase [Nicotiana tabacum] 414887 Seq. No. Seq. ID uC-osflcyp168b04a1 Method BLASTN NCBI GI g5257255 BLAST score 72 3.0e-32 E value Match length 168 % identity 87 NCBI Description Oryza sativa genomic DNA, chromosome 8, clone:P0026F07 414888 Seq. No. Seq. ID uC-osflcyp168b04b1 Method BLASTX NCBI GI g3126854 BLAST score 451 E value 4.0e-45 95 Match length 91 % identity NCBI Description (AF061577) chlorophyll a/b binding protein [Oryza sativa] 414889 Seq. No. Seq. ID uC-osflcyp168b05a1 Method BLASTX NCBI GI q3549652 BLAST score 168

```
Match length
                  39
% identity
                 (AJ224982) MAP3K epsilon protein kinase [Arabidopsis
NCBI Description
                  thaliana]
                  414890
Seq. No.
                  uC-osflcyp168b05b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3549652
BLAST score
                  311
E value
                  2.0e-28
Match length
                  143
% identity
                  49
NCBI Description (AJ224982) MAP3K epsilon protein kinase [Arabidopsis
                  thaliana]
Seq. No.
                  414891
                  uC-osflcyp168b06b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2829911
BLAST score
                  234
E value
                  2.0e-19
Match length
                  90
% identity
                  54
NCBI Description (AC002291) Unknown protein [Arabidopsis thaliana]
Seq. No.
                  414892
                  uC-osflcyp168b07b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2905643
BLAST score
                  239
E value
                  4.0e-20
Match length
                  104
% identity
                  46
NCBI Description (AF045244) ribitol kinase [Klebsiella pneumoniae]
Seq. No.
                  414893
Seq. ID
                  uC-osflcyp168b08a1
Method
                  BLASTX
NCBI GI
                  g1350986
                  373
BLAST score
E value
                  1.0e-35
Match length
                  78
                  95
% identity
NCBI Description 40S RIBOSOMAL PROTEIN S3A (CYC07 PROTEIN)
                  >gi 483431 dbj BAA05059 (D26060) cyc07 [Oryza sativa]
                  414894
Seq. No.
Seq. ID
                  uC-osflcyp168b08b1
                  BLASTX
Method
NCBI GI
                  g1350986
BLAST score
                  147
E value
                  1.0e-09
Match length
                  76
% identity
                  46
NCBI Description 40S RIBOSOMAL PROTEIN S3A (CYC07 PROTEIN)
                  >gi 483431 dbj BAA05059 (D26060) cyc07 [Oryza sativa]
```

```
414895
Seq. No.
                  uC-osflcyp168b09b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4322940
BLAST score
                  326
                  2.0e-30
E value
Match length
                  131
% identity
                  42
NCBI Description (AF096299) DNA-binding protein 2 [Nicotiana tabacum]
Seq. No.
                  414896
                  uC-osflcyp168b10b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2224915
BLAST score
                  235
                  1.0e-19
E value
Match length
                  50
% identity
                  78
NCBI Description (U95968) beta-expansin [Oryza sativa]
Seq. No.
                  414897
                  uC-osflcyp168b11a1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2129753
BLAST score
                  316
E value
                  6.0e-29
                  77
Match length
                  78
% identity
                  threonine synthase (EC 4.2.99.2) precursor - Arabidopsis
NCBI Description
                  thaliana (fragment) >gi_1448917 (L41666) threonine synthase
                  [Arabidopsis thaliana]
                  414898
Seq. No.
                  uC-osflcyp168b11b1
Seq. ID
                  BLASTX
Method
NCBI GI
                  q2129753
BLAST score
                  199
E value
                  2.0e-15
                  69
Match length
                  64
% identity
NCBI Description threonine synthase (EC 4.2.99.2) precursor - Arabidopsis
                  thaliana (fragment) >gi_1448917 (L41666) threonine synthase
                  [Arabidopsis thaliana]
                  414899
Seq. No.
Seq. ID
                  uC-osflcyp168b12b1
                  BLASTX
Method
NCBI GI
                  q1771160
BLAST score
                  384
E value
                  5.0e-37
Match length
                  145
% identity
                  52
NCBI Description
                  (X98929) SBT1 [Lycopersicon esculentum]
                  >gi 3687305 emb CAA06999.1 (AJ006378) subtilisin-like
```

protease [Lycopersicon esculentum]

NCBI GI

BLAST score

```
414900
Seq. No.
Seq. ID
                  uC-osflcyp168c01a1
Method
                  BLASTX
NCBI GI
                  g2827711
BLAST score
                  264
E value
                  5.0e-23
Match length
                  69
% identity
                  74
                 (AL021684) oxoglutarate dehydrogenase - like protein
NCBI Description
                  [Arabidopsis thaliana]
                  414901
Seq. No.
                  uC-osflcyp168c01b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2827711
BLAST score
                  636
E value
                  1.0e-66
Match length
                  147
                  76
% identity
NCBI Description (AL021684) oxoglutarate dehydrogenase - like protein
                  [Arabidopsis thaliana]
Seq. No.
                  414902
Seq. ID
                  uC-osflcyp168c02a1
Method
                  BLASTX
NCBI GI
                  q2055376
BLAST score
                  185
E value
                  1.0e-13
Match length
                  34
% identity
                  100
NCBI Description (U32109) MADS box protein [Oryza sativa]
                  414903
Seq. No.
                  uC-osflcyp168c02b1
Seq. ID
Method
                  BLASTN
                  g2286112
NCBI GI
                  55
BLAST score
E value
                  1.0e-21
                  59
Match length
                  98
% identity
NCBI Description Oryza sativa MADS box protein (OsMADS8) mRNA, complete cds
Seq. No.
                   414904
Seq. ID
                  uC-osflcyp168c03a1
Method
                  BLASTN
NCBI GI
                  g5912298
BLAST score
                  193
                  1.0e-104
E value
                  207
Match length
                  99
% identity
NCBI Description Oryza sativa mRNA for gigantea homologue, partial
Seq. No.
                   414905
Seq. ID
                  uC-osflcyp168c06a1
Method
                  BLASTN
```

g5257255

E value 2.0e-30 Match length 225 % identity 83

NCBI Description Oryza sativa genomic DNA, chromosome 8, clone:P0026F07

Seq. No. 414906

Seq. ID uC-osflcyp168c06b1

Method BLASTX
NCBI GI g2624328
BLAST score 316
E value 2.0e-29
Match length 79
% identity 80

NCBI Description (AJ002894) OsGRP2 [Oryza sativa]

Seq. No. 414907

Seq. ID uC-osflcyp168c11a1

Method BLASTX
NCBI GI g2501190
BLAST score 279
E value 1.0e-24
Match length 74
% identity 80

NCBI Description THIAMINE BIOSYNTHETIC ENZYME 1-2 PRECURSOR

>gi_2130147_pir__S61420 thiamine biosynthetic enzyme thi1-2 - maize >gi_596080 (U17351) thiamine biosynthetic enzyme

[Zea mays]

Seq. No. 414908

Seq. ID uC-osflcyp168c12a1

Method BLASTN
NCBI GI g5257255
BLAST score 158
E value 2.0e-83
Match length 324
% identity 88

NCBI Description Oryza sativa genomic DNA, chromosome 8, clone:P0026F07

Seq. No. 414909

Seq. ID uC-osflcyp168d01b1

Method BLASTX
NCBI GI g1314711
BLAST score 430
E value 2.0e-42
Match length 105
% identity 77

NCBI Description (U54615) calcium-dependent protein kinase [Arabidopsis

thaliana] >gi 3068712 (AF049236) calcium dependent protein

kinase [Arabidopsis thaliana]

Seq. No. 414910

Seq. ID uC-osflcyp168d02b1

Method BLASTX
NCBI GI g1362150
BLAST score 369
E value 2.0e-35
Match length 88

```
% identity
NCBI Description
                   hypothetical protein (clone AFN3) - wild oat (fragment)
                   >gi 726478 (U20000) putative ORF1 [Avena fatua]
Seq. No.
                   414911
Seq. ID
                   uC-osflcyp168d03a1
Method
                   BLASTN
NCBI GI
                   g4159705
BLAST score
                   36
E value
                   1.0e-10
Match length
                   76
% identity
                   87
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
                  MGD8, complete sequence
Seq. No.
                   414912
Seq. ID
                   uC-osflcyp168d03b1
Method
                   BLASTX
NCBI GI
                   g3668069
BLAST score
                   678
E value
                   2.0e-71
Match length
                   150
% identity
                   85
NCBI Description (U28007) Pto kinase interactor 1 [Lycopersicon esculentum]
Seq. No.
                   414913
Seq. ID
                  uC-osflcyp168d06a1
Method
                  BLASTX
NCBI GI
                  g829283
BLAST score
                  184
E value
                   2.0e-13
Match length
                  69
% identity
                   65
NCBI Description (Z15018) heat shock protein hsp82 [Oryza sativa]
Seq. No.
                  414914
Seq. ID
                  uC-osflcyp168d06b1
Method
                  BLASTN
NCBI GI
                  q20255
BLAST score
                  109
E value
                  1.0e-54
Match length
                  149
                  93
% identity
NCBI Description O.sativa gene for heat shock protein 82 HSP82
Seq. No.
                  414915
Seq. ID
                  uC-osflcyp168d07b1
Method
                  BLASTX
NCBI GI
                  g4894182
```

NCBI GI 94894182
BLAST score 539
E value 3.0e-55
Match length 130
% identity 76

NCBI Description (AJ242551) 12-oxophytodienoate reductase [Lycopersicon

esculentum]

Seq. No. 414916

```
uC-osflcyp168d09b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3202030
BLAST score
                  555
E value
                  3.0e-57
Match length
                  124
% identity
NCBI Description
                  (AF069318) geranylgeranyl hydrogenase [Mesembryanthemum
                  crystallinum]
Seq. No.
                  414917
Seq. ID
                  uC-osflcyp168d12a1
Method
                  BLASTN
NCBI GI
                  q450548
BLAST score
                  70
E value
                  5.0e-31
Match length
                  189
                  87
% identity
                  O.sativa (pRSAM-1) gene for S-adenosyl methionine
NCBI Description
                  synthetase
                  414918
Seq. No.
Seq. ID
                  uC-osflcyp168d12b1
Method
                  BLASTX
NCBI GI
                  q1170937
BLAST score
                  196
E value
                  2.0e-15
Match length
                  52
% identity
                  79
NCBI Description S-ADENOSYLMETHIONINE SYNTHETASE 1 (METHIONINE
                  ADENOSYLTRANSFERASE 1) (ADOMET SYNTHETASE 1)
                  >gi 450549 emb CAA81481 (Z26867) S-adenosyl methionine
                  synthetase [Oryza sativa]
Seq. No.
                  414919
Seq. ID
                  uC-osflcyp168e01a1
Method
                  BLASTX
NCBI GI
                  g2130069
BLAST score
                  155
E value
                   3.0e-10
Match length
                  30
% identity
                  100
NCBI Description catalase (EC 1.11.1.6) catA - rice
                  >gi 1261858_dbj_BAA06232_ (D29966) catalase [Oryza sativa]
Seq. No.
                   414920
Seq. ID
                  uC-osflcyp168e01b1
Method
                  BLASTX
NCBI GI
                  g2130069
BLAST score
                  861
E value
                  7.0e-93
Match length
                  160
                  99
% identity
NCBI Description catalase (EC 1.11.1.6) catA - rice
```

Seq. No. 414921

>gi_1261858 dbj BAA06232 (D29966) catalase [Oryza sativa]



Seq. ID uC-osflcyp168e03b1 Method BLASTX NCBI GI q4586021 BLAST score 374 E value 9.0e-36 76 Match length % identity 88 NCBI Description (AC007170) putative cytoplasmic aconitate hydratase [Arabidopsis thaliana] Seq. No. 414922 Seq. ID uC-osflcyp168e05a1 Method BLASTN NCBI GI q3618307 BLAST score 248 E value 1.0e-137 296 Match length % identity 96 NCBI Description Oryza sativa mRNA for zinc finger protein, complete cds, clone:C60910 Seq. No. 414923 Seq. ID uC-osflcyp168e05b1 Method BLASTN NCBI GI q3618307 BLAST score 100 E value 2.0e-49 Match length 132 % identity 94 NCBI Description Oryza sativa mRNA for zinc finger protein, complete cds, clone:C60910 414924 Seq. No. Seq. ID uC-osflcyp168e06a1 Method BLASTX NCBI GI g2341033 BLAST score 215 3.0e-17 E value 69 Match length % identity 59 NCBI Description (AC000104) Similar to Babesia aldo-keto reductase (gb_M93122). [Arabidopsis thaliana] 414925 Seq. No. Seq. ID uC-osflcyp168e06b1

Method BLASTX NCBI GI g4091008 BLAST score 178 E value 2.0e-19 Match length 105 % identity

NCBI Description (AF040700) methionyl-tRNA synthetase [Oryza sativa]

414926 Seq. No.

Seq. ID uC-osflcyp168e07a1

Method BLASTX NCBI GI g1136122

Match length

% identity

94

43

BLAST score 295 1.0e-26 E value 58 Match length 98 % identity NCBI Description (X91807) alfa-tubulin [Oryza sativa] Seq. No. 414927 Seq. ID uC-osflcyp168e07b1 Method BLASTX NCBI GI g1136122 BLAST score 562 6.0e-58 E value Match length 112 91 % identity NCBI Description (X91807) alfa-tubulin [Oryza sativa] Seq. No. 414928 Seq. ID uC-osflcyp168e08b1 Method BLASTX NCBI GI g3023816 BLAST score 522 E value 2.0e-53 Match length 100 100 % identity NCBI Description GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC >gi 968996 (U31676) glyceraldehyde-3-phosphate dehydrogenase [Oryza sativa] Seq. No. 414929 Seq. ID uC-osflcyp168e09b1 Method BLASTX NCBI GI g5410350 BLAST score 159 E value 5.0e-11 36 Match length 86 % identity NCBI Description (AF124045) unknown [Sorghum bicolor] Seq. No. 414930 Seq. ID uC-osflcyp168e10b1 Method BLASTN NCBI GI g3618307 BLAST score 58 E value 2.0e-24 Match length 102 90 % identity NCBI Description Oryza sativa mRNA for zinc finger protein, complete cds, clone:C60910 414931 Seq. No. Seq. ID uC-osflcyp168e11a1 BLASTX Method NCBI GI g3201615 BLAST score 156 E value 3.0e-10

Seq. No.

414937

```
NCBI Description (AC004669) unknown protein [Arabidopsis thaliana]
Seq. No.
                  414932
                  uC-osflcyp168e11b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3201615
BLAST score
                  376
E value
                  4.0e-36
Match length
                  87
% identity
                  79
NCBI Description (AC004669) unknown protein [Arabidopsis thaliana]
                   414933
Seq. No.
                  uC-osflcyp168e12a1
Seq. ID
Method
                  BLASTX
NCBI GI
                   g2341033
                  268
BLAST score
E value
                   2.0e-23
Match length
                  78
% identity
                   64
                  (AC000104) Similar to Babesia aldo-keto reductase
NCBI Description
                   (gb M93122). [Arabidopsis thaliana]
Seq. No.
                   414934
Seq. ID
                  uC-osflcyp168e12b1
Method
                  BLASTX
NCBI GI
                   q2341033
BLAST score
                   214
E value
                   2.0e-17
Match length
                   64
                   77
% identity
                  (AC000104) Similar to Babesia aldo-keto reductase
NCBI Description
                   (gb M93122). [Arabidopsis thaliana]
Seq. No.
                   414935
Seq. ID
                   uC-osflcyp168f01b1
Method
                   BLASTX
NCBI GI
                   q1084455
BLAST score
                   374
E value
                   5.0e-58
Match length
                   116
                   97
% identity
NCBI Description peptidylprolyl isomerase (EC 5.2.1.8) Cyp2 - rice
                   >gi_600767 (L29469) cyclophilin 2 [Oryza sativa]
Seq. No.
                   414936
Seq. ID
                   uC-osflcyp168f02a1
Method
                   BLASTN
                   g2331132
NCBI GI
BLAST score
                   285
E value
                   1.0e-159
                   328
Match length
                   97
% identity
NCBI Description Oryza sativa glycine-rich protein (OSGRP2) mRNA, complete
                   cds
```

```
Seq. ID
                  uC-osflcyp168f02b1
                  BLASTX
Method
NCBI GI
                  g2624326
BLAST score
                  469
E value
                  4.0e-47
Match length
                  92
% identity
                  99
NCBI Description (AJ002893) OsGRP1 [Oryza sativa]
Seq. No.
                  414938
Seq. ID
                  uC-osflcyp168f03b1
Method
                  BLASTX
NCBI GI
                  g2498586
BLAST score
                  595
E value
                  9.0e-62
Match length
                  131
                  90
% identity
NCBI Description MAJOR POLLEN ALLERGEN ORY S 1 PRECURSOR (ORY S I)
                  >gi 1173557 (U31771) Ory s 1 [Oryza sativa]
                  414939
Seq. No.
Seq. ID
                  uC-osflcyp168f07a1
Method
                  BLASTX
NCBI GI
                  g3695375
BLAST score
                  150
E value
                  7.0e-10
Match length
                  41
                  56
% identity
NCBI Description (AF096370) contains similarity to the major intrinsic
                  protein domain (Pfam: PF00230 MIP, E-value: 5.7e-111)
                  [Arabidopsis thaliana]
Seq. No.
                  414940
Seq. ID
                  uC-osflcyp168f07b1
Method
                  BLASTX
NCBI GI
                  q1928981
BLAST score
                  411
E value
                  3.0e-40
Match length
                  122
% identity
                  64
NCBI Description (U92651) tonoplast intrinsic protein bobTIP26-1 [Brassica
                  oleracea var. botrytis]
Seq. No.
                  414941
Seq. ID
                  uC-osflcyp168f08a1
Method
                  BLASTN
NCBI GI
                  g886400
BLAST score
                  265
E value
                  1.0e-147
Match length
                  349
% identity
                  93
NCBI Description Oryza sativa MADS-box protein (MADS2) mRNA, complete cds
Seq. No.
                  414942
Seq. ID
                  uC-osflcyp168f08b1
Method
                  BLASTX
```

NCBI GI g886401

```
BLAST score
                   312
E value
                   1.0e-28
Match length
                  83
% identity
                  83
NCBI Description (L37526) MADS box protein [Oryza sativa]
Seq. No.
                  414943
Seq. ID
                  uC-osflcyp168f09a1
Method
                  BLASTN
NCBI GI
                  g1261857
BLAST score
                  129
E value
                  4.0e-66
Match length
                  212
% identity
                  91
NCBI Description Rice CatA gene for catalase, complete cds
Seq. No.
                   414944
Seq. ID
                  uC-osflcyp168f11a1
Method
                  BLASTX
NCBI GI
                  g4895232
BLAST score
                  190
E value
                  2.0e-14
Match length
                  47
% identity
                  72
NCBI Description (AC007660) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  414945
Seq. ID
                  uC-osflcyp168q01b1
Method
                  BLASTX
NCBI GI
                  g2384758
BLAST score
                  678
E value
                  2.0e-71
Match length
                  134
% identity
                  97
NCBI Description (AF016896) GDP dissociation inhibitor protein OsGDI1 [Oryza
                  sativa]
Seq. No.
                  414946
Seq. ID
                  uC-osflcyp168g02a1
Method
                  BLASTN
NCBI GI
                  g5257255
BLAST score
                  120
E value
                  7.0e-61
Match length
                  228
% identity
                  89
NCBI Description Oryza sativa genomic DNA, chromosome 8, clone:P0026F07
Seq. No.
                  414947
Seq. ID
                  uC-osflcyp168g03b1
Method
                  BLASTX
NCBI GI
                  g4204300
BLAST score
                  198
E value
                  2.0e-15
Match length
                  68
% identity
```

NCBI Description (AC003027) Unknown protein [Arabidopsis thaliana]

E value

3.0e-29

```
414948
Seq. No.
Seq. ID
                   uC-osflcyp168g08a1
Method
                   BLASTX
NCBI GI
                   g2982268
BLAST score
                   167
E value
                   8.0e-12
Match length
                   44
% identity
                   77
                  (AF051217) probable 40S ribosomal protein S15 [Picea
NCBI Description
                   mariana]
Seq. No.
                   414949
Seq. ID
                   uC-osflcyp168g08b1
Method
                   BLASTN
NCBI GI
                   q218130
BLAST score
                   62
E value
                   2.0e-26
Match length
                   98
% identity
                   92
NCBI Description Rice mRNA for Ribosomal protein S15
Seq. No.
                   414950
Seq. ID
                   uC-osflcyp168g09b1
Method
                  BLASTX
NCBI GI
                   q4530585
BLAST score
                   281
E value
                   8.0e-25
Match length
                   78
% identity
                   65
NCBI Description (AF130978) B12D protein [Ipomoea batatas]
Seq. No.
                   414951
Seq. ID
                   uC-osflcyp168h01b1
Method
                   BLASTX
NCBI GI
                   q1019946
BLAST score
                   346
E value
                   1.0e-32
                   107
Match length
% identity
                   64
NCBI Description (U37060) ascorbate peroxidase [Gossypium hirsutum]
Seq. No.
                   414952
Seq. ID
                   uC-osflcyp168h02b1
Method
                  BLASTX
                  g510876
NCBI GI
BLAST score
                   700
E value
                   1.0e-79
Match length
                  164
% identity
                   86
NCBI Description (X80051) NADP dependent malic enzyme [Phaseolus vulgaris]
Seq. No.
                   414953
Seq. ID
                  uC-osflcyp168h03a1
Method
                  BLASTX
NCBI GI
                  g4768911
BLAST score
                  317
```

Match length 61 % identity NCBI Description (AF131201) plasma membrane MIP protein [Zea mays] Seq. No. 414954 Seq. ID uC-osflcyp168h03b1 Method BLASTX NCBI GI g1632822 BLAST score 526 E value 7.0e-54Match length 100 % identity 100 NCBI Description (Y08962) transmembrane protein [Oryza sativa] >gi 1667594 (U77297) transmembrane protein [Oryza sativa] Seq. No. 414955 Seq. ID uC-osflcyp168h04b1 Method BLASTX NCBI GI g4160292 BLAST score 180 E value 3.0e-13 Match length 49 % identity 67 NCBI Description (Y18209) alpha-N-acetylglucosaminidase [Nicotiana tabacum] Seq. No. 414956 Seq. ID uC-osflcyp168h07a1 Method BLASTN NCBI GI g2331130 BLAST score 201 E value 1.0e-109 Match length 205 % identity 100 NCBI Description Oryza sativa glycine-rich protein (OSGRP1) mRNA, complete cds Seq. No. 414957 Seq. ID uC-osflcyp168h07b1 Method BLASTN NCBI GI g2331130 BLAST score 114 E value 3.0e-57 Match length 182 % identity 96 NCBI Description Oryza sativa glycine-rich protein (OSGRP1) mRNA, complete cds Seq. No. 414958 Seq. ID uC-osflcyp168h09a1 Method BLASTX NCBI GI g3913641 BLAST score 398 E value 8.0e-39 Match length 76 % identity 100 FRUCTOSE-1,6-BISPHOSPHATASE, CHLOROPLAST PRECURSOR NCBI Description

(D-FRUCTOSE-1,6-BISPHOSPHATE 1-PHOSPHOHYDROLASE) (FBPASE)



>gi_3041777_dbj_BAA25423_ (AB007194)
fructose-1,6-bisphosphatase [Oryza sativa]

Seq. No. 414959

Seq. ID uC-osflcyp168h09b1

Method BLASTX
NCBI GI g3913641
BLAST score 703
E value 2.0e-74
Match length 135
% identity 99

NCBI Description FRUCTOSE-1,6-BISPHOSPHATASE, CHLOROPLAST PRECURSOR

(D-FRUCTOSE-1, 6-BISPHOSPHATE 1-PHOSPHOHYDROLASE) (FBPASE)

>gi_3041777_dbj_BAA25423_ (AB007194)

fructose-1,6-bisphosphatase [Oryza sativa]

Seq. No. 414960

Seq. ID uC-osflcyp168h10a1

Method BLASTX
NCBI GI g466160
BLAST score 341
E value 4.0e-32
Match length 80
% identity 82

NCBI Description HYPOTHETICAL 9.8 KD PROTEIN ZK652.3 IN CHROMOSOME III

>gi_630771_pir__S44903 ZK652.3 protein - Caenorhabditis
elegans >gi 289769 (L14429) putative [Caenorhabditis

elegans]

Seq. No. 414961

Seq. ID uC-osflcyp168h10b1

Method BLASTX
NCBI GI g466160
BLAST score 361
E value 2.0e-34
Match length 81
% identity 86

NCBI Description HYPOTHETICAL 9.8 KD PROTEIN ZK652.3 IN CHROMOSOME III

>gi_630771_pir__S44903 ZK652.3 protein - Caenorhabditis
elegans >gi_289769 (L14429) putative [Caenorhabditis

elegans]

Seq. No. 414962

Seq. ID uC-osflcyp169a01b1

Method BLASTX
NCBI GI g3335333
BLAST score 345
E value 2.0e-32
Match length 104
% identity 69

NCBI Description (AC004512) Similar to chloroplast membrane-associated 30KD

protein precursor (IM30) gb_M73744 from Pisum sativum. ESTs gb_N37557, gb_W43887 and gb_AA042479 come from this

gene. [Arabidopsis thaliana]

Seq. No. 414963

Seq. ID uC-osflcyp169a02b1

Method BLASTX NCBI GI g5932542 BLAST score 385 E value 5.0e-37 132 Match length % identity 60 NCBI Description

(AC009465) putative ribosomal protein s19 or s24

[Arabidopsis thaliana]

Seq. No. 414964

Seq. ID uC-osflcyp169a04a1

Method BLASTN NCBI GI q218207 BLAST score 124 E value 3.0e-63 180 Match length % identity 92

NCBI Description Oryza sativa mRNA for the small subunit of

ribulose-1,5-bisphosphate carboxylase, complete cds, clone

p0SSS1139

Seq. No. 414965

Seq. ID uC-osflcyp169a04b1

Method BLASTX NCBI GI g132105 BLAST score 726 E value 5.0e-77 154 Match length % identity 88

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR

(RUBISCO SMALL SUBUNIT C) $>gi_68094$ _pir_RKRZS9 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538 (D00643) small subunit of ribulose-1,5-bisphosphate carboxylase (RuBPC) [Oryza sativa] >gi 2407283 (AF017364)

ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa] >gi 226375 prf 1508256A ribulose bisphosphate

carboxylase S [Oryza sativa]

Seq. No. 414966

Seq. ID uC-osflcyp169a05a1

Method BLASTXNCBI GI q1184112 BLAST score 372 E value 8.0e-36 Match length 98 % identity 76

NCBI Description (U46138) Zn-induced protein [Oryza sativa]

Seq. No. 414967

Seq. ID uC-osflcyp169a05b1

Method BLASTN NCBI GI g6016845 BLAST score 232 1.0e-128 E value

Match length 256 % identity 98

```
NCBI Description Oryza sativa genomic DNA, chromosome 1, clone:P0711E10
                  414968
Seq. No.
Seq. ID
                  uC-osflcyp169a06a1
Method
                  BLASTX
NCBI GI
                  g1504052
BLAST score
                  323
E value
                  8.0e-30
                  79
Match length
% identity
                  81
NCBI Description (D87042) Calcium-dependent protein kinase [Zea mays]
                  414969
Seq. No.
Seq. ID
                  uC-osflcyp169a07b1
Method
                  BLASTX
NCBI GI
                  g2129946
                  210
BLAST score
E value
                  1.0e-16
                  59
Match length
                  76
% identity
                  ADP-ribosylation factor homolog GTP-binding protein NTGB1 -
NCBI Description
                  common tobacco (fragment) >gi 1184987 (U46927) NTGB1
                  [Nicotiana tabacum]
Seq. No.
                  414970
Seq. ID
                  uC-osflcyp169a08a1
Method
                  BLASTX
NCBI GI
                  g2911042
BLAST score
                  441
E value
                  9.0e-44
                  100
Match length
% identity
                  84
NCBI Description (AL021961) Phosphoglycerate dehydrogenase - like protein
                  [Arabidopsis thaliana]
                  414971
Seq. No.
Seq. ID
                  uC-osflcyp169a08b1
Method
                  BLASTX
NCBI GI
                  g2911042
BLAST score
                  562
E value
                  7.0e-58
Match length
                  155
% identity
NCBI Description (AL021961) Phosphoglycerate dehydrogenase - like protein
                  [Arabidopsis thaliana]
Seq. No.
                  414972
Seq. ID
                  uC-osflcyp169a10b1
Method
                  BLASTN
NCBI GI
                  g6016845
BLAST score
                  77
                  4.0e-35
E value
                  169
Match length
% identity
NCBI Description Oryza sativa genomic DNA, chromosome 1, clone:P0711E10
Seq. No.
                  414973
```



```
uC-osflcyp169a11a1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1076746
                  270
BLAST score
E value
                  5.0e-36
Match length
                  111
                  78
% identity
NCBI Description
                  heat shock protein 70 - rice (fragment)
                  >gi 763160 emb CAA47948 (X67711) heat shock protein 70
                  [Oryza sativa]
                  414974
Seq. No.
Seq. ID
                  uC-osflcyp169a11b1
Method
                  BLASTX
NCBI GI
                  q100440
BLAST score
                  286
E value
                  4.0e-26
                  54
Match length
% identity
                  98
                  heat shock protein 70 (clone D7) - potato (fragment)
NCBI Description
                  >gi 100441 pir__S21363 heat shock protein 70 (clone D3) -
                  potato (fragment) >gi_21477_emb_CAA78036_ (Z11984) 70-kD
                  heat shock protein [Solanum tuberosum]
Seq. No.
                  414975
                  uC-osflcyp169a12b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1399275
BLAST score
                  279
E value
                  4.0e-25
                  73
Match length
                  71
% identity
NCBI Description
                 (U31835) calmodulin-domain protein kinase CDPK isoform 6
                  [Arabidopsis thaliana] >gi_2623752 (AC002329) CDPK6
                  (calmodulin-domain protein kinase isoform 6) [Arabidopsis
                  thaliana]
                  414976
Seq. No.
Seq. ID
                  uC-osflcyp169b02a1
Method
                  BLASTX
NCBI GI
                  g4191782
BLAST score
                  235
E value
                  1.0e-19
Match length
                  58
% identity
                  74
NCBI Description (AC005917) WD-40 repeat protein [Arabidopsis thaliana]
                  414977
Seq. No.
Seq. ID
                  uC-osflcyp169b02b1
                  BLASTX
Method
```

Method BLASTX
NCBI GI 94191782
BLAST score 361
E value 3.0e-57
Match length 131
% identity 85

NCBI Description (AC005917) WD-40 repeat protein [Arabidopsis thaliana]

```
414978
Seq. No.
Seq. ID
                  uC-osflcyp169b03b1
Method
                  BLASTX
NCBI GI
                  g2832783
BLAST score
                  429
                  4.0e-72
E value
Match length
                  164
% identity
                  79
NCBI Description (AJ225806) potassium channel beta subunit [Egeria densa]
Seq. No.
                  414979
                  uC-osflcyp169b04a1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2191187
                  235
BLAST score
E value
                  1.0e-19
Match length
                  122
% identity
                   41
NCBI Description (AF007271) contains similarity to a DNAJ-like domain
                   [Arabidopsis thaliana]
                   414980
Seq. No.
Seq. ID
                  uC-osflcyp169b05b1
Method
                  BLASTX
NCBI GI
                   g1167836
BLAST score
                   316
E value
                   4.0e-36
Match length
                  110
% identity
NCBI Description (Z68893) protein with incomplete signal sequence [Holcus
                   lanatus]
                   414981
Seq. No.
Seq. ID
                  uC-osflcyp169b06a1
Method
                  BLASTN
NCBI GI
                  g487300
BLAST score
                  149
                   5.0e-78
E value
Match length
                   331
                   88
% identity
NCBI Description Rice mRNA EN290, partial sequence
Seq. No.
                   414982
Seq. ID
                   uC-osflcyp169b06b1
Method
                  BLASTX
NCBI GI
                   g3915865
BLAST score
                   458
E value
                   4.0e-53
                  118
Match length
                   89
% identity
NCBI Description 40S RIBOSOMAL PROTEIN S4
Seq. No.
                   414983
Seq. ID
                  uC-osflcyp169b08a1
Method
                  BLASTN
NCBI GI
                   g3618315
```

71

BLAST score

E value 2.0e-31
Match length 95
% identity 94

NCBI Description Oryza sativa mRNA for zinc finger protein, complete cds,

clone:R2931

Seq. No. 414984

Seq. ID uC-osflcyp169b08b1

Method BLASTX
NCBI GI g3618316
BLAST score 509
E value 1.0e-57
Match length 143
% identity 82

NCBI Description (AB001886) zinc finger protein [Oryza sativa]

Seq. No. 414985

Seq. ID uC-osflcyp169b09a1

Method BLASTX
NCBI GI g2072555
BLAST score 237
E value 9.0e-20
Match length 44
% identity 100

NCBI Description (AF001396) metallothionein-like protein [Oryza sativa]

>gi_6103441_gb_AAF03603.1_ (AF147786) metallothionein-like

protein [Oryza sativa]

Seq. No. 414986

Seq. ID uC-osflcyp169b09b1

Method BLASTX
NCBI GI g2072555
BLAST score 237
E value 9.0e-20
Match length 44
% identity 100

NCBI Description (AF001396) metallothionein-like protein [Oryza sativa]

>gi_6103441_gb_AAF03603.1_ (AF147786) metallothionein-like

protein [Oryza sativa]

Seq. No. 414987

Seq. ID uC-osflcyp169b10b1

Method BLASTX
NCBI GI g3075488
BLAST score 457
E value 1.0e-45
Match length 109
% identity 81

NCBI Description (AF058796) chlorophyll a/b-binding protein [Oryza sativa]

Seq. No. 414988

Seq. ID uC-osflcyp169b11a1

Method BLASTN
NCBI GI g3885889
BLAST score 44
E value 2.0e-15
Match length 88

```
% identity
NCBI Description Oryza sativa histone H3 mRNA, complete cds
                  414989
Seq. No.
                  uC-osflcyp169b11b1
Seq. ID
                  BLASTX
Method
NCBI GI
                  q1053047
BLAST score
                  444
                  3.0e-44
E value
Match length
                  88
                  100
% identity
                  (U38425) histone H3 [Glycine max] >gi_1053049 (U38426)
NCBI Description
                  histone H3 [Glycine max] >gi_1053051 (U38427) histone H3
                  [Glycine max]
                  414990
Seq. No.
                  uC-osflcyp169b12b1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g2773153
BLAST score
                  247
                  1.0e-136
E value
Match length
                  259
                  99
% identity
                  Oryza sativa abscisic acid- and stress-inducible protein
NCBI Description
                  (Asr1) mRNA, complete cds
Seq. No.
                  414991
                  uC-osflcyp169c01b1
Seq. ID
                  BLASTX
Method
NCBI GI
                  g3201627
BLAST score
                  800
E value
                  1.0e-85
                  180
Match length
                  81
% identity
                 (AC004669) putative SWH1 protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   414992
                  uC-osflcyp169c02b1
Seq. ID
Method
                  BLASTX
NCBI GI
                   a4039152
BLAST score
                   169
E value
                   1.0e-11
Match length
                   53
% identity
                   58
                   (AF104221) low temperature and salt responsive protein
NCBI Description
                   LTI6B [Arabidopsis thaliana] >gi 4325219_gb_AAD17303_
                   (AF122006) hydrophobic protein [Arabidopsis thaliana]
Seq. No.
                   414993
Seq. ID
                   uC-osflcyp169c03a1
Method
                   BLASTX
NCBI GI
                   q131773
BLAST score
                   210
E value
                   1.0e-16
                   57
Match length
% identity
                   81
NCBI Description 40S RIBOSOMAL PROTEIN S14 (CLONE MCH2)
```

Seq. No. 414994 Seq. ID uC-osflcyp169c03b1 Method BLASTX q730633 NCBI GI 297 BLAST score E value 3.0e-49 136 Match length 78 % identity NCBI Description 40S RIBOSOMAL PROTEIN S14 >gi 396252 emb CAA50506 (X71384) 40S ribosomal protein S14 [Podocoryne carnea] 414995 Seq. No. uC-osflcyp169c04a1 Seq. ID Method BLASTN NCBI GI g1261857 328 BLAST score E value 0.0e + 00363 Match length % identity NCBI Description Rice CatA gene for catalase, complete cds Seq. No. 414996 Seq. ID uC-osflcyp169c04b1 Method BLASTX NCBI GI q2130069 BLAST score 352 4.0e-61 E value Match length 120 99 % identity NCBI Description catalase (EC 1.11.1.6) catA - rice >gi 1261858_dbj_BAA06232_ (D29966) catalase [Oryza sativa] Seq. No. 414997 uC-osflcyp169c05a1 Seq. ID Method BLASTX NCBI GI g3892058 215 BLAST score E value 3.0e-17 Match length 66 % identity 56 (AC002330) putative glutamate-/aspartate-binding peptide NCBI Description [Arabidopsis thaliana] Seq. No. 414998 uC-osflcyp169c06b1 Seq. ID Method BLASTX NCBI GI g2501353 BLAST score 358 E value 1.0e-40 Match length 115 76 % identity TRANSKETOLASE, CHLOROPLAST (TK) >gi 1084440_pir__S54300 NCBI Description transketolase (EC 2.2.1.1) 3 - Craterostigma plantagineum (fragment) >gi 664901 emb CAA86607_ (Z46646) transketolase

>qi 82724 pir B30097 ribosomal protein S14 (clone MCH2) -

maize

% identity

NCBI Description

96

[Craterostigma plantagineum]

414999 Seq. No. Seq. ID uC-osflcyp169c08b1 Method BLASTX NCBI GI q5103831 205 BLAST score 6.0e-16 E value 71 Match length 54 % identity (AC007591) ESTs gb_H37032, gb_R6425, gb_Z34651, gb_N37268, NCBI Description gb_AA713172 and gb_Z34241 come from this gene. [Arabidopsis thaliana] 415000 Seq. No. uC-osflcyp169c10b1 Seq. ID Method BLASTX g2911052 NCBI GI 425 BLAST score 4.0e-44E value 145 Match length 66 % identity NCBI Description (AL021961) putative protein [Arabidopsis thaliana] 415001 Seq. No. uC-osflcyp169c12b1 Seq. ID BLASTN Method g5670155 NCBI GI 400 BLAST score 0.0e + 00E value 438 Match length % identity NCBI Description Oryza sativa subsp. japonica BAC clone 34K24, complete sequence 415002 Seq. No. Seq. ID uC-osflcyp169d01a1 BLASTX Method q2407279 NCBI GI 167 BLAST score 1.0e-11 E value Match length 38 87 % identity NCBI Description (AF017362) aldolase [Oryza sativa] 415003 Seq. No. Seq. ID uC-osflcyp169d01b1 Method BLASTX NCBI GI q3913018 BLAST score 786 E value 5.0e-84Match length 158

54151

aldolase [Oryza sativa]

FRUCTOSE-BISPHOSPHATE ALDOLASE, CHLOROPLAST PRECURSOR

(ALDP) >gi_218155_dbj_BAA02730_ (D13513) chloroplastic

```
415004
Seq. No.
                  uC-osflcyp169d02a1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q5002357
BLAST score
                  145
                  6.0e-09
E value
Match length
                  42
                  64
% identity
                  (AF150957) heat-shock protein ClpP [Azospirillum
NCBI Description
                  brasilense]
                  415005
Seq. No.
                  uC-osflcyp169d03b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3193303
BLAST score
                  266
                  3.0e-23
E value
                  106
Match length
                   50
% identity
                  (AF069298) similar to several proteins containing a tandem
NCBI Description
                  repeat region such as Plasmodium falciparum GGM tandem
                   repeat protein (GB:U27807); partial CDS [Arabidopsis
                   thaliana]
                   415006
Seq. No.
                  uC-osflcyp169d04b1
Seq. ID
Method
                  BLASTX
NCBI GI
                   g2286153
                   265
BLAST score
                   2.0e-23
E value
Match length
                  82
                   68
% identity
NCBI Description (AF007581) cytoplasmic malate dehydrogenase [Zea mays]
                   415007
Seq. No.
Seq. ID
                   uC-osflcyp169d06b1
Method
                   BLASTX
NCBI GI
                   g3603473
                   229
BLAST score
                   7.0e-19
E value
Match length
                   45
                   100
% identity
NCBI Description (AF090698) elicitor-responsive gene-3 [Oryza sativa]
                   415008
Seq. No.
Seq. ID
                   uC-osflcyp169d07b1
Method
                   BLASTX
                   g2494041
NCBI GI
                   354
BLAST score
E value
                   2.0e-33
                   94
Match length
                   70
% identity
                   DIAMINOPIMELATE EPIMERASE (DAP EPIMERASE)
NCBI Description
                   >gi 1653875 dbj_BAA18785_ (D90917) diaminopimelate
                   epimerase [Synechocystis sp.]
```

415009

Seq. No.

Method

BLASTX

```
uC-osflcyp169d08a1
Seq. ID
                  BLASTX
Method
                  q6015065
NCBI GI
BLAST score
                  324
                  6.0e-30
E value
                  70
Match length
                  89
% identity
                  ELONGATION FACTOR 2 (EF-2) >gi 2369714_emb_CAB09900_
NCBI Description
                  (Z97178) elongation factor 2 [Beta vulgaris]
                  415010
Seq. No.
                  uC-osflcyp169d08b1
Seq. ID
                  BLASTX
Method
                  q6015065
NCBI GI
BLAST score
                   630
                   6.0e-66
E value
                  135
Match length
                   90
% identity
NCBI Description ELONGATION FACTOR 2 (EF-2) >gi_2369714_emb_CAB09900_
                   (Z97178) elongation factor 2 [Beta vulgaris]
                   415011
Seq. No.
                   uC-osflcyp169d11b1
Seq. ID
                   BLASTX
Method
NCBI GI
                   q4753653
                   588
BLAST score
                   7.0e-61
E value
                   157
Match length
                   74
% identity
NCBI Description (AL049751) putative protein [Arabidopsis thaliana]
                   415012
Seq. No.
                   uC-osflcyp169d12b1
Seq. ID
Method
                   BLASTX
                   q3193303
NCBI GI
BLAST score
                   343
E value
                   3.0e-32
                   100
Match length
                   65
% identity
                  (AF069298) similar to several proteins containing a tandem
NCBI Description
                   repeat region such as Plasmodium falciparum GGM tandem
                   repeat protein (GB:U27807); partial CDS [Arabidopsis
                   thaliana]
                   415013
Seq. No.
                   uC-osflcyp169e01a1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g1136122
BLAST score
                   247
                   6.0e-21
E value
                   53
Match length
                   89
% identity
NCBI Description (X91807) alfa-tubulin [Oryza sativa]
                   415014
Seq. No.
                   uC-osflcyp169e01b1
Seq. ID
```

```
NCBI GI
                  g416222
BLAST score
                  385
E value
                  4.0e-37
Match length
                  117
% identity
NCBI Description (D16504) alpha-tubulin [Chlorella vulgaris]
                  415015
Seq. No.
Seq. ID
                  uC-osflcyp169e03b1
                  BLASTX
Method
NCBI GI
                  g4115371
BLAST score
                  503
                  7.0e-51
E value
Match length
                  125
                  74
% identity
NCBI Description (AC005967) unknown protein [Arabidopsis thaliana]
                  415016
Seq. No.
Seq. ID
                  uC-osflcyp169e04b1
Method
                  BLASTX
NCBI GI
                  q5360230
BLAST score
                  558
E value
                  1.0e-84
Match length
                  155
                  97
% identity
NCBI Description (AB015287) Ran [Oryza sativa]
                  415017
Seq. No.
                  uC-osflcyp169e05b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g90626
BLAST score
                  308
                   6.0e-29
E value
Match length
                  80
% identity
                   91
NCBI Description histone H4 (clone 53) - mouse >gi_51311_emb_CAA31622_
                   (X13236) histone H4 (AA 1 - 103) [Mus musculus]
                   415018
Seq. No.
Seq. ID
                   uC-osflcyp169e06b1
Method
                  BLASTX
NCBI GI
                   g2982289
                  574
BLAST score
                   2.0e-59
E value
                  130
Match length
% identity
                   87
NCBI Description (AF051229) 60S ribosomal protein L17 [Picea mariana]
                   415019
Seq. No.
                   uC-osflcyp169e09a1
Seq. ID
                   BLASTX
Method
NCBI GI
                   g120668
                   388
BLAST score
E value
                   2.0e-37
Match length
                   81
% identity
                   90
NCBI Description GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC
```



>gi_82399_pir__A24159 glyceraldehyde-3-phosphate
dehydrogenase (EC 1.2.1.12), cytosolic - barley (fragment)
>gi_167044 (M36650) glyceraldehyde-3-phosphate
dehydrogenase [Hordeum vulgare] >gi_225347_prf__1301218A
dehydrogenase,glyceraldehydephosphate [Hordeum vulgare var.
distichum]

Seq. No. 415020

Seq. ID uC-osflcyp169e09b1

Method BLASTX
NCBI GI g462141
BLAST score 361
E value 6.0e-44
Match length 107
% identity 84

NCBI Description GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE (GAPDH)

>gi_1085816_pir__S38570 glyceraldehyde-3-phosphate
dehydrogenase (EC 1.2.1.12) - Atriplex nummularia
>gi 409575 (U02886) glyceraldehyde-3-phosphate

dehydrogenase [Atriplex nummularia] >gi_414607_emb_CAA53269_ (X75597)

glyceraldehyde-3-phosphate dehydrogenase [Atriplex

nummularia]

Seq. No. 415021

Seq. ID uC-osflcyp169e10b1

Method BLASTX
NCBI GI g2702281
BLAST score 442
E value 7.0e-44
Match length 109
% identity 37

NCBI Description (AC003033) putative protein disulfide isomerase precursor

[Arabidopsis thaliana]

Seq. No. 415022

Seq. ID uC-osflcyp169e11b1

Method BLASTX
NCBI GI g1848212
BLAST score 586
E value 9.0e-61
Match length 129
% identity 51

NCBI Description (Y11209) protein disulfide-isomerase precursor [Nicotiana

tabacum]

Seq. No. 415023

Seq. ID uC-osflcyp169f01a1

Method BLASTN
NCBI GI g2196541
BLAST score 249
E value 1.0e-138
Match length 340
% identity 97

NCBI Description Oryza sativa glycine-rich protein mRNA, complete cds

Seq. No. 415024

```
uC-osflcyp169f01b1
Seq. ID
                  BLASTX
Method
NCBI GI
                  q2293480
BLAST score
                  418
                  4.0e-41
E value
Match length
                  84
                  98
% identity
NCBI Description
                 (AF011331) glycine-rich protein [Oryza sativa]
                  415025
Seq. No.
                  uC-osflcyp169f02b1
Seq. ID
                  BLASTX
Method
NCBI GI
                  g2739370
BLAST score
                  394
E value
                  3.0e - 38
Match length
                  129
                  57
% identity
NCBI Description (AC002505) putative pectinesterase [Arabidopsis thaliana]
Seq. No.
                   415026
                  uC-osflcyp169f03b1
Seq. ID
                  BLASTN
Method
NCBI GI
                   q5441872
BLAST score
                   48
                   1.0e-17
E value
Match length
                   68
                   46
% identity
                  Oryza sativa genomic DNA, chromosome 2, clone:P0437H03
NCBI Description
                   (contig a)
Seq. No.
                   415027
                   uC-osflcyp169f04b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   q1903021
BLAST score
                   788
E value
                   3.0e-84
Match length
                   172
                   87
% identity
NCBI Description (Y10216) hypothetical 3-isopropylmalate dehydrogenase
                   [Arabidopsis thaliana]
                   415028
Seq. No.
                   uC-osflcyp169f05b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2673914
BLAST score
                   234
E value
                   2.0e-19
Match length
                   84
                   52
% identity
NCBI Description (AC002561) hypothetical protein [Arabidopsis thaliana]
                   415029
Seq. No.
                   uC-osflcyp169f07a1
Seq. ID
                   BLASTX
Method
                   g2407279
NCBI GI
BLAST score
                   345
```

2.0e-32

E value

Seq. No.

415035

```
67
Match length
                  100
% identity
NCBI Description (AF017362) aldolase [Oryza sativa]
                  415030
Seq. No.
                  uC-osflcyp169f07b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3913018
BLAST score
                  610
E value
                  1.0e-63
Match length
                  128
                  97
% identity
NCBI Description FRUCTOSE-BISPHOSPHATE ALDOLASE, CHLOROPLAST PRECURSOR
                  (ALDP) >gi 218155 dbj BAA02730 (D13513) chloroplastic
                  aldolase [Oryza sativa]
                  415031
Seq. No.
                  uC-osflcyp169f10b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g5689613
BLAST score
                  314
E value
                  9.0e-29
                  79
Match length
% identity
                  75
NCBI Description (AJ242807) cellulase [Brassica napus]
                  415032
Seq. No.
                  uC-osflcyp169g01b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2791806
BLAST score
                  194
                  2.0e-22
E value
                  109
Match length
% identity
                  59
NCBI Description (AF041433) bet3 [Mus musculus]
                   415033
Seq. No.
Seq. ID
                  uC-osflcyp169g02b1
Method
                  BLASTX
NCBI GI
                  g1808694
BLAST score
                  354
E value
                  1.0e-33
                  118
Match length
                   58
% identity
NCBI Description (Y10787) hypothetical protein [Sporobolus stapfianus]
                   415034
Seq. No.
Seq. ID
                  uC-osflcyp169g05b1
Method
                  BLASTX
NCBI GI
                  g4938503
BLAST score
                  222
                   6.0e-27
E value
                  82
Match length
                   76
% identity
NCBI Description (AL078465) hnRNP-like protein [Arabidopsis thaliana]
```

Method

BLASTX

```
uC-osflcyp169g06b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1084427
BLAST score
                  310
                  3.0e-28
E value
Match length
                  65
                  74
% identity
NCBI Description
                  gip1 protein - garden petunia >gi_825524_emb_CAA60677_
                  (X87225) gip1 [Petunia x hybrida]
Seq. No.
                  415036
                  uC-osflcyp169g07b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q6056205
BLAST score
                  505
                  3.0e-51
E value
Match length
                  137
% identity
                 (AC009400) unknown protein [Arabidopsis thaliana]
NCBI Description
                  415037
Seq. No.
                  uC-osflcyp169g08b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1808694
                  154
BLAST score
E value
                  4.0e-10
                   63
Match length
% identity
NCBI Description (Y10787) hypothetical protein [Sporobolus stapfianus]
Seq. No.
                   415038
                  uC-osflcyp169g09b1
Seq. ID
Method
                  BLASTX
NCBI GI
                   g1076800
BLAST score
                   475
                   8.0e-48
E value
Match length
                   116
                   78
% identity
NCBI Description L-ascorbate peroxidase (EC 1.11.1.11), cytosolic isozyme -
                  maize >gi_600116_emb_CAA84406_ (Z34934) cytosolic ascorbate
                   peroxidase [Zea mays] >qi 1096503 prf 2111423A ascorbate
                  peroxidase [Zea mays]
                   415039
Seq. No.
                   uC-osflcyp169g11b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g4467099
BLAST score
                   434
E value
                   7.0e-43
Match length
                   130
% identity
                   73
                  (AL035538) glycine hydroxymethyltransferase like protein
NCBI Description
                   [Arabidopsis thaliana]
                   415040
Seq. No.
                   uC-osflcyp169g12b1
Seq. ID
```

g1917019 NCBI GI BLAST score 465 E value 1.0e-46Match length 111 % identity 84 NCBI Description (U92045) ribosomal protein S6 RPS6-1 [Zea mays] Seq. No. 415041 Seq. ID uC-osflcyp169h01b1 Method BLASTX NCBI GI g2160161 BLAST score 404 E value 2.0e-39 Match length 126 % identity 11 NCBI Description (AC000132) F21M12.7 gene product [Arabidopsis thaliana] Seq. No. 415042 Seq. ID uC-osflcyp169h02b1 Method BLASTN NCBI GI g6063530 BLAST score 74 E value 3.0e - 33Match length 136 % identity 89 NCBI Description Oryza sativa genomic DNA, chromosome 3, clone:P0043E01 Seq. No. 415043 uC-osflcyp169h03a1 Seq. ID Method BLASTN g1752830 NCBI GI BLAST score 40 E value 4.0e-13 Match length 40 % identity 100 NCBI Description Oryza sativa DNA for metallothionein-like protein, complete cds Seq. No. 415044 Seq. ID uC-osflcyp169h03b1 Method BLASTX NCBI GI g2497903 220 BLAST score E value 7.0e-18 Match length 59 % identity 68 NCBI Description METALLOTHIONEIN-LIKE PROTEIN TYPE 2 >gi_1752831_dbj_BAA14038.1_ (D89931) metallothionein-like
protein [Oryza sativa] >gi_1815628 (U43530) metallothionein-like type 2 [Oryza sativa]

Seq. No. 415045

Seq. ID uC-osflcyp169h04b1

Method BLASTX
NCBI GI g2499819
BLAST score 386
E value 2.0e-50

Seq. ID

119 Match length % identity ASPARTIC PROTEINASE ORYZASIN 1 PRECURSOR NCBI Description >gi_2130068_pir__S66516 aspartic proteinase 1 precursor rice >gi_1030715_dbj_BAA06876_ (D32165) aspartic protease
[Oryza sativa] >gi_1711289_dbj_BAA06875_ (D32144) aspartic protease [Oryza sativa] 415046 Seq. No. uC-osflcyp169h08a1 Seq. ID Method BLASTN q3560532 NCBI GI 89 BLAST score 2.0e-42 E value Match length 155 91 % identity NCBI Description Oryza sativa 24-methylene lophenol C24(1)methyltransferase mRNA, complete cds Seq. No. 415047 uC-osflcyp169h08b1 Seq. ID Method BLASTX NCBI GI q3560533 BLAST score 469 4.0e-47 E value Match length 101 88 % identity (AF042333) 24-methylene lophenol C24(1)methyltransferase NCBI Description [Oryza sativa] Seq. No. 415048 uC-osflcyp169h12b1 Seq. ID Method BLASTX NCBI GI g1711572 BLAST score 440 E value 1.0e-43 Match length 135 % identity 65 NCBI Description SUCCINYL-COA LIGASE (GDP-FORMING), ALPHA-CHAIN PRECURSOR (SUCCINYL-COA SYNTHETASE, ALPHA CHAIN) (SCS-ALPHA) >gi 1076415 pir S30579 succinate--CoA ligase (GDP-forming) (EC 6.2.1.4) alpha chain - Arabidopsis thaliana (fragment) >qi 16510 emb CAA48891 (X69138) succinate--CoA ligase (GDP-forming) [Arabidopsis thaliana] Seq. No. 415049 uC-osflcyp170a02a1 Seq. ID BLASTX Method q5802606 NCBI GI 408 BLAST score E value 9.0e-40 88 Match length % identity NCBI Description (AF174486) methylenetetrahydrofolate reductase [Zea mays] Seq. No. 415050

54160

uC-osflcyp170a02b1

```
BLASTX
Method
                  q5802606
NCBI GI
                  290
BLAST score
E value
                  2.0e-29
                  153
Match length
                  53
% identity
NCBI Description (AF174486) methylenetetrahydrofolate reductase [Zea mays]
                  415051
Seq. No.
                  uC-osflcyp170a03a1
Seq. ID
Method
                  BLASTX
                  q5734741
NCBI GI
                  169
BLAST score
                  5.0e-13
E value
Match length
                  60
                  63
% identity
                  (AC007651) Similar to Ubiquitin Conjugating Enzyme
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                  415052
                  uC-osflcyp170a05b1
Seq. ID
                  BLASTX
Method
NCBI GI
                   q4006829
BLAST score
                   337
                   9.0e-32
E value
Match length
                  76
% identity
NCBI Description (AC005970) putative protein kinase [Arabidopsis thaliana]
                   415053
Seq. No.
                   uC-osflcyp170a08b1
Seq. ID
                   BLASTX
Method
NCBI GI
                   q5802606
BLAST score
                   262
                   6.0e-26
E value
Match length
                   86
                   78
% identity
NCBI Description (AF174486) methylenetetrahydrofolate reductase [Zea mays]
Seq. No.
                   415054
                   uC-osflcyp170a09a1
Seq. ID
                   BLASTX
Method
                   q1620982
NCBI GI
                   205
BLAST score
                   4.0e-16
E value
Match length
                   58
% identity
                   76
NCBI Description (Y08860) 40S ribosomal protein S5 [Nicotiana
                   plumbaginifolia]
                   415055
Seq. No.
                   uC-osflcyp170a10b1
Seq. ID
                   BLASTX
Method
NCBI GI
                   g5815410
                   512
BLAST score
                   5.0e-52
E value
                   128
Match length
```

```
% identity
                  (AF177392) blast and wounding induced mitogen-activated
NCBI Description
                  protein kinase [Oryza sativa]
                  415056
Seq. No.
                  uC-osflcyp170b01b1
Seq. ID
                  BLASTX
Method
                  g2407281
NCBI GI
                  364
BLAST score
                  6.0e-35
E value
                  87
Match length
                  85
% identity
                  (AF017363) ribulose 1,5-bisphosphate carboxylase small
NCBI Description
                  subunit [Oryza sativa]
                  415057
Seq. No.
                  uC-osflcyp170b02a1
Seq. ID
Method
                  BLASTN
                  g4107008
NCBI GI
                  382
BLAST score
                   0.0e+00
E value
                   423
Match length
                   97
% identity
NCBI Description Oryza sativa mRNA for OSK1, complete cds
                   415058
Seq. No.
                   uC-osflcyp170b02b1
Seq. ID
Method
                   BLASTX
                   g4107009
NCBI GI
                   502
BLAST score
                   1.0e-75
E value
                   156
Match length
                   87
% identity
NCBI Description (D82039) OSK1 [Oryza sativa]
                   415059
Seq. No.
                   uC-osflcyp170b03a1
Seq. ID
Method
                   BLASTX
                   g1617197
NCBI GI
                   282
BLAST score
                   5.0e-25
E value
                   71
Match length
                   72
% identity
NCBI Description (Z72488) CP12 [Nicotiana tabacum]
                   415060
Seq. No.
                   uC-osflcyp170b08a1
Seq. ID
                   BLASTX
Method
                   q3297808
NCBI GI
                   252
BLAST score
                   2.0e-21
E value
                   86
Match length
 % identity
NCBI Description (AL031032) putative protein [Arabidopsis thaliana]
 Seq. No.
                   415061
                   uC-osflcyp170b10b1
 Seq. ID
```

```
BLASTX
Method
                   q1710841
NCBI GI
                   452
BLAST score
                   3.0e-45
E value
Match length
                   92
                   96
% identity
                   ADENOSYLHOMOCYSTEINASE (S-ADENOSYL-L-HOMOCYSTEINE
NCBI Description
                   HYDROLASE) (ADOHCYASE) >gi_758247_emb_CAA56278_ (X79905) S-adenosylhomocysteine hydrolase [Phalaenopsis sp.]
                   415062
Seq. No.
                   uC-osflcyp170b12b1
Seq. ID
                   BLASTN
Method
                   g2773153
NCBI GI
                   249
BLAST score
                   1.0e-137
E value
                   397
Match length
                   91
% identity
NCBI Description Oryza sativa abscisic acid- and stress-inducible protein
                   (Asr1) mRNA, complete cds
                    415063
Seq. No.
                   uC-osflcyp170c01a1
Seq. ID
                   BLASTX
Method
                    g4531444
NCBI GI
                    193
BLAST score
                    1.0e-18
E value
                   99
Match length
                    57
% identity
NCBI Description (AC006224) putative protein kinase [Arabidopsis thaliana]
                    415064
Seq. No.
                    uC-osflcyp170c03a1
Seq. ID
                    BLASTX
Method
                    g5734776
NCBI GI
                    273
BLAST score
                    7.0e-24
E value
                    177
Match length
                    18
% identity
NCBI Description (AC007980) 53021 [Arabidopsis thaliana]
Seq. No.
                    415065
                    uC-osflcyp170c12a1
Seq. ID
                    BLASTX
Method
                    q289920
NCBI GI
                    259
BLAST score
E value
                    2.0e-22
Match length
                    60
 % identity
                   (L07119) chlorophyll A/B binding protein [Gossypium
NCBI Description
                    hirsutum]
                    415066
 Seq. No.
                    uC-osflcyp170c12b1
 Seq. ID
                    BLASTX
Method
                    g320618
 NCBI GI
 BLAST score
                    403
```

5.0e-40 E value 88 Match length 95 % identity chlorophyll a/b-binding protein I precursor - rice NCBI Description >gi_218172_dbj_BAA00536_ (D00641) type I light-harvesting chlorophyll a/b-binding protein [Oryza sativa] >gi_227611_prf__1707316A chlorophyll a/b binding protein 1 [Oryza sativa] 415067 Seq. No. uC-osflcyp170d01b1 Seq. ID BLASTX Method q5679336 NCBI GI 143 BLAST score 3.0e-09 E value Match length 30 73 % identity (AF171223) putative zinc finger protein [Oryza sativa] NCBI Description 415068 Seq. No. uC-osflcyp170d03b1 Seq. ID BLASTX Method g129555 NCBI GI 154 BLAST score 5.0e-10 E value Match length 111 32 % identity PEROXISOME ASSEMBLY FACTOR-1 (PAF-1) (PEROXIN-2) NCBI Description >gi_2143903_pir__B53782 peroxisome assembly factor-1 - rat >gi_57645_emb_CAA41054_ (X57988) peroxisome assembly factor-1 [Rattus rattus] >gi_1109647_dbj_BAA06306_ (D30616) PAF-1 [Rattus norvegicus] >gi_227548_prf__1706355A peroxisome assembly factor 1 [Cricetulus griseus] 415069 Seq. No. uC-osflcyp170d04a1 Seq. ID Method BLASTN q1943914 NCBI GI 35 BLAST score 5.0e-10 E value 59 Match length 90 % identity Leishmania mexicana amazonensis organelle-type Ca2+-ATPase NCBI Description gene, complete cds 415070 Seq. No. Seq. ID uC-osflcyp170d04b1 Method BLASTX NCBI GI q3914212 357 BLAST score 1.0e-42 E value Match length 126

% identity 69 5-OXOPROLINASE (5-OXO-L-PROLINASE) (PYROGLUTAMASE) NCBI Description

(5-OPASE) >gi 1732065 (U70825) 5-oxo-L-prolinase [Rattus

norvegicus]

```
Seq. No.
                  uC-osflcyp170d05b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1903364
                  294
BLAST score
                  2.0e-26
E value
Match length
                  129
                  50
% identity
NCBI Description
                  (AC000104) EST gb T45093 comes from this gene. [Arabidopsis
                  thaliana]
                  415072
Seq. No.
                  uC-osflcyp170d07a1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2245058
BLAST score
                  150
E value
                  2.0e-09
Match length
                  83
                   40
% identity
NCBI Description
                 (Z97342) hypothetical protein [Arabidopsis thaliana]
                  415073
Seq. No.
                  uC-osflcyp170d09a1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2244990
BLAST score
                   406
E value
                   2.0e-39
Match length
                  85
% identity
                   96
NCBI Description (Z97340) putative protein [Arabidopsis thaliana]
                   415074
Seq. No.
Seq. ID
                  uC-osflcyp170d12b1
Method
                  BLASTX
NCBI GI
                   g2275219
BLAST score
                   362
E value
                   2.0e-34
Match length
                  141
                   73
% identity
NCBI Description (AC002337) unknown protein [Arabidopsis thaliana]
Seq. No.
                   415075
                   uC-osflcyp170e01b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g4887131
BLAST score
                   252
E value
                   2.0e-24
Match length
                  114
                   57
% identity
NCBI Description (AF134732) 60S ribosomal protein L1 [Prunus armeniaca]
Seq. No.
                   415076
Seq. ID
                  uC-osflcyp170e02a1
Method
                  BLASTX
NCBI GI
                   g129916
BLAST score
                  248
E value
                   5.0e-23
```

Method

NCBI GI

BLASTX

g3182921

```
Match length
                   68
                   93
% identity
                   PHOSPHOGLYCERATE KINASE, CYTOSOLIC >gi 66911 pir TVWTGY
NCBI Description
                   phosphoglycerate kinase (EC 2.7.2.3), cytosolic - wheat
                   >gi_21835_emb_CAA33302_ (X15232) phosphoglycerate kinase
                   (AA 1 - 401) [Triticum aestivum]
                   415077
Seq. No.
Seq. ID
                   uC-osflcyp170e03a1
                   BLASTX
Method
NCBI GI
                   q3036951
                   339
BLAST score
                   1.0e-31
E value
                   67
Match length
% identity
                   97
                   (AB012639) light harvesting chlorophyll a/b-binding protein
NCBI Description
                   [Nicotiana sylvestris]
                   415078
Seq. No.
Seq. ID
                   uC-osflcyp170e03b1
                   BLASTX
Method
NCBI GI
                   q320618
BLAST score
                   342
E value
                   8.0e-32
Match length
                   74
% identity
                   92
                   chlorophyll a/b-binding protein I precursor - rice
NCBI Description
                   >gi_218172_dbj_BAA00536_ (D00641) type I light-harvesting
chlorophyll a/b-binding protein [Oryza sativa]
                   >gi_227611_prf__1707316A chlorophyll a/b binding protein 1
                   [Oryza sativa]
Seq. No.
                   415079
Seq. ID
                   uC-osflcyp170e04a1
Method
                   BLASTX
NCBI GI
                   q4097569
                   236
BLAST score
                   1.0e-19
E value
                   95
Match length
                   56
% identity
NCBI Description (U64915) GMFP4 [Glycine max]
                   415080
Seq. No.
Seq. ID
                   uC-osflcyp170e07a1
Method
                   BLASTX
NCBI GI
                   g3337356
BLAST score
                   144
                   7.0e-09
E value
                   43
Match length
% identity
                   (AC004481) putative protein transport protein SEC61 alpha
NCBI Description
                   subunit [Arabidopsis thaliana]
                   415081
Seq. No.
Seq. ID
                   uC-osflcyp170e07b1
```

```
346
BLAST score
E value
                  1.0e-32
                  69
Match length
                  97
% identity
                  ASPARAGINE SYNTHETASE [GLUTAMINE-HYDROLYZING]
NCBI Description
                  (GLUTAMINE-DEPENDENT ASPARAGINE SYNTHETASE) >gi 1432054
                  (U55873) asparagine synthetase [Oryza sativa]
                  >gi_1902992_dbj_BAA18951_ (D83378) asparagine synthetase
                  [Oryza sativa]
                  415082
Seq. No.
                  uC-osflcyp170e11a1
Seq. ID
Method
                  BLASTN
                  g1261857
NCBI GI
                  331
BLAST score
E value
                  0.0e+00
                  370
Match length
                  98
% identity
NCBI Description Rice CatA gene for catalase, complete cds
                  415083
Seq. No.
                  uC-osflcyp170e11b1
Seq. ID
                  BLASTN
Method
                  g1261857
NCBI GI
BLAST score
                  341
                  0.0e + 00
E value
Match length
                  352
                  99
% identity
NCBI Description Rice CatA gene for catalase, complete cds
                  415084
Seq. No.
                  uC-osflcyp170e12a1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3746065
                  233
BLAST score
E value
                  3.0e-19
Match length
                  67
% identity
NCBI Description (AC005311) putative lipase [Arabidopsis thaliana]
                  415085
Seq. No.
Seq. ID
                  uC-osflcyp170e12b1
Method
                  BLASTX
NCBI GI
                  g2832660
                  221
BLAST score
                   3.0e-18
E value
Match length
                  132
% identity
NCBI Description (AL021710) lipase-like protein [Arabidopsis thaliana]
Seq. No.
                   415086
Seq. ID
                  uC-osflcyp170f01a1
```

Method BLASTX
NCBI GI g3789940
BLAST score 197
E value 4.0e-15
Match length 41

% identity 24

NCBI Description (AF093504) tetra-ubiquitin [Saccharum hybrid cultivar

H32-85601

Seq. No. 415087

Seq. ID uC-osflcyp170f02b1

Method BLASTX
NCBI GI g3335355
BLAST score 659
E value 3.0e-69
Match length 138
% identity 28

NCBI Description (AC004512) Match to polyubiquitin DNA gb_L05401 from A.

thaliana. Contains insertion of mitochondrial NADH

dehydrogenase gb_X82618 and gb_X98301. May be a pseudogene with an expressed insert. EST gb AA586248 comes from this

region. [Arabi

Seq. No. 415088

Seq. ID uC-osflcyp170f04a1

Method BLASTN
NCBI GI g11957
BLAST score 490
E value 0.0e+00
Match length 519
% identity 98

NCBI Description Rice complete chloroplast genome

Seq. No. 415089

Seq. ID uC-osflcyp170f04b1

Method BLASTN
NCBI GI g11957
BLAST score 152
E value 4.0e-80
Match length 164
% identity 99

NCBI Description Rice complete chloroplast genome

Seq. No. 415090

Seq. ID uC-osflcyp170f05b1

Method BLASTX
NCBI GI g1076641
BLAST score 286
E value 5.0e-26
Match length 79
% identity 70

NCBI Description tau-protein kinase (EC 2.7.1.135) homolog - common tobacco

>gi_456356_emb_CAA54803_ (X77763) shaggy like protein kinase [Nicotiana tabacum] >gi_1094395_prf__2106142A

Ser/Thr protein kinase [Nicotiana tabacum]

Seq. No. 415091

Seq. ID uC-osflcyp170f06a1

Method BLASTX NCBI GI g1519251 BLAST score 299 E value 6.0e-27

```
62
Match length
% identity
NCBI Description (U65957) GF14-c protein [Oryza sativa]
Seq. No.
                   415092
Seq. ID
                   uC-osflcyp170f06b1
Method
                  BLASTX
NCBI GI
                   g1519251
BLAST score
                   656
E value
                   7.0e-69
Match length
                  132
                   98
% identity
NCBI Description (U65957) GF14-c protein [Oryza sativa]
Seq. No.
                   415093
Seq. ID
                  uC-osflcyp170f09a1
Method
                  BLASTN
NCBI GI
                  g1658312
BLAST score
                  119
E value
                   4.0e-60
Match length
                  147
% identity
                   48
NCBI Description O.sativa osr40g2 gene
Seq. No.
                   415094
Seq. ID
                  uC-osflcyp170f09b1
Method
                  BLASTN
NCBI GI
                  g1658312
BLAST score
                  65
E value
                  1.0e-28
Match length
                  81
% identity
                  95
NCBI Description O.sativa osr40g2 gene
Seq. No.
                   415095
Seq. ID
                  uC-osflcyp170g01b1
Method
                  BLASTX
NCBI GI
                  g5081779
BLAST score
                  233
E value
                  6.0e-20
Match length
                  57
% identity
                  75
NCBI Description (AF150630) cellulose synthase [Gossypium hirsutum]
                  415096
Seq. No.
Seq. ID
                  uC-osflcyp170g02a1
Method
                  BLASTX
NCBI GI
                  g1076820
BLAST score
                  287
E value
                  1.0e-25
Match length
                  59
                  92
% identity
NCBI Description phosphoglycerate mutase (EC 5.4.2.1) - maize
Seq. No.
                  415097
Seq. ID
                  uC-osflcyp170g03a1
Method
                  BLASTN
```

```
g2072554
NCBI GI
                  71
BLAST score
                  1.0e-31
E value
                  191
Match length
                  84
% identity
                  Oryza sativa metallothionein-like protein mRNA, complete
NCBI Description
                  415098
Seq. No.
                  uC-osflcyp170g03b1
Seq. ID
Method
                  BLASTX
                  g2072555
NCBI GI
                  203
BLAST score
                  2.0e-16
E value
                  37
Match length
                  100
% identity
                   (AF001396) metallothionein-like protein [Oryza sativa]
NCBI Description
                  >gi_6103441_gb_AAF03603.1_ (AF147786) metallothionein-like
                  protein [Oryza sativa]
                   415099
Seq. No.
                  uC-osflcyp170g04a1
Seq. ID
                  BLASTX
Method
                   q1416512
NCBI GI
BLAST score
                   145
                   5.0e-09
E value
Match length
                   33
                   79
% identity
                  (D63167) CTP:phosphocholine cytidylyltransferase [Brassica
NCBI Description
                   napus]
                   415100
Seq. No.
                   uC-osflcyp170g06a1
Seq. ID
Method
                   BLASTN
                   q2331130
NCBI GI
BLAST score
                   200
E value
                   1.0e-108
                   208
Match length
% identity
                   99
                   Oryza sativa glycine-rich protein (OSGRP1) mRNA, complete
NCBI Description
                   415101
Seq. No.
                   uC-osflcyp170g06b1
Seq. ID
                   BLASTX
Method
                   g2331133
NCBI GI
BLAST score
                   157
E value
                   1.0e-12
                   50
Match length
% identity
NCBI Description (AF010580) glycine-rich protein [Oryza sativa]
Seq. No.
                   415102
                   uC-osflcyp170g09a1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2245001
BLAST score
                   221
```

% identity

```
E value
                  6.0e-18
Match length
                  44
% identity
                  93
NCBI Description (Z97341) hypothetical protein [Arabidopsis thaliana]
                  415103
Seq. No.
                  uC-osflcyp170g09b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2245001
BLAST score
                  323
E value
                  9.0e-30
Match length
                  73
% identity
NCBI Description (Z97341) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  415104
                  uC-osflcyp170g10b1
Seq. ID
Method
                  BLASTN
NCBI GI
                  q968995
BLAST score
                  86
E value
                  7.0e-41
Match length
                  94
% identity
                  99
NCBI Description Oryza sativa clone glyceraldehyde-3-phosphate dehydrogenase
                  (Gpc) mRNA, complete cds
                  415105
Seq. No.
                  uC-osflcyp170h02a1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2493650
BLAST score
                  273
E value
                  5.0e-24
Match length
                  60
% identity
                  90
NCBI Description
                  RUBISCO SUBUNIT BINDING-PROTEIN BETA SUBUNIT (60 KD
                  CHAPERONIN BETA SUBUNIT) (CPN-60 BETA)
                  >gi_1167858_emb_CAA93139_ (Z68903) chaperonin [Secale
                  cereale]
Seq. No.
                  415106
Seq. ID
                  uC-osflcyp170h02b1
Method
                  BLASTX
NCBI GI
                  g81601
BLAST score
                  154
E value
                  1.0e-10
Match length
                  36
                  92
% identity
NCBI Description chaperonin 60 beta - Arabidopsis thaliana
Seq. No.
                  415107
Seq. ID
                  uC-osflcyp170h03b1
Method
                  BLASTX
NCBI GI
                  g6016726
BLAST score
                  155
E value
                  8.0e-12
Match length
                  67
```

```
(AC009325) unknown protein [Arabidopsis thaliana]
NCBI Description
                  >gi 6091713 gb AAF03425.1 AC010797 1 (AC010797) unknown
                  protein [Arabidopsis thaliana]
                  415108
Seq. No.
                  uC-osflcyp170h04a1
Seq. ID
Method
                  BLASTX
                  g6015059
NCBI GI
                  469
BLAST score
                  7.0e-47
E value
                  91
Match length
                  100
% identity
                  ELONGATION FACTOR 1-ALPHA (EF-1-ALPHA) >gi 2996096
NCBI Description
                  (AF030517) translation elongation factor-1 alpha; EF-1
                  alpha [Oryza sativa]
                  415109
Seq. No.
                  uC-osflcyp170h04b1
Seq. ID
Method
                  BLASTX
                  q2662343
NCBI GI
                  393
BLAST score
                  2.0e-38
E value
                  78
Match length
                  97
% identity
NCBI Description (D63581) EF-1 alpha [Oryza sativa]
                  415110
Seq. No.
Seq. ID
                  uC-osflcyp170h06b1
Method
                  BLASTX
                  g2655008
NCBI GI
BLAST score
                  167
E value
                  1.0e-11
                  80
Match length
                  44
% identity
NCBI Description (AF017144) (1-4)-beta-mannan endohydrolase [Lycopersicon
                  esculentum]
Seq. No.
                  415111
                  uC-osflcyp170h07a1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3337356
BLAST score
                  271
                  9.0e-24
E value
                  55
Match length
                  96
% identity
NCBI Description (AC004481) putative protein transport protein SEC61 alpha
                  subunit [Arabidopsis thaliana]
Seq. No.
                  415112
                  uC-osflcyp170h07b1
Seq. ID
                  BLASTX
Method
NCBI GI
                  q3337356
BLAST score
                  372
E value
                  7.0e-36
                  72
Match length
% identity
NCBI Description (AC004481) putative protein transport protein SEC61 alpha
```

NCBI Description

subunit [Arabidopsis thaliana]

Seq. No. 415113 uC-osflcyp170h08b1 Seq. ID Method BLASTX g4427003 NCBI GI BLAST score 149 9.0e-10 E value Match length 66 47 % identity (AF127664) NBD-like protein [Arabidopsis thaliana] NCBI Description Seq. No. 415114 uC-osflcyp171a02b1 Seq. ID BLASTX Method NCBI GI q1076531 BLAST score 155 3.0e-10 E value Match length 65 52 % identity hypothetical protein, pollen allergen homolog - garden pea NCBI Description >gi_2129891_pir__S65056 pollen allergen homolog precursor (clone PPA1) - garden pea >gi_732905_emb_CAA59470_ (X85187) homology with pollen allergens [Pisum sativum] 415115 Seq. No. uC-osflcyp171a03b1 Seq. ID BLASTX Method g4455323 NCBI GI BLAST score 222 6.0e-18 E value 78 Match length 55 % identity (AL035525) aminopeptidase-like protein [Arabidopsis NCBI Description thaliana] 415116 Seq. No. uC-osflcyp171a04a1 Seq. ID Method BLASTN g5714761 NCBI GI 39 BLAST score 2.0e-12 E value 43 Match length 98 % identity NCBI Description Oryza sativa subsp. indica serine/threonine protein phosphatase PP2A-4 catalytic subunit (PP2A) gene, complete 415117 Seq. No. uC-osflcyp171a04b1 Seq. ID Method BLASTX g3063447 NCBI GI 384 BLAST score 6.0e-37 E value Match length 169 % identity

54173

(AC003981) F22013.9 [Arabidopsis thaliana]

Seq. ID

```
415118
Seq. No.
                  uC-osflcyp171a07b1
Seq. ID
                  BLASTX
Method
                  g4680675
NCBI GI
                  184
BLAST score
                  2.0e-13
E value
                  159
Match length
                  31
% identity
                  (AF132952) CGI-18 protein [Homo sapiens]
NCBI Description
Seq. No.
                  415119
                  uC-osflcyp171a08b1
Seq. ID
                  BLASTX
Method
                  g5882732
NCBI GI
                  178
BLAST score
                  2.0e-23
E value
                  120
Match length
                  55
% identity
                  (AC008263) Similar to gb_AF135422 GDP-mannose
NCBI Description
                  pyrophosphorylase A (GMPPA) from Homo sapiens. ESTs
                  gb_AA712990, gb_N65247, gb_N38149, gb_T04179, gb_Z38092,
                   gb_T76473, gb_N96403, gb_AA394551 and gb_AA728527 come from
                   415120
Seq. No.
                  uC-osflcyp171a10b1
Seq. ID
                  BLASTX
Method
                  g4680212
NCBI GI
                   150
BLAST score
                   4.0e-12
E value
                   52
Match length
% identity
                   81
NCBI Description (AF114171) hypothetical protein [Sorghum bicolor]
                   415121
Seq. No.
                   uC-osflcyp171a11b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g1350680
BLAST score
                   362
                   1.0e-48
E value
                   129
Match length
                   77
% identity
NCBI Description 60S RIBOSOMAL PROTEIN L1
                   415122
Seq. No.
                   uC-osflcyp171b02b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   q4539383
BLAST score
                   276
                   3.0e-24
E value
                   175
Match length
% identity
                   (AL035526) putative protein (fragment) [Arabidopsis
NCBI Description
                   thaliana]
                   415123
Seq. No.
```

54174

uC-osflcyp171b04b1

Match length

103

```
BLASTX
Method
                  g4115534
NCBI GI
                  221
BLAST score
                  8.0e-18
E value
                  149
Match length
                  39
% identity
                  (AB012114) UDP-glycose:flavonoid glycosyltransferase [Vigna
NCBI Description
                  mungo]
                  415124
Seq. No.
                  uC-osflcyp171b05a1
Seq. ID
Method
                  BLASTX
                  g485517
NCBI GI
                  170
BLAST score
                  6.0e-12
E value
Match length
                  37
                  92
% identity
NCBI Description ADP, ATP carrier protein - rice
                  415125
Seq. No.
                  uC-osflcyp171b05b1
Seq. ID
                  BLASTX
Method
                  g485517
NCBI GI
                   886
BLAST score
                   9.0e-96
E value
Match length
                   179
                   94
% identity
NCBI Description ADP, ATP carrier protein - rice
                   415126
Seq. No.
                   uC-osflcyp171b06b1
Seq. ID
                   BLASTX
Method
                   g5080810
NCBI GI
                   529
BLAST score
                   7.0e-54
E value
                   135
Match length
% identity
                   78
NCBI Description (AC007258) Very similar to helicases [Arabidopsis thaliana]
                   415127
Seq. No.
                   uC-osflcyp171b09b1
Seq. ID
                   BLASTX
Method
                   q5903092
NCBI GI
                   453
BLAST score
                   5.0e-45
E value
                   128
Match length
% identity
NCBI Description (AC008017) Highly similar to developmental protein DG1118
                   [Arabidopsis thaliana]
                   415128
Seq. No.
                   uC-osflcyp171b10b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g1731181
BLAST score
                   240
                   5.0e-20
E value
```

Seq. No.

415133

% identity 44 HYPOTHETICAL 75.5 KD PROTEIN C14A4.3 IN CHROMOSOME II NCBI Description >gi_3874230_emb_CAA90107.1_ (Z49909) weak similarity with a B. Flavum translocation protein (Swiss Prot accession number P38376); cDNA EST yk220e10.5 comes from this gene; cDNA EST yk549e12.3 comes from this gene; cDNA EST yk618d6.3 comes from this gene 415129 Seq. No. uC-osflcyp171b11a1 Seq. ID Method BLASTX NCBI GI g283008 378 BLAST score 2.0e-36 E value Match length 73 % identity 100 sucrose synthase (EC 2.4.1.13) - rice NCBI Description >gi 20366 emb CAA46017 (X64770) sucrose synthase [Oryza sativa] 415130 Seq. No. uC-osflcyp171b11b1 Seq. ID Method BLASTX NCBI GI g283008 BLAST score 695 2.0e-73 E value Match length 153 % identity 90 sucrose synthase (EC 2.4.1.13) - rice NCBI Description >gi 20366 emb CAA46017 (X64770) sucrose synthase [Oryza sativa] Seq. No. 415131 uC-osflcyp171b12b1 Seq. ID Method BLASTX NCBI GI g5922612 BLAST score 482 E value 2.0e-48 171 Match length 61 % identity (AP000492) EST AU078118(E3904) corresponds to a region of NCBI Description the predicted gene.; similar to Arabidopsis thaliana BAC IG002P16; No definition line found. (AF007270) [Oryza sativa] 415132 Seq. No. uC-osflcyp171c02b1 Seq. ID Method BLASTN NCBI GI q4164148 BLAST score 527 E value 0.0e + 00Match length 527 % identity 100 Oryza sativa mRNA for iron-superoxide dismutase, complete NCBI Description

uC-osflcyp171c03b1 Seq. ID BLASTX Method g3687235 NCBI GI 389 BLAST score 2.0e-37 E value 83 Match length 93 % identity (AC005169) putative copia-like transposable element NCBI Description [Arabidopsis thaliana] 415134 Seq. No. uC-osflcyp171c05b1 Seq. ID BLASTX Method NCBI GI q4678328 179 BLAST score 1.0e-13 E value 53 Match length 64 % identity NCBI Description (AL049658) aldehyde dehydrogenase (NAD+)-like protein [Arabidopsis thaliana] Seq. No. 415135 uC-osflcyp171c07a1 Seq. ID Method BLASTX NCBI GI q5107826 BLAST score 146 E value 4.0e-09 Match length 32 % identity 84 NCBI Description (AF149413) similar to malate dehydrogenases; Pfam PF00390, Score=1290.5. E=0, N=1 [Arabidopsis thaliana] 415136 Seq. No. uC-osflcyp171c07b1 Seq. ID Method BLASTX NCBI GI q2911148 BLAST score 769 E value 4.0e-82 172 Match length % identity 86 NCBI Description (AB005808) NADP-malic enzyme [Aloe arborescens] 415137 Seq. No. Seq. ID uC-osflcyp171c08b1 Method BLASTX NCBI GI g4467147 563 BLAST score 6.0e-58E value 170 Match length 64 % identity NCBI Description (AL035540) putative protein [Arabidopsis thaliana] Seq. No. 415138 Seq. ID uC-osflcyp171c10a1 Method BLASTX NCBI GI g1931642

54177

233

BLAST score

```
3.0e-19
E value
                  77
Match length
% identity
                   58
                  (U95973) Ser/Thr protein kinase isolog [Arabidopsis
NCBI Description
                  thaliana]
                   415139
Seq. No.
Seq. ID
                  uC-osflcyp171c10b1
Method
                  BLASTX
NCBI GI
                   g1350680
                   378
BLAST score
                   3.0e-36
E value
                   111
Match length
                   65
% identity
NCBI Description 60S RIBOSOMAL PROTEIN L1
                   415140
Seq. No.
                   uC-osflcyp171c11a1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2388580
BLAST score
                   184
                   2.0e-13
E value
Match length
                   60
% identity
                   50
                  (AC000098) Similar to Sequence 10 from patent 5477002
NCBI Description
                   (gb_1253956). [Arabidopsis thaliana]
                   415141
Seq. No.
                   uC-osflcyp171d01b1
Seq. ID
Method
                   BLASTX
                   g4127348
NCBI GI
BLAST score
                   432
                   1.0e-42
E value
Match length
                   157
% identity
                   53
NCBI Description (AJ010449) glutathione transferase [Alopecurus myosuroides]
                   415142
Seq. No.
                   uC-osflcyp171d02b1
Seq. ID
                   BLASTX
Method
                   g4263704
NCBI GI
                   368
BLAST score
                   5.0e - 35
E value
                   142
Match length
                   51
% identity
                  (AC006223) putative sugar starvation-induced protein
NCBI Description
                   [Arabidopsis thaliana]
                   415143
Seq. No.
Seq. ID
                   uC-osflcyp171d04a1
                   BLASTX
Method
                   g6016877
NCBI GI
                   222
BLAST score
                   4.0e-18
E value
Match length
                   48
% identity
NCBI Description (AP000570) ESTs AU077642(E30706), AU077641(E30706)
```

```
correspond to a region of the predicted gene.; hypothetical
                  protein [Oryza sativa]
                  415144
Seq. No.
                  uC-osflcyp171d04b1
Seq. ID
Method
                  BLASTX
                  q6016877
NCBI GI
BLAST score
                  222
E value
                  6.0e-18
Match length
                  48
                  79
% identity
                  (AP000570) ESTs AU077642(E30706), AU077641(E30706)
NCBI Description
                  correspond to a region of the predicted gene.; hypothetical
                  protein [Oryza sativa]
                  415145
Seq. No.
                  uC-osflcyp171d09b1
Seq. ID
                  BLASTX
Method
NCBI GI
                  g4960150
BLAST score
                  408
                  3.0e-41
E value
Match length
                  101
% identity
                  89
                  (AF153277) DNA-directed RNA polymerase IIa [Nicotiana
NCBI Description
                  tabacum] >gi_4960152_gb_AAD34614.1_AF153278_1 (AF153278)
                  DNA-directed RNA polymerase IIb [Nicotiana tabacum]
Seq. No.
                  415146
                  uC-osflcyp171d11a1
Seq. ID
                  BLASTX
Method
NCBI GI
                  g2801536
                  257
BLAST score
                   4.0e-22
E value
                  69
Match length
% identity
                   67
NCBI Description (AF039531) lysophospholipase homolog [Oryza sativa]
Seq. No.
                  415147
                  uC-osflcyp171d11b1
Seq. ID
                  BLASTX
Method
NCBI GI
                  g1710780
                  615
BLAST score
                   5.0e-64
E value
                  164
Match length
                   72
% identity
NCBI Description 40S RIBOSOMAL PROTEIN S9 (S7) >gi 1321917 emb CAA65433
                   (X96613) cytoplasmic ribosomal protein S7 [Podospora
                   anserina]
```

Method BLASTX
NCBI GI g1151244
BLAST score 242
E value 1.0e-29
Match length 111

415148

uC-osflcyp171d12b1

Match length 11 % identity 57

Seq. No.

Seq. ID

```
NCBI Description (U43377) GTP-binding protein [Arabidopsis thaliana]
                  415149
Seq. No.
                  uC-osflcyp171e01a1
Seq. ID
                  BLASTX
Method
                  q2435522
NCBI GI
                  207
BLAST score
E value
                  3.0e-16
Match length
                  66
                  64
% identity
NCBI Description (AF024504) contains similarity to other AMP-binding enzymes
                  [Arabidopsis thaliana]
                  415150
Seq. No.
                  uC-osflcyp171e01b1
Seq. ID
Method
                  BLASTX
                  g4926866
NCBI GI
                  304
BLAST score
E value
                  1.0e-27
                  99
Match length
                  58
% identity
NCBI Description (AC007509) putative amp-binding protein [Arabidopsis
                  thaliana]
Seq. No.
                   415151
                   uC-osflcyp171e02a1
Seq. ID
Method
                  BLASTX
                   g4926866
NCBI GI
                  207
BLAST score
                   3.0e-16
E value
                   62
Match length
                   66
% identity
NCBI Description (AC007509) putative amp-binding protein [Arabidopsis
                   thaliana]
                   415152
Seq. No.
                   uC-osflcyp171e02b1
Seq. ID
                   BLASTX
Method
NCBI GI
                   g1917019
                   675
BLAST score
E value
                   4.0e-71
                   153
Match length
                   86
% identity
NCBI Description (U92045) ribosomal protein S6 RPS6-1 [Zea mays]
                   415153
Seq. No.
Seq. ID
                   uC-osflcyp171e03a1
                   BLASTX
Method
                   g5688947
NCBI GI
BLAST score
                   253
                   1.0e-21
E value
Match length
                   48
% identity
                  (AB017428) succinate dehydrogenase iron-protein subunit
NCBI Description
                   (SDHB) [Oryza sativa] >gi_5688949_dbj_BAA82750.1_
                   (AB017429) succinate dehydrogenase iron-protein subunit
```

(SDHB) [Oryza sativa]

415154 Seq. No. Seq. ID uC-osflcyp171e03b1 Method BLASTX NCBI GI g5688947 BLAST score 590 E value 4.0e-61 Match length 127 % identity 86

NCBI Description (AB017428) succinate dehydrogenase iron-protein subunit

(SDHB) [Oryza sativa] >gi 5688949 dbj BAA82750.1_

(AB017429) succinate dehydrogenase iron-protein subunit

(SDHB) [Oryza sativa]

Seq. No. 415155

Seq. ID uC-osflcyp171e04b1

Method BLASTX
NCBI GI g5596468
BLAST score 412
E value 3.0e-40
Match length 144
% identity 53

NCBI Description (AL096882) putative protein [Arabidopsis thaliana]

Seq. No. 415156

Seq. ID uC-osflcyp171e05b1

Method BLASTX
NCBI GI g4587514
BLAST score 712
E value 2.0e-75
Match length 163
% identity 82

NCBI Description (AC007060) Similar to W08E3.3 gi_3880615 putative

GTP-binding protein from C. elegans cosmid gb_Z92773. EST gb AA597331 comes from this gene. [Arabidopsis thaliana]

Seq. No. 415157

Seq. ID uC-osflcyp171e06a1

Method BLASTN
NCBI GI g2961436
BLAST score 297
E value 1.0e-166
Match length 327
% identity 88

NCBI Description Oryza sativa MADS box protein (MADS4) mRNA, complete cds

Seq. No. 415158

Seq. ID uC-osflcyp171e06b1

Method BLASTN
NCBI GI g2961436
BLAST score 125
E value 4.0e-64
Match length 129
% identity 99

NCBI Description Oryza sativa MADS box protein (MADS4) mRNA, complete cds

Seq. No. 415159

uC-osflcyp171e07b1 Seq. ID BLASTN Method g4966303 NCBI GI BLAST score 44 3.0e-15 E value 76 Match length 48 % identity NCBI Description Caenorhabditis elegans cosmid F16B3 415160 Seq. No. uC-osflcyp171e08a1 Seq. ID Method BLASTX NCBI GI q482311 BLAST score 165 2.0e-11 E value Match length 48 71 % identity photosystem II oxygen-evolving complex protein 1 - rice NCBI Description (strain Nihonbare) >gi_739292_prf__2002393A oxygen-evolving complex protein 1 [Oryza sativa] Seq. No. 415161 uC-osflcyp171e08b1 Seq. ID Method BLASTX NCBI GI q131388 394 BLAST score 3.0e-38 E value 131 Match length % identity 66 OXYGEN-EVOLVING ENHANCER PROTEIN 1 PRECURSOR (OEE1) (33 KD NCBI Description SUBUNIT OF OXYGEN EVOLVING SYSTEM OF PHOTOSYSTEM II) (33 KD THYLAKOID MEMBRANE PROTEIN) >gi_100831_pir__\$16260 photosystem II oxygen-evolving complex protein 1 - common wheat x Sanduri wheat >gi_21844_emb_CAA40670_ (X57408) 33kDa oxygen evolving protein of photosystem II [Triticum aestivum] 415162 Seq. No. uC-osflcyp171e09b1 Seq. ID BLASTX Method g4895198 NCBI GI BLAST score 161 9.0e-11 E value 132 Match length % identity NCBI Description (AC007661) unknown protein [Arabidopsis thaliana] 415163 Seq. No. Seq. ID uC-osflcyp171e10b1 BLASTN Method g2443456 NCBI GI 100 BLAST score 9.0e-49E value Match length 147

54182

NCBI Description Oryza sativa ethylene responsive element binding protein

(Os-EREBP1) mRNA, complete cds

93

% identity

```
Seq. No.
                  415164
Seq. ID
                  uC-osflcyp171e12a1
Method
                  BLASTX
NCBI GI
                  g4572673
BLAST score
                  313
E value
                  1.0e-28
                  96
Match length
                  67
% identity
NCBI Description (AC006954) putative sarcosine oxidase [Arabidopsis
                  thaliana]
Seq. No.
                  415165
Seq. ID
                  uC-osflcyp171e12b1
Method
                  BLASTX
                  g4572673
NCBI GI
BLAST score
                  470
E value
                  5.0e-47
Match length
                  167
% identity
                  53
NCBI Description (AC006954) putative sarcosine oxidase [Arabidopsis
                  thaliana]
                  415166
Seq. No.
Seq. ID
                  uC-osflcyp171f01a1
Method
                  BLASTX
NCBI GI
                  g1706260
BLAST score
                  363
                  2.0e-34
E value
                  69
Match length
% identity
                  94
NCBI Description CYSTEINE PROTEINASE 1 PRECURSOR >gi 2118131 pir S59597
                  cysteine proteinase 1 precursor - maize
                  >gi 643597 dbj BAA08244 (D45402) cysteine proteinase [Zea
                  mays]
Seq. No.
                  415167
Seq. ID
                  uC-osflcyp171f01b1
Method
                  BLASTX
NCBI GI
                  g1706260
BLAST score
                  403
                  3.0e-39
E value
                  85
Match length
                  91
% identity
NCBI Description CYSTEINE PROTEINASE 1 PRECURSOR >gi 2118131 pir S59597
                  cysteine proteinase 1 precursor - maize
                  >gi_643597_dbj_BAA08244_ (D45402) cysteine proteinase [Zea
                  mays]
Seq. No.
                  415168
Seq. ID
                  uC-osflcyp171f02a1
Method
                  BLASTX
NCBI GI
                  g1706260
                  247
BLAST score
E value
                  6.0e-21
Match length
                  47
                  89
% identity
```

```
NCBI Description CYSTEINE PROTEINASE 1 PRECURSOR >gi_2118131_pir__S59597
                   cysteine proteinase 1 precursor - maize
                   >gi_643597_dbj_BAA08244_ (D45402) cysteine proteinase [Zea
                   mays]
                   415169
Seq. No.
                   uC-osflcyp171f02b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   q3914422
                   623
BLAST score
E value
                   5.0e-65
                   120
Match length
                   93
% identity
                  PROFILIN >gi_2154728_emb_CAA69669_ (Y08389) profilin 2 [Cynodon dactylon] >gi_2154730_emb_CAA69670_ (Y08390)
NCBI Description
                   profilin 1 [Cynodon dactylon]
                   415170
Seq. No.
                   uC-osflcyp171f05a1
Seq. ID
Method
                   BLASTX
                   q2696804
NCBI GI
                   393
BLAST score
                   4.0e-38
E value
                   73
Match length
% identity
                   100
NCBI Description (AB009665) water channel protein [Oryza sativa]
                   415171
Seq. No.
                   uC-osflcyp171f05b1
Seq. ID
                   BLASTX
Method
NCBI GI
                   g2894534
BLAST score
                   824
E value
                   2.0e-88
Match length
                   161
                   98
% identity
NCBI Description (AJ224327) aquaporin [Oryza sativa]
Seq. No.
                   415172
                   uC-osflcyp171f06b1
Seq. ID
                   BLASTX
Method
NCBI GI
                   g5902359
BLAST score
                   722
                   1.0e-76
E value
                   173
Match length
                   77
% identity
NCBI Description (AC009322) Heat-shock protein [Arabidopsis thaliana]
                   415173
Seq. No.
                   uC-osflcyp171f07b1
Seq. ID
                   BLASTX
Method
                   g548493
NCBI GI
                   374
BLAST score
                   9.0e-36
E value
Match length
                   122
                   54
% identity
NCBI Description EXOPOLYGALACTURONASE PRECURSOR (EXOPG) (PECTINASE)
                    (GALACTURAN 1,4-ALPHA-GALACTURONIDASE)
```

```
>gi_629854_pir__S30067 polygalacturonase - maize
>gi_288612_emb_CAA47052_ (X66422) polygalacturonase [Zea mays]
```

Seq. No. 415174

Seq. ID uC-osflcyp171f08a1

Method BLASTX
NCBI GI g2058273
BLAST score 697
E value 1.0e-73
Match length 138
% identity 100

NCBI Description (D83527) YK426 [Oryza sativa]

Seq. No. 415175

Seq. ID uC-osflcyp171f08b1

Method BLASTX
NCBI GI g2058273
BLAST score 310
E value 2.0e-28
Match length 64
% identity 97

NCBI Description (D83527) YK426 [Oryza sativa]

Seq. No. 415176

Seq. ID uC-osflcyp171f09a1

Method BLASTX
NCBI GI g4191782
BLAST score 315
E value 8.0e-29
Match length 93
% identity 61

NCBI Description (AC005917) WD-40 repeat protein [Arabidopsis thaliana]

Seq. No. 415177

Seq. ID uC-osflcyp171f10a1

Method BLASTN
NCBI GI g2832716
BLAST score 53
E value 8.0e-21
Match length 93
% identity 89

NCBI Description Lolium temulentum mRNA for alkaline/neutral invertase

Seq. No. 415178

Seq. ID uC-osflcyp171f10b1

Method BLASTX
NCBI GI g2832717
BLAST score 929
E value 1.0e-101
Match length 174
% identity 97

NCBI Description (AJ003114) alkaline/neutral invertase [Lolium temulentum]

Seq. No. 415179

Seq. ID uC-osflcyp171f12b1

Method BLASTX

```
q2073375
NCBI GI
                  511
BLAST score
                  2.0e-88
E value
Match length
                  164
                  99
% identity
                  (D85317) farnesyl pyrophosphate synthase [Oryza sativa]
NCBI Description
                  >gi 4063829 dbj BAA36276_ (AB021747) farnesyl diphosphate
                  synthase [Oryza sativa]
                  415180
Seq. No.
                  uC-osflcyp171g02b1
Seq. ID
Method
                  BLASTX
                  q1246823
NCBI GI
                  507
BLAST score
                  2.0e-51
E value
                  151
Match length
                   63
% identity
NCBI Description (X89865) unknown [Phoenix dactylifera]
                  415181
Seq. No.
                  uC-osflcyp171g03a1
Seq. ID
                  BLASTX
Method
NCBI GI
                  g3935181
                   292
BLAST score
E value
                   3.0e-26
                  79
Match length
% identity
                   66
NCBI Description (AC004557) F17L21.24 [Arabidopsis thaliana]
                   415182
Seq. No.
                   uC-osflcyp171g04a1
Seq. ID
                   BLASTX
Method
                   g2104949
NCBI GI
                   225
BLAST score
E value
                   2.0e-18
Match length
                   48
% identity
NCBI Description (U96716) MAP kinase-like protein [Selaginella lepidophylla]
                   415183
Seq. No.
Seq. ID
                   uC-osflcyp171g05b1
Method
                   BLASTN
                   q6006355
NCBI GI
                   177
BLAST score
                   1.0e-94
E value
Match length
                   205
                   97
% identity
NCBI Description Oryza sativa genomic DNA, chromosome 6, clone:P0493C11
Seq. No.
                   415184
                   uC-osflcyp171g08a1
Seq. ID
Method
                   BLASTX
                   g3790593
NCBI GI
                   147
BLAST score
                   4.0e-09
E value
Match length
                   66
```

42

% identity

```
(AF079185) RING-H2 finger protein RHY1a [Arabidopsis
NCBI Description
                  thaliana]
                  415185
Seq. No.
                  uC-osflcyp171g10b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3402684
BLAST score
                  399
E value
                  1.0e-38
Match length
                  142
% identity
                  58
NCBI Description (AC004697) hypothetical protein [Arabidopsis thaliana]
                  415186
Seq. No.
                  uC-osflcyp171g11a1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2498077
                  251
BLAST score
E value
                  1.0e-21
                  50
Match length
                  86
% identity
                  NUCLEOSIDE DIPHOSPHATE KINASE I (NDK I) (NDP KINASE I)
NCBI Description
                  (PP18) >gi_1777930 (U55019) nucleoside diphosphate kinase
                  [Saccharum officinarum]
                  415187
Seq. No.
                  uC-osflcyp171g11b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2498077
BLAST score
                  694
                  3.0e-73
E value
                  147
Match length
                  84
% identity
NCBI Description NUCLEOSIDE DIPHOSPHATE KINASE I (NDK I) (NDP KINASE I)
                  (PP18) >gi 1777930 (U55019) nucleoside diphosphate kinase
                  [Saccharum officinarum]
                  415188
Seq. No.
Seq. ID
                  uC-osflcyp171g12b1
Method
                  BLASTX
                  g3023816
NCBI GI
                  662
BLAST score
                  2.0e-69
E value
Match length
                  145
% identity
                  89
NCBI Description GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC
                  >gi 968996 (U31676) glyceraldehyde-3-phosphate
                  dehydrogenase [Oryza sativa]
                  415189
Seq. No.
Seq. ID
                  uC-osflcyp171h05b1
                  BLASTX
Method
                  g6041819
NCBI GI
BLAST score
                  245
E value
                  1.0e-20
                  142
Match length
                  39
% identity
```

```
NCBI Description (AC009918) unknown protein [Arabidopsis thaliana]
Seq. No.
                  415190
                  uC-osflcyp171h06b1
Seq. ID
                  BLASTX
Method
                  g4490309
NCBI GI
                  307
BLAST score
E value
                  7.0e-28
Match length
                  116
                  51
% identity
                 (AL035678) peroxidase ATP17a-like protein [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  415191
                  uC-osflcyp171h08b1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g6016845
BLAST score
                  41
E value
                  2.0e-13
Match length
                  73
                  89
% identity
NCBI Description Oryza sativa genomic DNA, chromosome 1, clone:P0711E10
                  415192
Seq. No.
                  uC-osflcyp171h10b1
Seq. ID
Method
                  BLASTX
                  g4508069
NCBI GI
                  293
BLAST score
                  3.0e-26
E value
                  96
Match length
                   64
% identity
NCBI Description (AC005882) 12246 [Arabidopsis thaliana]
                  415193
Seq. No.
                  uC-osflcyp171h11a1
Seq. ID
                  BLASTX
Method
NCBI GI
                  q548493
                  322
BLAST score
E value
                   1.0e-29
                  73
Match length
                  77
% identity
NCBI Description EXOPOLYGALACTURONASE PRECURSOR (EXOPG) (PECTINASE)
                  (GALACTURAN 1,4-ALPHA-GALACTURONIDASE)
                   >gi_629854_pir S30067 polygalacturonase - maize
                   >gi 288612 emb CAA47052 (X66422) polygalacturonase [Zea
                   mays]
                   415194
Seq. No.
Seq. ID
                   uC-osflcyp171h12a1
Method
                   BLASTN
                  q4105602
NCBI GI
                  125
BLAST score
                   6.0e-64
E value
Match length
                   197
% identity
                   91
NCBI Description Oryza sativa metallothionein (MTe) gene, complete cds
```

```
415195
Seq. No.
                  uC-osflcyp171h12b1
Seq. ID
                  BLASTN
Method
                  q4097337
NCBI GI
                  362
BLAST score
                  0.0e + 00
E value
                  439
Match length
                  99
% identity
NCBI Description Oryza sativa metallothionein-like protein mRNA, complete
                  cds
                   415196
Seq. No.
                   uC-osflcyp172a02a1
Seq. ID
                   BLASTX
Method
                   q2649345
NCBI GI
                   408
BLAST score
                   7.0e-40
E value
Match length
                   135
                   61
% identity
NCBI Description (AE001019) tryptophan synthase, subunit beta (trpB-1)
                   [Archaeoglobus fulgidus]
                   415197
Seq. No.
                   uC-osflcyp172a05a1
Seq. ID
                   BLASTN
Method
                   g5360229
NCBI GI
BLAST score
                   402
                   0.0e + 00
E value
                   406
Match length
                   100
% identity
NCBI Description Oryza sativa mRNA for Ran, complete cds
                   415198
Seq. No.
                   uC-osflcyp172a05b1
 Seq. ID
                   BLASTX
Method
                   q5360230
NCBI GI
 BLAST score
                   704
                   2.0e-74
 E value
Match length
                   129
 % identity
 NCBI Description (AB015287) Ran [Oryza sativa]
                    415199
 Seq. No.
                   uC-osflcyp172a07b1
 Seq. ID
                    BLASTX
 Method
                    q3851003
 NCBI GI
 BLAST score
                    213
 E value
                    2.0e-17
 Match length
                    72
 % identity
 NCBI Description (AF069910) pyruvate dehydrogenase E1 beta subunit isoform 3
                    [Zea mays]
                    415200
 Seq. No.
                    uC-osflcyp172a08b1
 Seq. ID
                    BLASTX
 Method
                    g2262101
 NCBI GI
```

```
BLAST score
                  250
E value
                  2.0e-21
Match length
                  110
                  55
% identity
                 (AC002343) kinesin heavy chain isolog [Arabidopsis
NCBI Description
                  thaliana]
                  415201
Seq. No.
                  uC-osflcyp172a09a1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g5803242
BLAST score
                  78
E value
                  1.0e-35
Match length
                  262
                  44
% identity
NCBI Description Oryza sativa genomic DNA, chromosome 6, clone:P0535G04
                  415202
Seq. No.
Seq. ID
                  uC-osflcyp172a09b1
                  BLASTX
Method
NCBI GI
                  g4680207
BLAST score
                  148
E value
                  2.0e-09
                  73
Match length
% identity
                  42
                  (AF114171) disease resistance protein RPM1 homolog [Sorghum
NCBI Description
                  bicolor]
Seq. No.
                  415203
Seq. ID
                  uC-osflcyp172a11b1
Method
                  BLASTX
NCBI GI
                  g2623310
BLAST score
                  169
E value
                  5.0e-12
                  100
Match length
                  42
% identity
                  (AC002409) unknown protein [Arabidopsis thaliana]
NCBI Description
                  >gi 3402721 (AC004261) unknown protein [Arabidopsis
                  thaliana]
                  415204
Seq. No.
Seq. ID
                  uC-osflcyp172b04a1
Method
                  BLASTN
NCBI GI
                  g4680335
BLAST score
                  36
E value
                  8.0e-11
Match length
                  44
                  95
% identity
NCBI Description Oryza sativa subsp. indica BAC clone 16F19 php20725 region,
                  complete sequence
                  415205
```

Seq. No. 415205 Seq. ID uC-osf

Seq. ID uC-osflcyp172b05b1

Method BLASTX
NCBI GI g2289961
BLAST score 296
E value 1.0e-26

Match length

66

```
97
Match length
                  63
% identity
NCBI Description (U82434) AtRAB8 [Arabidopsis thaliana]
                  415206
Seq. No.
Seq. ID
                  uC-osflcyp172b06b1
Method
                  BLASTX
NCBI GI
                  g4581181
BLAST score
                  381
E value
                  2.0e-36
Match length
                  180
                  43
% identity
NCBI Description (AC006220) unknown protein [Arabidopsis thaliana]
Seq. No.
                  415207
                  uC-osflcyp172b07a1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1170937
BLAST score
                  207
E value
                  2.0e-16
Match length
                  36
                  100
% identity
                  S-ADENOSYLMETHIONINE SYNTHETASE 1 (METHIONINE
NCBI Description
                  ADENOSYLTRANSFERASE 1) (ADOMET SYNTHETASE 1)
                  >gi_450549_emb_CAA81481_ (Z26867) S-adenosyl methionine
                  synthetase [Oryza sativa]
                   415208
Seq. No.
                  uC-osflcyp172b07b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1170937
BLAST score
                  720
                  2.0e-76
E value
Match length
                  137
% identity
                  99
                  S-ADENOSYLMETHIONINE SYNTHETASE 1 (METHIONINE
NCBI Description
                  ADENOSYLTRANSFERASE 1) (ADOMET SYNTHETASE 1)
                  >qi 450549 emb CAA81481 (Z26867) S-adenosyl methionine
                   synthetase [Oryza sativa]
                   415209
Seq. No.
Seq. ID
                   uC-osflcyp172b09b1
                  BLASTX
Method
NCBI GI
                   g4432864
BLAST score
                  539
E value
                   4.0e-55
                  161
Match length
                   60
% identity
NCBI Description (AC006300) hypothetical protein [Arabidopsis thaliana]
                   415210
Seq. No.
Seq. ID
                   uC-osflcyp172b11a1
Method
                   BLASTX
NCBI GI
                   g623586
BLAST score
                   206
E value
                   3.0e-16
```

```
% identity
NCBI Description (L29273) putative [Nicotiana tabacum]
                  415211
Seq. No.
Seq. ID
                  uC-osflcyp172b11b1
Method
                  BLASTX
NCBI GI
                  g4567198
BLAST score
                  281
                  8.0e-25
E value
Match length
                  57
                  95
% identity
                  (AC007168) putative GTP-binding protein [Arabidopsis
NCBI Description
                  thaliana]
                  415212
Seq. No.
                  uC-osflcyp172b12b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3929545
BLAST score
                  865
                  3.0e-93
E value
Match length
                  169
% identity
                  98
NCBI Description (AF067194) S-adenosylmethionine decarboxylase [Oryza
                  sativa]
Seq. No.
                  415213
                  uC-osflcyp172c02b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g5579092
BLAST score
                  404
                  3.0e-39
E value
Match length
                  157
                   51
% identity
NCBI Description (AF100954) gibberellin 2-oxidase-like protein [Pisum
                  sativum]
                   415214
Seq. No.
Seq. ID
                  uC-osflcyp172c03b1
                  BLASTN
Method
                  g4097337
NCBI GI
BLAST score
                  423
                  0.0e+00
E value
                   430
Match length
                   100
% identity
NCBI Description Oryza sativa metallothionein-like protein mRNA, complete
                   cds
                   415215
Seq. No.
Seq. ID
                  uC-osflcyp172c04a1
Method
                  BLASTN
NCBI GI
                  g20181
BLAST score
                  160
                   1.0e-84
E value
Match length
                  188
% identity
                   96
NCBI Description Rice cab2R gene for light harvesting chlorophyll
                   a/b-binding protein
```

```
415216
Seq. No.
                   uC-osflcyp172c04b1
Seq. ID
                   BLASTX
Method
NCBI GI
                   g115787
                   714
BLAST score
                   1.0e-75
E value
Match length
                   158
% identity
                   89
                   CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I
NCBI Description
                   CAB-2) (LHCP) >gi_82461_pir__S03706 chlorophyll a/b-binding protein 2R precursor - rice >gi_20182_emb_CAA32109_
                   (X13909) chlorophyll a/b-binding preprotein (AA -28 to 235)
                   [Oryza sativa]
                   415217
Seq. No.
                   uC-osflcyp172c05b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g1076486
BLAST score
                   211
                   1.0e-16
E value
Match length
                   50
% identity
                   74
                   cim1 protein - soybean >gi_555616 (U03860) cytokinin
NCBI Description
                   induced message [Glycine max]
                    415218
Seq. No.
                   uC-osflcyp172c06a1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g4539408
BLAST score
                   187
                    5.0e-14
E value
                    49
Match length
                    78
% identity
NCBI Description (AL049524) putative alpha NAC [Arabidopsis thaliana]
                    415219
Seq. No.
Seq. ID
                    uC-osflcyp172c06b1
                   {\tt BLASTX}
Method
NCBI GI
                    g4539408
BLAST score
                    416
E value
                    6.0e-41
Match length
                    119
                    72
% identity
NCBI Description (AL049524) putative alpha NAC [Arabidopsis thaliana]
                    415220
Seq. No.
Seq. ID
                    uC-osflcyp172c07a1
Method
                    BLASTX
NCBI GI
                    g2191197
                    250
BLAST score
E value
                    2.0e-21
                    77
Match length
% identity
                    73
                   (AF007271) contains similarity to Synechococcus PCC7942
NCBI Description
                    chromosomal region used as basis of neutral siteII
                    recombinational cloning vector (PID:g1174192) [Arabidopsis
```

Seq. ID

thaliana]

```
415221
Seq. No.
Seq. ID
                  uC-osflcyp172c07b1
                  BLASTX
Method
NCBI GI
                  g2191197
BLAST score
                  325
E value
                  2.0e-30
Match length
                  89
% identity
                  80
                  (AF007271) contains similarity to Synechococcus PCC7942
NCBI Description
                  chromosomal region used as basis of neutral siteII
                  recombinational cloning vector (PID:g1174192) [Arabidopsis
                  thalianal
                  415222
Seq. No.
                  uC-osflcyp172c08b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4539460
BLAST score
                  199
E value
                  3.0e-15
Match length
                  153
% identity
NCBI Description (AL049500) putative protein [Arabidopsis thaliana]
Seq. No.
                  415223
                  uC-osflcyp172c09b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3386605
BLAST score
                  324
                  5.0e-30
E value
Match length
                  113
                  58
% identity
NCBI Description (AC004665) hypothetical protein [Arabidopsis thaliana]
                  415224
Seq. No.
Seq. ID
                  uC-osflcyp172c10b1
Method
                  BLASTX
NCBI GI
                  g2104535
BLAST score
                  665
                  7.0e-70
E value
                  175
Match length
                  70
% identity
NCBI Description (AF001308) T10M13.13 [Arabidopsis thaliana]
                  415225
Seq. No.
Seq. ID
                  uC-osflcyp172c12b1
                  BLASTX
Method
NCBI GI
                  q4731111
BLAST score
                  309
E value
                  3.0e-28
                  79
Match length
% identity
NCBI Description (AF064707) exhydrolase II [Zea mays]
Seq. No.
                   415226
```

uC-osflcyp172d01b1

Method

BLASTX

```
BLASTX
 Method
 NCBI GI
                   g1346109
 BLAST score
                   440
 E value
                   1.0e-43
 Match length
                   111
                   81
 % identity
 NCBI Description
                   GUANINE NUCLEOTIDE-BINDING PROTEIN BETA SUBUNIT-LIKE
                   PROTEIN (GPB-LR) (RWD) >gi 540535_dbj_BAA07404_ (D38231)
                   RWD [Oryza sativa]
                    415227
 Seq. No.
 Seq. ID
                   uC-osflcyp172d02b1
                   BLASTX
 Method
 NCBI GI
                   g3426039
 BLAST score
                   665
                   7.0e-70
 E value
                   164
 Match length
                   74
 % identity
 NCBI Description (AC005168) unknown protein [Arabidopsis thaliana]
 Seq. No.
                    415228
 Seq. ID
                   uC-osflcyp172d04b1
 Method
                   BLASTX
. NCBI GI
                   q3063460
 BLAST score
                   450
 E value
                   1.0e-44
                   158
 Match length
                   56
 % identity
 NCBI Description (AC003981) F22013.22 [Arabidopsis thaliana]
                    415229
 Seq. No.
 Seq. ID
                   uC-osflcyp172d05b1
 Method
                   BLASTX
 NCBI GI
                   g5823020
 BLAST score
                   251
                    4.0e-23
 E value
                   117
 Match length
                   54
 % identity
 NCBI Description (AF089849) senescence-specific cysteine protease [Brassica
                   napus]
                    415230
 Seq. No.
 Seq. ID
                   uC-osflcyp172d06a1
 Method
                   BLASTX
 NCBI GI
                   g2501190
 BLAST score
                   275
 E value
                    3.0e-24
                   75
 Match length
 % identity
                   77
 NCBI Description THIAMINE BIOSYNTHETIC ENZYME 1-2 PRECURSOR
                   >gi 2130147 pir S61420 thiamine biosynthetic enzyme thi1-2
                    - maize >gi_596080 (U17351) thiamine biosynthetic enzyme
                    [Zea mays]
 Seq. No.
                    415231
 Sea. ID
                   uC-osflcyp172d06b1
```

g2501189 NCBI GI 430 BLAST score 2.0e-42 E value Match length 122 72 % identity THIAMINE BIOSYNTHETIC ENZYME 1-1 PRECURSOR NCBI Description >gi_2130146_pir__S61419 thiamine biosynthetic enzyme thi1-1 - maize >gi_596078 (U17350) thiamine biosynthetic enzyme [Zea mays] Seq. No. 415232 uC-osflcyp172d07a1 Seq. ID BLASTX Method q3668097 NCBI GI BLAST score 171 4.0e-12 E value 41 Match length 73 % identity (AC004667) putative glycine cleavage system protein H NCBI Description precursor [Arabidopsis thaliana] 415233 Seq. No. uC-osflcyp172d07b1 Seq. ID Method BLASTX q3668097 NCBI GI BLAST score 534 2.0e-54 E value Match length 139 75 % identity NCBI Description (AC004667) putative glycine cleavage system protein H precursor [Arabidopsis thaliana] Seq. No. 415234 Seq. ID uC-osflcyp172d08a1 Method BLASTX NCBI GI q4584110 354 BLAST score E value 1.0e-33 127 Match length 50 % identity NCBI Description (AJ133639) SAH7 protein [Arabidopsis thaliana] 415235 Seq. No. Seq. ID uC-osflcyp172d08b1 BLASTX Method NCBI GI g3860323 349 BLAST score E value 8.0e-33 77 Match length 83 % identity NCBI Description (AJ012688) hypothetical protein [Cicer arietinum]

415236 Seq. No.

Seq. ID uC-osflcyp172d09a1

BLASTN Method NCBI GI g4884509

BLAST score 55

```
6.0e-22
E value
Match length
                  75
                  93
% identity
                  Oryza sativa mRNA for class III chitinase homologue
NCBI Description
                  (OsChib3H-a), complete cds, clone:C60571
                  415237
Seq. No.
Seq. ID
                  uC-osflcyp172d11b1
Method
                  BLASTX
NCBI GI
                  g4510347
BLAST score
                  181
                  4.0e-13
E value
                  65
Match length
                   60
% identity
                  (AC006921) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                  415238
Seq. No.
                  uC-osflcyp172d12b1
Seq. ID
                  BLASTX
Method
NCBI GI
                  q1009234
BLAST score
                  432
                   1.0e-42
E value
Match length
                  153
% identity
NCBI Description (L38829) SUP2 gene product [Nicotiana tabacum]
                   415239
Seq. No.
                  uC-osflcyp172e02a1
Seq. ID
Method
                  BLASTX
NCBI GI
                   g4337196
BLAST score
                  189
E value
                   3.0e-14
Match length
                   81
                   38
% identity
NCBI Description (AC006403) putative serine/threonine receptor kinase
                   [Arabidopsis thaliana]
                   415240
Seq. No.
                   uC-osflcyp172e04b1
Seq. ID
Method
                   BLASTX
                   g4835789
NCBI GI
BLAST score
                   582
E value
                   4.0e-60
Match length
                   176
% identity
                   63
                   (AC007296) Strong similarity to gi 3367522 F8K4.9 from
NCBI Description
                   Arabidopsis thaliana BAC gb AC004392. EST gb_W43487 comes
                   from this gene
                   415241
Seq. No.
                   uC-osflcyp172e08b1
Seq. ID
Method
                   BLASTX
                   g4102727
NCBI GI
                   274
BLAST score
E value
                   5.0e-24
Match length
                   71
                   72
% identity
```

```
(AF015782) blight-associated protein pl2 precursor [Citrus
NCBI Description
                  jambhiri]
                  415242
Seq. No.
                  uC-osflcyp172e10a1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g313141
BLAST score
                  37
                  3.0e-11
E value
Match length
                  49
% identity
                  94
NCBI Description Z.mays ZmPRO3 mRNA for profilin
                  415243
Seq. No.
                  uC-osflcyp172e10b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3914422
BLAST score
                  599
E value
                  3.0e-62
Match length
                  118
                  92
% identity
                  PROFILIN >gi_2154728_emb_CAA69669 (Y08389) profilin 2
NCBI Description
                   [Cynodon dactylon] >gi_2154730_emb_CAA69670_ (Y08390)
                  profilin 1 [Cynodon dactylon]
                   415244
Seq. No.
                  uC-osflcyp172e11b1
Seq. ID
Method
                  BLASTX
NCBI GI
                   g2623310
BLAST score
                   237
                   9.0e-20
E value
                   157
Match length
                   43
% identity
                   (AC002409) unknown protein [Arabidopsis thaliana]
NCBI Description
                   >qi 3402721 (AC004261) unknown protein [Arabidopsis
                   thaliana]
                   415245
Seq. No.
                   uC-osflcyp172f02a1
Seq. ID
                   BLASTX
Method
NCBI GI
                   q4105563
                   215
BLAST score
                   3.0e-17
E value
                   51
Match length
                   82
% identity
NCBI Description (AF047490) zeta-carotene desaturase precursor [Zea mays]
                   415246
Seq. No.
Seq. ID
                   uC-osflcyp172f02b1
                   BLASTX
Method
                   g4105563
NCBI GI
BLAST score
                   610
E value
                   2.0e-63
                   160
Match length
                   79
% identity
NCBI Description (AF047490) zeta-carotene desaturase precursor [Zea mays]
```

```
Seq. ID
                  uC-osflcyp172f03a1
                  BLASTX
Method
NCBI GI
                  g3023271
BLAST score
                  262
                  6.0e-23
E value
Match length
                  54
                  93
% identity
NCBI Description GLUTATHIONE-DEPENDENT FORMALDEHYDE DEHYDROGENASE (FDH)
                  (FALDH) (GSH-FDH) >gi 1675394 (U77637) class III ADH enzyme
                  [Oryza sativa]
                  415248
Seq. No.
                  uC-osflcyp172f03b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3023271
BLAST score
                  761
E value
                  4.0e-81
                  160
Match length
                  93
% identity
NCBI Description GLUTATHIONE-DEPENDENT FORMALDEHYDE DEHYDROGENASE (FDH)
                   (FALDH) (GSH-FDH) >gi 1675394 (U77637) class III ADH enzyme
                  [Oryza sativa]
                  415249
Seq. No.
Seq. ID
                  uC-osflcyp172f05b1
                  BLASTX
Method
NCBI GI
                  g4139172
BLAST score
                  304
E value
                  9.0e-48
Match length
                  123
                  81
% identity
NCBI Description (AF092952) beta 1 tubulin [Cyanophora paradoxa]
                  415250
Seq. No.
Seq. ID
                  uC-osflcyp172f06a1
                  BLASTN
Method
NCBI GI
                  g5852170
BLAST score
                  397
E value
                  0.0e + 00
                  397
Match length
% identity
                  100
NCBI Description Oryza sativa indica(GLA4) genomic DNA, chromosome 4, BAC
                  clone:t17804
                  415251
Seq. No.
Seq. ID
                  uC-osflcyp172f06b1
Method
                  BLASTN
NCBI GI
                  g5852170
BLAST score
                  397
                  0.0e + 00
E value
Match length
                  438
% identity
                  97
NCBI Description Oryza sativa indica(GLA4) genomic DNA, chromosome 4, BAC
                  clone:t17804
Seq. No.
                  415252
```

Seq. No.

```
Seq. ID
                  uC-osflcyp172f10b1
                  BLASTX
Method
NCBI GI
                  g2130069
BLAST score
                  911
                  1.0e-98
E value
Match length
                  169
% identity
                  99
                  catalase (EC 1.11.1.6) catA - rice
NCBI Description
                  >gi 1261858 dbj BAA06232 (D29966) catalase [Oryza sativa]
Seq. No.
                  415253
Seq. ID
                  uC-osflcyp172f11b1
Method
                  BLASTX
NCBI GI
                  g398849
BLAST score
                  754
E value
                  3.0e-80
Match length
                  139
                  99
% identity
NCBI Description (X74656) beta-5 tubulin [Zea mays]
Seq. No.
                  415254
Seq. ID
                  uC-osflcyp172f12b1
Method
                  BLASTX
NCBI GI
                  q82080
BLAST score
                  398
E value
                  9.0e-39
                  117
Match length
                  67
% identity
NCBI Description
                  chlorophyll a/b-binding protein type III precursor - tomato
                  >gi 226872 prf 1609235A chlorophyll a/b binding protein
                  [Lycopersicon esculentum]
                  415255
Seq. No.
Seq. ID
                  uC-osflcyp172g01a1
Method
                  BLASTX
NCBI GI
                  g2511590
BLAST score
                  167
E value
                  6.0e-12
Match length
                  55
                  76
% identity
NCBI Description
                 (Y13692) multicatalytic endopeptidase complex, proteasome
                  component, beta subunit [Arabidopsis thaliana] >gi_3421111
                   (AF043534) 20S proteasome beta subunit PBD1 [Arabidopsis
                  thaliana]
                  415256
Seq. No.
Seq. ID
                  uC-osflcyp172g01b1
                  BLASTX
Method
NCBI GI
                  g2244837
BLAST score
                  340
E value
                  5.0e-32
Match length
                  84
% identity
                  76
NCBI Description
                  (Z97337) proteasome chain protein [Arabidopsis thaliana]
                  >gi_2511572_emb_CAA73618.1_ (Y13175) multicatalytic
                  endopeptidase [Arabidopsis thaliana] >gi 3421114 (AF043535)
```

20S proteasome beta subunit PBD2 [Arabidopsis thaliana]

415257 Seq. No. Seq. ID uC-osflcyp172g03b1 Method BLASTX NCBI GI q4587556 BLAST score 362 7.0e-42E value 147 Match length 61 % identity (AC006577) Similar to gi_1653162 (p)ppGpp NCBI Description 3-pyrophosphohydrolase from Synechocystis sp genome gb D90911. EST gb W43807 comes from this gene. [Arabidopsis thaliana] Seq. No. 415258 uC-osflcyp172g04a1 Seq. ID Method BLASTX NCBI GI q5817000 BLAST score 152 E value 7.0e-10 40 Match length 68 % identity NCBI Description (AL110123) putative protein [Arabidopsis thaliana] Seq. No. 415259 uC-osflcyp172g07b1 Seq. ID Method BLASTX NCBI GI q4559339 521 BLAST score 5.0e-53E value Match length 153 % identity (AC007087) putative ATP-dependent RNA helicase [Arabidopsis NCBI Description thaliana] Seq. No. 415260 Seq. ID uC-osflcyp172g09b1 Method BLASTX NCBI GI g2275202 BLAST score 382 E value 8.0e-37 Match length 136 % identity 55 (AC002337) acyl-CoA synthetase isolog [Arabidopsis NCBI Description thaliana] Seq. No. 415261 Seq. ID uC-osflcyp172g10a1 Method BLASTX NCBI GI g2384671 BLAST score 220 7.0e-18 E value Match length 69

[Arabidopsis thaliana]

62

% identity

NCBI Description

(AF012657) putative potassium transporter AtKT2p

BLAST score

```
415262
Seq. No.
Seq. ID
                  uC-osflcyp172g11b1
Method
                  BLASTX
NCBI GI
                  g5524756
BLAST score
                  686
                  2.0e-77
E value
                  154
Match length
% identity
                  57
NCBI Description (AJ243528) putative glyoxalase I [Triticum aestivum]
Seq. No.
                  415263
                  uC-osflcyp172h02b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2245015
BLAST score
                  540
E value
                  3.0e-55
Match length
                  143
% identity
                  69
NCBI Description (Z97341) glucosyltransferase like protein [Arabidopsis
                  thaliana]
Seq. No.
                  415264
Seq. ID
                  uC-osflcyp172h04a1
Method
                  BLASTX
NCBI GI
                  q4580389
BLAST score
                  406
E value
                  9.0e-40
Match length
                  118
% identity
                  65
NCBI Description (AC007171) unknown protein [Arabidopsis thaliana]
Seq. No.
                  415265
Seq. ID
                  uC-osflcyp172h04b1
Method
                  BLASTX
NCBI GI
                  q4580389
BLAST score
                  359
E value
                  4.0e-34
Match length
                  101
% identity
                  67
NCBI Description (AC007171) unknown protein [Arabidopsis thaliana]
Seq. No.
                  415266
Seq. ID
                  uC-osflcyp172h07b1
Method
                  BLASTX
NCBI GI
                  g4803836
BLAST score
                  158
E value
                  4.0e-21
                  116
Match length
% identity
NCBI Description (AB026987) a dynamin-like protein ADL3 [Arabidopsis
                  thaliana]
                  415267
Seq. No.
Seq. ID
                  uC-osflcyp172h08b1
Method
                  BLASTX
NCBI GI
                  g1173027
```

```
3.0e-41
E value
Match length
                  102
                  86
% identity
                  60S RIBOSOMAL PROTEIN L31 >gi_915313 (U23784) ribosomal
NCBI Description
                  protein L31 [Nicotiana glutinosa]
                  415268
Seq. No.
                  uC-osflcyp172h09a1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3559805
BLAST score
                  163
                  4.0e-11
E value
                  33
Match length
                  79
% identity
                  (AJ006787) putative phytochelatin synthetase [Arabidopsis
NCBI Description
                  thaliana]
                  415269
Seq. No.
                  uC-osflcyp172h09b1
Seq. ID
Method
                  BLASTX
                  q6041808
NCBI GI
                  213
BLAST score
E value
                   6.0e-27
Match length
                  78
                   73
% identity
NCBI Description (AC009755) unknown protein [Arabidopsis thaliana]
                   415270
Seq. No.
                  uC-osflcyp172h10a1
Seq. ID
                  BLASTX
Method
NCBI GI
                   g4895232
BLAST score
                   245
                   8.0e-21
E value
Match length
                  60
% identity
                   72
NCBI Description (AC007660) hypothetical protein [Arabidopsis thaliana]
                   415271
Seq. No.
                   uC-osflcyp172h10b1
Seq. ID
                   BLASTX
Method
NCBI GI
                   g4895232
                   255
BLAST score
                   8.0e-22
E value
                  134
Match length
                   49
% identity
NCBI Description (AC007660) hypothetical protein [Arabidopsis thaliana]
                   415272
Seq. No.
                   uC-osflcyp172h12b1
Seq. ID
                   BLASTX
Method
                   g2792216
NCBI GI
                   347
BLAST score
                   1.0e-32
E value
                   135
Match length
                   51
% identity
```

NCBI Description (AF032686) NBS-LRR type resistance protein [Hordeum

vulgare]

BLAST score

505

```
415273
Seq. No.
                  uC-osflcyp173a01a1
Seq. ID
Method
                  BLASTX
                  g1871182
NCBI GI
                  154
BLAST score
                  6.0e-10
E value
                  39
Match length
% identity
                  (U90439) phospholipase D isolog [Arabidopsis thaliana]
NCBI Description
                  415274
Seq. No.
                  uC-osflcyp173a01b1
Seq. ID
                  BLASTX
Method
                  q1871182
NCBI GI
BLAST score
                  622
E value
                  7.0e-65
                  156
Match length
                   71
% identity
                  (U90439) phospholipase D isolog [Arabidopsis thaliana]
NCBI Description
                  415275
Seq. No.
                  uC-osflcyp173a02a1
Seq. ID
Method
                  BLASTX
                  q5031981
NCBI GI
BLAST score
                   188
                   2.0e-15
E value
                   96
Match length
                   46
% identity
                  26S proteasome-associated pad1 homolog >gi 1923256 (U86782)
NCBI Description
                   26S proteasome-associated pad1 homolog [Homo sapiens]
                   415276
Seq. No.
Seq. ID
                   uC-osflcyp173a02b1
Method
                  BLASTX
NCBI GI
                   g2505940
                   662
BLAST score
                   2.0e-69
E value
                  156
Match length
                   83
% identity
NCBI Description (Y13071) 26S proteasome, non-ATPase subunit [Mus musculus]
                   415277
Seq. No.
                   uC-osflcyp173a03a1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2829889
                   269
BLAST score
                   2.0e-23
E value
                   76
Match length
% identity
NCBI Description (AC002396) Hypothetical protein [Arabidopsis thaliana]
                   415278
Seq. No.
                   uC-osflcyp173a03b1
Seq. ID
                   BLASTX
Method
                   g2829889
NCBI GI
```

```
4.0e-51
E value
Match length
                  146
                  70
% identity
                 (AC002396) Hypothetical protein [Arabidopsis thaliana]
NCBI Description
                  415279
Seq. No.
Seq. ID
                  uC-osflcyp173a04a1
Method
                  BLASTX
NCBI GI
                  q5734636
BLAST score
                  239
E value
                  3.0e-20
                  79
Match length
                  52
% identity
                 (AP000391) Similar to putative lipase (AC006232) [Oryza
NCBI Description
                  sativa]
                  415280
Seq. No.
Seq. ID
                  uC-osflcyp173a04b1
Method
                  BLASTX
NCBI GI
                  g5734634
BLAST score
                  303
E value
                  1.0e-27
Match length
                  95
                  58
% identity
NCBI Description (AP000391) Similar to putative lipase (AC006232) [Oryza
                  sativa]
                  415281
Seq. No.
                  uC-osflcyp173a08b1
Seq. ID
                  {\tt BLASTX}
Method
                  g68843
NCBI GI
BLAST score
                  326
                  3.0e-30
E value
Match length
                  86
                  77
% identity
NCBI Description phospholipid transfer protein homolog - rice
                  >gi 4139635 pdb 1RZL Rice Nonspecific Lipid Transfer
                  Protein >gi 5107522 pdb 1BV2 Lipid Transfer Protein From
                  Rice Seeds, Nmr, 14 Structures
                  415282
Seq. No.
Seq. ID
                  uC-osflcyp173a09a1
Method
                  BLASTX
NCBI GI
                  q2829889
                  159
BLAST score
                  1.0e-10
E value
                  49
Match length
% identity
NCBI Description (AC002396) Hypothetical protein [Arabidopsis thaliana]
                   415283
Seq. No.
Seq. ID
                  uC-osflcyp173a09b1
Method
                  BLASTX
NCBI GI
                  q4884932
BLAST score
                  273
E value
                   6.0e-24
```

Match length

```
% identity
NCBI Description
                  (AF141659) AtHVA22a [Arabidopsis thaliana]
                  >gi 4884944 gb AAD31885.1 AF141977 1 (AF141977) AtHVA22a
                  [Arabidopsis thaliana]
                  415284
Seq. No.
Seq. ID
                  uC-osflcyp173b01a1
Method
                  BLASTX
NCBI GI
                  q2369766
BLAST score
                  148
E value
                  3.0e-09
Match length
                  32
% identity
NCBI Description (AJ001304) hypothetical protein [Citrus x paradisi]
Seq. No.
                  415285
Seq. ID
                  uC-osflcyp173b01b1
Method
                  BLASTN
NCBI GI
                  q4680189
BLAST score
                  41
                  2.0e-13
E value
Match length
                  76
                  89
% identity
NCBI Description Oryza sativa subsp. indica putative dnaJ-like protein,
                  putative myb-related protein, putative farnesyl
                  pyrophosphate synthase, and hypothetical protein genes,
                  complete cds
Seq. No.
                  415286
Seq. ID
                  uC-osflcyp173b04b1
Method
                  BLASTX
NCBI GI
                  g4415926
BLAST score
                  554
                  7.0e-57
E value
                  172
Match length
                  66
% identity
NCBI Description (AC006282) unknown protein [Arabidopsis thaliana]
Seq. No.
                  415287
Seq. ID
                  uC-osflcyp173b05a1
Method
                  BLASTX
NCBI GI
                  g693920
BLAST score
                  415
E value
                  1.0e-40
Match length
                  80
                  97
% identity
                 (U21113) chlorophyll a/b binding protein [Solanum
NCBI Description
                  tuberosuml
                  415288
Seq. No.
Seq. ID
                  uC-osflcyp173b05b1
Method
                  BLASTX
NCBI GI
                  g3036951
BLAST score
                  830
E value
                  3.0e-89
Match length
                  158
% identity
                  99
```

(AB012639) light harvesting chlorophyll a/b-binding protein NCBI Description [Nicotiana sylvestris] 415289 Seq. No. Seq. ID uC-osflcyp173b07b1 Method BLASTX g3643602 NCBI GI 294 BLAST score E value 2.0e-26 Match length 99 58 % identity (AC005395) putative tonoplast intrinsic protein NCBI Description [Arabidopsis thaliana] 415290 Seq. No. uC-osflcyp173b09a1 Seq. ID Method BLASTN NCBI GI g4138731 36 BLAST score E value 1.0e-10 Match length 92 85 % identity NCBI Description Zea mays mRNA for proline-rich protein Seq. No. 415291 uC-osflcyp173b09b1 Seq. ID Method BLASTN g4138731 NCBI GI BLAST score 54 3.0e-21 E value Match length 375 21 % identity NCBI Description Zea mays mRNA for proline-rich protein 415292 Seq. No. Seq. ID uC-osflcyp173b11b1 Method BLASTX NCBI GI g2501189 BLAST score 333 E value 4.0e-31 Match length 105 % identity 69 THIAMINE BIOSYNTHETIC ENZYME 1-1 PRECURSOR NCBI Description >gi 2130146 pir S61419 thiamine biosynthetic enzyme thi1-1 - maize >gi_596078 (U17350) thiamine biosynthetic enzyme [Zea mays] Seq. No. 415293 Seq. ID uC-osflcyp173c01b1 Method BLASTX NCBI GI g4559353 BLAST score 678 2.0e-71E value Match length 153 82 % identity (AC006585) putative extragenic suppressor protein NCBI Description

54207

[Arabidopsis thaliana]

```
Seq. No.
                  415294
Seq. ID
                  uC-osflcyp173c02a1
Method
                  BLASTN
NCBI GI
                  g5679837
BLAST score
                  144
                  4.0e-75
E value
Match length
                  385
% identity
                  84
NCBI Description Oryza sativa chromosome 4 BAC 11332 genomic sequences
                  415295
Seq. No.
Seq. ID
                  uC-osflcyp173c02b1
Method
                  BLASTX
NCBI GI
                  q5679840
BLAST score
                  905
                  5.0e-98
E value
Match length
                  171
                  97
% identity
NCBI Description (AJ243961) 11332.4 [Oryza sativa]
                  415296
Seq. No.
Seq. ID
                  uC-osflcyp173c03b1
Method
                  BLASTX
NCBI GI
                  q3367523
BLAST score
                  263
                  1.0e-22
E value
Match length
                  88
                  57
% identity
NCBI Description (AC004392) ESTs gb_AA728658 and gb_N95943 come from this
                  gene. [Arabidopsis thaliana]
                  415297
Seq. No.
                  uC-osflcyp173c05b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g575605
                  275
BLAST score
                  3.0e-24
E value
                  160
Match length
% identity
                   41
NCBI Description (D42065) cationic peroxidase isozyme 40K precursor
                   [Nicotiana tabacum]
                   415298
Seq. No.
Seq. ID
                  uC-osflcyp173c06a1
Method
                  BLASTX
                  g1076724
NCBI GI
                   247
BLAST score
                   7.0e-21
E value
                   67
Match length
% identity
                   69
NCBI Description LHCI-680, photosystem I antenna protein - barley
                   >gi 666054 emb CAA59049 (X84308) LHCI-680, photosystem I
                   antenna protein [Hordeum vulgare]
Seq. No.
                   415299
Seq. ID
                   uC-osflcyp173c06b1
```

```
BLASTX
Method
                  q1076724
NCBI GI
                  619
BLAST score
E value
                  5.0e-69
                  146
Match length
                  83
% identity
                  LHCI-680, photosystem I antenna protein - barley
NCBI Description
                  >gi_666054_emb_CAA59049_ (X84308) LHCI-680, photosystem I
                  antenna protein [Hordeum vulgare]
Seq. No.
                  415300
                  uC-osflcyp173c08b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q5031281
BLAST score
                  283
                   3.0e-25
E value
                  98
Match length
                   57
% identity
                  (AF139499) unknown [Prunus armeniaca]
NCBI Description
                   415301
Seq. No.
                  uC-osflcyp173c09b1
Seq. ID
Method
                  BLASTX
                   q6091726
NCBI GI
BLAST score
                   162
                   7.0e-11
E value
Match length
                  73
                   49
% identity
                  (AC010797) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   415302
Seq. No.
                   uC-osflcyp173c10b1
Seq. ID
Method
                   BLASTX
                   q4510396
NCBI GI
                   362
BLAST score
E value
                   2.0e-34
Match length
                   155
% identity
                  (AC006587) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   415303
Seq. No.
Seq. ID
                   uC-osflcyp173d01b1
Method
                   BLASTX
NCBI GI
                   g4538920
BLAST score
                   390
                   9.0e-38
E value
Match length
                   131
% identity
                  (AL049483) nitrogen fixation like protein [Arabidopsis
NCBI Description
                   thaliana]
                   415304
Seq. No.
                   uC-osflcyp173d04b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2924781
BLAST score
                   603
E value
                   1.0e-62
```

Seq. No.

415310

```
141
Match length
% identity
                  75
                  (AC002334) putative cellulose synthase [Arabidopsis
NCBI Description
                  thaliana]
                  415305
Seq. No.
                  uC-osflcyp173d06a1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2662310
BLAST score
                  232
                  4.0e-19
E value
Match length
                  44
% identity
                  98
NCBI Description (AB009307) bpwl [Hordeum vulgare]
Seq. No.
                  415306
                  uC-osflcyp173d06b1
Seq. ID
Method
                  BLASTX
                  g2662310
NCBI GI
BLAST score
                  489
E value
                  3.0e-49
Match length
                  94
                  99
% identity
NCBI Description (AB009307) bpw1 [Hordeum vulgare]
                  415307
Seq. No.
                  uC-osflcyp173d07b1
Seq. ID
Method
                  BLASTX
                  g3785989
NCBI GI
BLAST score
                  612
E value
                  1.0e-63
Match length
                  146
% identity
NCBI Description (AC005560) unknown protein [Arabidopsis thaliana]
Seq. No.
                  415308
Seq. ID
                  uC-osflcyp173d08b1
Method
                  BLASTX
NCBI GI
                  g2493147
BLAST score
                  401
E value
                  5.0e-39
Match length
                  85
% identity
                  95
NCBI Description VACUOLAR ATP SYNTHASE 16 KD PROTEOLIPID SUBUNIT >gi 857574
                   (U27098) H+-ATPase [Oryza sativa]
Seq. No.
                   415309
Seq. ID
                  uC-osflcyp173d10a1
Method
                  BLASTX
NCBI GI
                  g1737492
                  229
BLAST score
E value
                  8.0e-19
                  60
Match length
% identity
NCBI Description (U81318) poly(A)-binding protein [Triticum aestivum]
```

```
uC-osflcyp173d10b1
Seq. ID
                    BLASTX
Method
NCBI GI
                    q5007080
BLAST score
                    339
                    1.0e-31
E value
                    89
Match length
                    81
% identity
                    (AF153689) poly(A)-binding protein [Oryza sativa]
NCBI Description
Seq. No.
                    415311
                    uC-osflcyp173d11b1
Seq. ID
Method
                    BLASTX
NCBI GI
                    q1652856
BLAST score
                    187
                    8.0e-14
E value
Match length
                    125
                    33
% identity
                    (D90909) hypothetical protein [Synechocystis sp.]
NCBI Description
                    415312
Seq. No.
                    uC-osflcyp173e01b1
Seq. ID
                    BLASTX
Method
                    g4538920
NCBI GI
                    277
BLAST score
E value
                    1.0e-27
                    130
Match length
% identity
                    58
                    (AL049483) nitrogen fixation like protein [Arabidopsis
NCBI Description
                    thaliana]
Seq. No.
                    415313
                    uC-osflcyp173e02a1
Seq. ID
Method
                    BLASTX
NCBI GI
                    g115787
BLAST score
                    265
E value
                    1.0e-46
Match length
                    98
                    96
% identity
                    CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I
NCBI Description
                    CAB-2) (LHCP) >gi_82461_pir__S03706 chlorophyll a/b-binding protein 2R precursor - rice >gi_20182_emb_CAA32109_
                     (X13909) chlorophyll a/b-binding preprotein (AA -28 to 235)
                     [Oryza sativa]
                     415314
Seq. No.
Seq. ID
                    uC-osflcyp173e02b1
Method
                    BLASTX
NCBI GI
                    g320618
BLAST score
                    685
E value
                     3.0e-72
Match length
                    146
% identity
                    89
                    chlorophyll a/b-binding protein I precursor - rice
NCBI Description
                    >gi_218172_dbj_BAA00536_ (D00641) type I light-harvesting
chlorophyll a/b-binding protein [Oryza sativa]
                     >gi 227611_prf__1707316A chlorophyll a/b binding protein 1
```

[Oryza sativa]

```
415315
Seq. No.
                  uC-osflcyp173e03b1
Seq. ID
Method
                  BLASTX
                  q4539545
NCBI GI
                  695
BLAST score
                  2.0e-73
E value
                  147
Match length
% identity
                  89
                  (Y16644) PRCI [Nicotiana tabacum]
NCBI Description
                  415316
Seq. No.
                  uC-osflcyp173e05b1
Seq. ID
                  BLASTX
Method
NCBI GI
                  a542157
BLAST score
                   612
E value
                  1.0e-63
                  138
Match length
                  87
% identity
NCBI Description ribosomal 5S RNA-binding protein - Rice
                  415317
Seq. No.
                  uC-osflcyp173e06a1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3860277
BLAST score
                   458
                   1.0e-45
E value
Match length
                   99
                   89
% identity
                   (ACO05824) putative ribosomal protein L10 [Arabidopsis
NCBI Description
                   thaliana] >gi 4314394_gb_AAD15604_ (AC006232) putative
                   ribosomal protein L10A [Arabidopsis thaliana]
                   415318
Seq. No.
Seq. ID
                   uC-osflcyp173e06b1
Method
                   BLASTX
NCBI GI
                   q3860277
BLAST score
                   550
E value
                   2.0e-56
Match length
                   151
% identity
                   71
                   (AC005824) putative ribosomal protein L10 [Arabidopsis
NCBI Description
                   thaliana] >gi 4314394 gb AAD15604 (AC006232) putative
                   ribosomal protein L10A [Arabidopsis thaliana]
Seq. No.
                   415319
Seq. ID
                   uC-osflcyp173e07b1
Method
                   BLASTX
                   q5869967
NCBI GI
                   734
BLAST score
                   4.0e-81
E value
Match length
                   166
                   91
% identity
NCBI Description (AJ010946) isovaleryl-CoA Dehydrogenase [Pisum sativum]
                   415320
Seq. No.
                   uC-osflcyp173e09a1
Seq. ID
```

```
BLASTX
Method
NCBI GI
                  q4539545
                  209
BLAST score
                  1.0e-16
E value
                  75
Match length
                  63
% identity
                  (Y16644) PRCI [Nicotiana tabacum]
NCBI Description
                  415321
Seq. No.
                  uC-osflcyp173e11b1
Seq. ID
Method
                  BLASTX
                  g6093778
NCBI GI
BLAST score
                  645
                  2.0e-67
E value
                  138
Match length
                  94
% identity
                  PROTEASOME COMPONENT C3 (MACROPAIN SUBUNIT C3)
NCBI Description
                  (MULTICATALYTIC ENDOPEPTIDASE COMPLEX SUBUNIT C3)
                  >gi_2511574_emb_CAA73619.1_ (Y13176) multicatalytic
                  endopeptidase [Arabidopsis thaliana] >gi 3421075 (AF043520)
                  20S proteasome subunit PAB1 [Arabidopsis thaliana]
                  >qi 4966368 qb AAD34699.1 AC006341 27 (AC006341) Identical
                  to gb Y13176 Arabidopsis thaliana mRNA for proteasome
                  subunit prc3. ESTs gb_H36972, gb_T22551 and gb_T13800 come
                  from this gene
                  415322
Seq. No.
Seq. ID
                  uC-osflcyp173e12b1
Method
                  BLASTN
NCBI GI
                  q3850817
                  272
BLAST score
                  1.0e-151
E value
Match length
                  291
% identity
                  99
NCBI Description Oryza sativa mRNA for U2 snRNP auxiliary factor, small
                  subunit 35a
                   415323
Seq. No.
Seq. ID
                  uC-osflcyp173f02b1
Method
                  BLASTX
NCBI GI
                   q5081608
BLAST score
                   261
                   2.0e-22
E value
                  151
Match length
                   37
% identity
NCBI Description (AF135439) formin binding protein 11 [Mus musculus]
Seq. No.
                   415324
                   uC-osflcyp173f03a1
Seq. ID
Method
                   BLASTX
                   g417154
NCBI GI
                   406
BLAST score
                   1.0e-39
E value
                  99
Match length
                   83
% identity
NCBI Description HEAT SHOCK PROTEIN 82 >gi_100685_pir__S25541 heat shock
                   protein 82 - rice (strain Taichung Native One)
```

>gi_20256_emb_CAA77978_ (Z11920) heat shock protein 82 (HSP82) [Oryza sativa]

Seq. No. 415325

Seq. ID uC-osflcyp173f03b1

Method BLASTX
NCBI GI g417154
BLAST score 330
E value 8.0e-47
Match length 166
% identity 62

NCBI Description HEAT SHOCK PROTEIN 82 >gi 100685 pir S25541 heat shock

protein 82 - rice (strain Taichung Native One)

>gi_20256_emb_CAA77978_ (Z11920) heat shock protein 82

(HSP82) [Oryza sativa]

Seq. No. 415326

Seq. ID uC-osflcyp173f04b1

Method BLASTX
NCBI GI g1777921
BLAST score 432
E value 1.0e-42
Match length 97
% identity 85

NCBI Description (U54774) glutamate decarboxylase [Nicotiana tabacum]

Seq. No. 415327

Seq. ID uC-osflcyp173f06a1

Method BLASTX
NCBI GI g1170937
BLAST score 251
E value 2.0e-21
Match length 50
% identity 92

NCBI Description S-ADENOSYLMETHIONINE SYNTHETASE 1 (METHIONINE

ADENOSYLTRANSFERASE 1) (ADOMET SYNTHETASE 1)

>gi_450549_emb_CAA81481_ (Z26867) S-adenosyl methionine

synthetase [Oryza sativa]

Seq. No. 415328

Seq. ID uC-osflcyp173f06b1

Method BLASTX
NCBI GI g1170937
BLAST score 771
E value 3.0e-82
Match length 145
% identity 100

NCBI Description S-ADENOSYLMETHIONINE SYNTHETASE 1 (METHIONINE

ADENOSYLTRANSFERASE 1) (ADOMET SYNTHETASE 1)

>gi_450549_emb_CAA81481_ (Z26867) S-adenosyl methionine

synthetase [Oryza sativa]

Seq. No. 415329

Seq. ID uC-osflcyp173f08a1

Method BLASTX NCBI GI g1729971 BLAST score 274

E value

```
3.0e-24
E value
Match length
                  56
                  88
% identity
                  TONOPLAST INTRINSIC PROTEIN, GAMMA (GAMMA TIP)
NCBI Description
                  (AQUAPORIN-TIP) >gi_1076745_pir__S52004 gamma-Tip protein -
                  rice >gi_473997_dbj_BAA05017_ (D25534) gamma-Tip [Oryza
                  sativa]
                  415330
Seq. No.
                  uC-osflcyp173f08b1
Seq. ID
Method
                  BLASTX
                  g1729971
NCBI GI
BLAST score
                  583
                  3.0e-60
E value
Match length
                  161
                  75
% identity
                  TONOPLAST INTRINSIC PROTEIN, GAMMA (GAMMA TIP)
NCBI Description
                   (AQUAPORIN-TIP) >gi 1076745 pir S52004 gamma-Tip protein -
                  rice >gi 473997_dbj_BAA05017_ (D25534) gamma-Tip [Oryza
                  sativa]
                  415331
Seq. No.
Seq. ID
                  uC-osflcyp173f09a1
                  BLASTX
Method
                  q6006897
NCBI GI
                  178
BLAST score
                  7.0e-13
E value
                   95
Match length
                   43
% identity
                  (AC008153) unknown protein [Arabidopsis thaliana]
NCBI Description
                   415332
Seq. No.
                  uC-osflcyp173f09b1
Seq. ID
                  BLASTX
Method
NCBI GI
                   g6006897
BLAST score
                   381
                   1.0e-36
E value
Match length
                   176
% identity
                   48
                  (AC008153) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   415333
                   uC-osflcyp173f10b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   q1777921
BLAST score
                   828
                   5.0e-89
E value
Match length
                   169
% identity
                   92
                  (U54774) glutamate decarboxylase [Nicotiana tabacum]
NCBI Description
                   415334
Seq. No.
                   uC-osflcyp173f11b1
Seq. ID
                   BLASTX
Method
                   g4432839
NCBI GI
                   351
BLAST score
                   5.0e-33
```

```
Match length
                   78
                   86
% identity
                   (AC006283) unknown protein [Arabidopsis thaliana]
NCBI Description
                   415335
Seq. No.
                   uC-osflcyp173f12a1
Seq. ID
Method
                   BLASTX
                   g4455361
NCBI GI
                   380
BLAST score
                   2.0e-36
E value
Match length
                   152
% identity
                   51
                   (AL035524) putative protein [Arabidopsis thaliana]
NCBI Description
                   415336
Seq. No.
                   uC-osflcyp173g02b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   q4220472
                   473
BLAST score
                   2.0e-47
E value
                   119
Match length
                   77
% identity
                   (AC006069) similar to yeast cccl protein [Arabidopsis
NCBI Description
                   thaliana]
                   415337
Seq. No.
                   uC-osflcyp173g03b1
Seq. ID
Method
                   BLASTX
                   g1620369
NCBI GI
BLAST score
                   206
                   4.0e-16
E value
                   51
Match length
                   71
% identity
                  (Y08781) peroxidase ATP22a [Arabidopsis thaliana]
NCBI Description
                   415338
Seq. No.
                   uC-osflcyp173g04b1
Seq. ID
Method
                   BLASTX
                   g231610
NCBI GI
                   590
BLAST score
                    4.0e-61
E value
Match length
                   141
                   83
% identity
NCBI Description ATP SYNTHASE GAMMA CHAIN, CHLOROPLAST PRECURSOR
                    >gi_67880_pir__PWNTG H+-transporting ATP synthase (EC
                   3.6.1.34) gamma chain precursor, chloroplast - common tobacco >gi_19785_emb_CAA45152_ (X63606) ATP synthase
                    (gamma subunit) [Nicotiana tabacum]
Seq. No.
                    415339
                   uC-osflcyp173g05b1
Seq. ID
Method
                   BLASTX
                    q3386604
NCBI GI
                    264
BLAST score
                    8.0e-23
E value
Match length
                    104
                    55
% identity
```

```
(AC004665) putative protein kinase [Arabidopsis thaliana]
NCBI Description
                  415340
Seq. No.
                  uC-osflcyp173g06a1
Seq. ID
                  BLASTX
Method
NCBI GI
                  q322854
                  410
BLAST score
                  5.0e-40
E value
                  89
Match length
                   93
% identity
                  pollen-specific protein - rice >gi_20310_emb_CAA78897_
NCBI Description
                   (Z16402) pollen specific gene [Oryza sativa]
                   415341
Seq. No.
                  uC-osflcyp173g06b1
Seq. ID
Method
                  BLASTX
                  g322854
NCBI GI
BLAST score
                   488
                   4.0e-49
E value
Match length
                  103
                   94
% identity
                  pollen-specific protein - rice >gi_20310_emb_CAA78897
NCBI Description
                   (Z16402) pollen specific gene [Oryza sativa]
                   415342
Seq. No.
                   uC-osflcyp173g08a1
Seq. ID
                   BLASTX
Method
                   g3345477
NCBI GI
                   188
BLAST score
                   4.0e-14
E value
                   35
Match length
% identity
                   97
                  (AB016283) carbonic anhydrase [Oryza sativa]
NCBI Description
                   415343
Seq. No.
                   uC-osflcyp173g08b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g606817
                   500
BLAST score
                   6.0e-67
E value
                   136
Match length
% identity
                   (U08404) carbonic anhydrase [Oryza sativa]
NCBI Description
                   >gi_5917783_gb_AAD56038.1_AF182806_1 (AF182806) carbonic
                   anhydrase 3 [Oryza sativa]
Seq. No.
                   415344
Seq. ID
                   uC-osflcyp173g09a1
Method
                   BLASTX
NCBI GI
                   q1620369
BLAST score
                   237
                   1.0e-19
E value
Match length
                   80
% identity
                  (Y08781) peroxidase ATP22a [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   415345
```

NCBI GI

```
Seq. ID
                  uC-osflcyp173g09b1
                  BLASTX
Method
                  g1483213
NCBI GI
BLAST score
                  472
                  9.0e-51
E value
                  158
Match length
% identity
                   61
                   (X96480) PAC [Arabidopsis thaliana]
NCBI Description
                  >gi_5729705_gb_AAD48512.1_AC007927_2 (AC007927) pale cress
                  protein [Arabidopsis thaliana]
Seq. No.
                   415346
Seq. ID
                  uC-osflcyp173g11b1
Method
                  BLASTN
                   g3618319
NCBI GI
BLAST score
                   478
                   0.0e+00
E value
Match length
                   493
% identity
                   100
                  Oryza sativa mRNA for zinc finger protein, complete cds,
NCBI Description
                   clone:S3574
Seq. No.
                   415347
                   uC-osflcyp173h03b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3894197
BLAST score
                   385
                   5.0e-37
E value
Match length
                   154
% identity
                   48
                  (AC005662) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   415348
Seq. No.
                   uC-osflcyp173h04a1
Seq. ID
                   BLASTX
Method
NCBI GI
                   g226263
                   169
BLAST score
                   8.0e-12
E value
                   31
Match length
                   97
% identity
                  chlorophyll a/b binding protein [Glycine max]
NCBI Description
                   415349
Seq. No.
                   uC-osflcyp173h04b1
Seq. ID
                   BLASTX
Method
                   g3036951
NCBI GI
                   496
BLAST score
                   4.0e-50
E value
                   95
Match length
                   98
% identity
                  (AB012639) light harvesting chlorophyll a/b-binding protein
NCBI Description
                   [Nicotiana sylvestris]
                   415350
Seq. No.
Seq. ID
                   uC-osflcyp173h05b1
                   BLASTX
Method
```

54218

g4115918

NCBI GI

E value

BLAST score

794

5.0e-85

```
BLAST score
                  295
                  2.0e-26
E value
                  73
Match length
% identity
                  77
                  (AF118222) similar to nascent polypeptide associated
NCBI Description
                  complex alpha chain [Arabidopsis thaliana]
                  415351
Seq. No.
                  uC-osflcyp173h07b1
Seq. ID
                  BLASTX
Method
                  g3236238
NCBI GI
                  529
BLAST score
                   6.0e - 54
E value
Match length
                  129
                  74
% identity
                   (AC004684) putative ARF1 GTPase activating protein
NCBI Description
                   [Arabidopsis thaliana] >gi 4519792 dbj BAA75744.1_
                   (AB017876) Aspl [Arabidopsis thaliana]
                   415352
Seq. No.
Seq. ID
                  uC-osflcyp173h09a1
                  BLASTX
Method
                  g3738302
NCBI GI
BLAST score
                   334
                   3.0e-31
E value
                   125
Match length
                   51
% identity
                  (AC005309) tubby-like protein [Arabidopsis thaliana]
NCBI Description
                   >gi_4249398 (AC006072) putative tubby protein [Arabidopsis
                   thaliana]
                   415353
Seq. No.
                   uC-osflcyp173h09b1
Seq. ID
                   BLASTX
Method
NCBI GI
                   g5777631
BLAST score
                   178
                   9.0e-13
E value
                   49
Match length
% identity
                   71
                  (AJ245900) CAA303719.1 protein [Oryza sativa]
NCBI Description
Seq. No.
                   415354
                   uC-osflcyp173h11a1
Seq. ID
                   BLASTN
Method
NCBI GI
                   q1136121
                   86
BLAST score
                   2.0e-40
E value
                   339
Match length
                   84
% identity
NCBI Description O.sativa mRNA for alpha-tubulin (clone OSTA-136)
                   415355
Seq. No.
                   uC-osflcyp173h11b1
Seq. ID
                   BLASTX
Method
                   g1136122
```

```
148
Match length
                  99
% identity
                  (X91807) alfa-tubulin [Oryza sativa]
NCBI Description
                  415356
Seq. No.
                  uC-osflcyp173h12b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g974782
                  835
BLAST score
                  8.0e-90
E value
Match length
                  170
% identity
                  94
                  (Z49150) cobalamine-independent methionine synthase
NCBI Description
                  [Solenostemon scutellarioides]
                  415357
Seq. No.
                  uC-osflcyp174a01b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2661412
BLAST score
                  680
                  1.0e-71
E value
Match length
                  185
% identity
                  71
                  (AJ000728) MAP kinase kinase [Lycopersicon esculentum]
NCBI Description
                  415358
Seq. No.
                  uC-osflcyp174a02a1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1236961
BLAST score
                  408
E value
                  9.0e-40
Match length
                  110
                  65
% identity
                  (U50201) prunasin hydrolase precursor [Prunus serotina]
NCBI Description
                  415359
Seq. No.
Seq. ID
                  uC-osflcyp174a02b1
Method
                  BLASTX
NCBI GI
                  q833835
BLAST score
                  588
                  8.0e-61
E value
Match length
                  180
% identity
                  60
NCBI Description
                  (U26025) amygdalin hydrolase isoform AH I precursor [Prunus
                  serotina]
Seq. No.
                  415360
Seq. ID
                  uC-osflcyp174a05b1
Method
                  BLASTX
NCBI GI
                  q4508073
BLAST score
                  258
E value
                   3.0e-22
Match length
                  121
% identity
NCBI Description
                  (AC005882) 43220 [Arabidopsis thaliana]
Seq. No.
                  415361
```

Seq. No.

415366

Seq. ID uC-osflcyp174a06a1 Method BLASTN NCBI GI g976256 BLAST score 448 E value 0.0e + 00Match length 473 % identity 98 NCBI Description Rice mRNA stearyl-ACP desaturase, complete cds 415362 Seq. No. Seq. ID uC-osflcyp174a06b1 Method BLASTX NCBI GI g3915029 BLAST score 962 1.0e-104 E value 183 Match length % identity 99 ACYL-[ACYL-CARRIER PROTEIN] DESATURASE PRECURSOR NCBI Description (STEAROYL-ACP DESATURASE) >qi 976257 dbj BAA07631 (D38753) stearyl-ACP desaturase [Oryza sativa] Seq. No. 415363 Seq. ID uC-osflcyp174a07a1 Method BLASTX NCBI GI g3041855 BLAST score 245 E value 1.0e-20 Match length 52 % identity 71 (ACO04537) similar to tumor suppressor p33ING1; similar to NCBI Description AF044076 (PID:g2829208) [Homo sapiens] 415364 Seq. No. uC-osflcyp174a07b1 Seq. ID Method BLASTX NCBI GI g2829208 291 BLAST score 5.0e-26 E value Match length 79 % identity 61 (AF044076) candidate tumor suppressor p33ING1 [Homo NCBI Description sapiens] >gi_5689257 dbj_BAA82886.1 (AB024401) p33 [Homo sapiens] 415365 Seq. No. uC-osflcyp174a08a1 Seq. ID Method BLASTX NCBI GI g3023713 BLAST score 385 E value 4.0e-37 76 Match length 99 % identity ENOLASE (2-PHOSPHOGLYCERATE DEHYDRATASE) NCBI Description (2-PHOSPHO-D-GLYCERATE HYDRO-LYASE) (OSE1) >gi 780372 (U09450) enolase [Oryza sativa]

```
Seq. ID
                  uC-osflcyp174a08b1
Method
                  BLASTX
NCBI GI
                  g3023713
BLAST score
                   740
                   1.0e-78
E value
Match length
                  159
                   91
% identity
NCBI Description
                  ENOLASE (2-PHOSPHOGLYCERATE DEHYDRATASE)
                   (2-PHOSPHO-D-GLYCERATE HYDRO-LYASE) (OSE1) >qi 780372
                   (U09450) enolase [Oryza sativa]
Seq. No.
                   415367
Seq. ID
                  uC-osflcyp174a09a1
Method
                  BLASTN
NCBI GI
                   g4097337
BLAST score
                   442
E value
                   0.0e + 00
Match length
                   445
% identity
                   100
NCBI Description
                  Oryza sativa metallothionein-like protein mRNA, complete
Seq. No.
                   415368
Seq. ID
                   uC-osflcyp174a09b1
Method
                   BLASTN
NCBI GI
                   q4097337
BLAST score
                   426
                   0.0e + 00
E value
Match length
                   500
% identity
                   100
NCBI Description
                  Oryza sativa metallothionein-like protein mRNA, complete
                   cds
                   415369
Seq. No.
                   uC-osflcyp174a10a1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g5882729
BLAST score
                   159
E value
                   1.0e-10
Match length
                   70
                   43
% identity
                  (AC008263) ESTs gb T04387, gb R84022 and gb T42239 come
NCBI Description
                   from this gene. [Arabidopsis thaliana]
                   415370
Seq. No.
                   uC-osflcyp174a11b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2827139
BLAST score
                   542
                   2.0e-55
E value
Match length
                   153
% identity
                   69
                   (AF027172) cellulose synthase catalytic subunit
NCBI Description
                   [Arabidopsis thaliana] >gi_4049343_emb_CAA22568.1
                   (AL034567) cellulose synthase catalytic subunit (RSW1)
```

[Arabidopsis thaliana]

NCBI GI

```
Seq. No.
                  415371
                  uC-osflcyp174b01b1
Seq. ID
Method
                  BLASTX
                  q4006978
NCBI GI
                  188
BLAST score
                  7.0e-14
E value
Match length
                  87
                  43
% identity
                  (AJ131335) pollen allergen (group II) [Cynodon dactylon]
NCBI Description
                  415372
Seq. No.
                  uC-osflcyp174b02b1
Seq. ID
Method
                  BLASTX
                  g2498586
NCBI GI
BLAST score
                   642
E value
                   4.0e-67
Match length
                  146
% identity
                  79
                  MAJOR POLLEN ALLERGEN ORY S 1 PRECURSOR (ORY S I)
NCBI Description
                  >gi 1173557 (U31771) Ory s 1 [Oryza sativa]
Seq. No.
                   415373
Seq. ID
                   uC-osflcyp174b03b1
Method
                   BLASTX
NCBI GI
                   g3695392
BLAST score
                   309
                   4.0e-28
E value
Match length
                   138
% identity
                   46
                  (AF096371) No definition line found [Arabidopsis thaliana]
NCBI Description
                   415374
Seq. No.
                   uC-osflcyp174b04b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g5257277
                   483
BLAST score
                   1.0e-48
E value
Match length
                   103
                   92
% identity
                  (AP000364) ESTs C98431(E0144), C71728(E0144) correspond to a
NCBI Description
                   region of the predicted gene.; Similar to Medicago sativa
                   S-adenosyl-L-methionine. (U20736) [Oryza sativa]
                   415375
Seq. No.
                   uC-osflcyp174b05a1
Seq. ID
                   BLASTX
Method
                   g4160294
NCBI GI
BLAST score
                   278
                   1.0e-24
E value
Match length
                   85
                   60
% identity
                  (Y18644) methyltransferase-like protein 1 [Mus musculus]
NCBI Description
Seq. No.
                   415376
                   uC-osflcyp174b05b1
Seq. ID
Method
                   BLASTX
```

54223

g2131358

Method

NCBI GI

BLAST score

BLASTX

587

g3885334

```
BLAST score
                  167
E value
                  2.0e-11
                  68
Match length
% identity
                  46
                  hypothetical protein YDL201w - yeast (Saccharomyces
NCBI Description
                                                         (X99000) ORF D1075
                  cerevisiae) >gi 1429356 emb CAA67468
                  [Saccharomyces cerevisiae] >qi 1431332 emb CAA98779
                  (274249) ORF YDL201w [Saccharomyces cerevisiae]
Seq. No.
                  415377
                  uC-osflcyp174b06b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2213600
                  353
BLAST score
                  3.0e-33
E value
                  128
Match length
                  52
% identity
                 (AC000348) T7N9.20 [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  415378
Seq. ID
                  uC-osflcyp174b07a1
                  BLASTX
Method
                  q1304215
NCBI GI
BLAST score
                  371
                  2.0e-35
E value
Match length
                  101
                  54
% identity
                  (D84392) precursor of rice 22 kDa protein of photosystem II
NCBI Description
                  (PSII-S) [Oryza sativa]
                  415379
Seq. No.
                  uC-osflcyp174b07b1
Seq. ID
Method
                  BLASTX
                  q1304215
NCBI GI
BLAST score
                  546
                  7.0e-56
E value
Match length
                  127
% identity
                   65
                  (D84392) precursor of rice 22 kDa protein of photosystem II
NCBI Description
                   (PSII-S) [Oryza sativa]
Seq. No.
                   415380
                  uC-osflcyp174b08a1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3885334
BLAST score
                  195
                  9.0e-15
E value
                  70
Match length
% identity
                   57
                  (AC005623) putative argonaute protein [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                   415381
                  uC-osflcyp174b08b1
Seq. ID
```

E value 1.0e-60
Match length 179
% identity 63
NCBI Description (AC00562

NCBI Description (AC005623) putative argonaute protein [Arabidopsis

thaliana]

Seq. No. 415382

Seq. ID uC-osflcyp174b09a1

Method BLASTX
NCBI GI g4678297
BLAST score 282
E value 6.0e-25
Match length 94
% identity 60

NCBI Description (AL049655) protein disulfide-isomerase-like protein

[Arabidopsis thaliana]

Seq. No. 415383

Seq. ID uC-osflcyp174b09b1

Method BLASTX
NCBI GI g2507460
BLAST score 196
E value 6.0e-15
Match length 77
% identity 44

NCBI Description PROTEIN DISULFIDE ISOMERASE PRECURSOR (PDI) (PROLYL

4-HYDROXYLASE BETA SUBUNIT) (CELLULAR THYROID HORMONE BINDING PROTEIN) (P55) >gi_2144545_pir__ISHUSS protein disulfide-isomerase (EC 5.3.4.1) precursor - human

>gi 190384 (M22806) prolyl 4-hydroxylase beta-subunit [Homo

sapiens]

Seq. No. 415384

Seq. ID uC-osflcyp174b10b1

Method BLASTX
NCBI GI g2842490
BLAST score 184
E value 2.0e-13
Match length 51
% identity 63

NCBI Description (AL021749) heat-shock protein [Arabidopsis thaliana]

Seq. No. 415385

Seq. ID uC-osflcyp174b11b1

Method BLASTX
NCBI GI g4914374
BLAST score 575
E value 2.0e-59
Match length 143
% identity 74

NCBI Description (AC007584) putative protein kinase [Arabidopsis thaliana]

Seq. No. 415386

Seq. ID uC-osflcyp174b12a1

Method BLASTX NCBI GI g4887131 BLAST score 192

```
1.0e-14
E value
Match length
                  76
                  53
% identity
NCBI Description
                 (AF134732) 60S ribosomal protein L1 [Prunus armeniaca]
Seq. No.
                  415387
                  uC-osflcyp174b12b1
Seq. ID
Method
                  BLASTX
                  g1350680
NCBI GI
BLAST score
                  442
                  1.0e-43
E value
Match length
                  133
                  68
% identity
NCBI Description 60S RIBOSOMAL PROTEIN L1
                  415388
Seq. No.
Seq. ID
                  uC-osflcyp174c01b1
Method
                  BLASTX
NCBI GI
                  g3212854
                  239
BLAST score
                  7.0e-20
E value
                  81
Match length
                  56
% identity
NCBI Description (AC004005) unknown protein [Arabidopsis thaliana]
Seq. No.
                  415389
Seq. ID
                  uC-osflcyp174c02a1
Method
                  BLASTX
NCBI GI
                  q2130069
BLAST score
                  274
                  5.0e-24
E value
Match length
                  62
                  87
% identity
NCBI Description
                  catalase (EC 1.11.1.6) catA - rice
                  >gi_1261858_dbj_BAA06232 (D29966) catalase [Oryza sativa]
                  415390
Seq. No.
                  uC-osflcyp174c02b1
Seq. ID
Method
                  BLASTX
                  g2130069
NCBI GI
BLAST score
                  776
                  6.0e-83
E value
Match length
                  161
                  90
% identity
NCBI Description
                  catalase (EC 1.11.1.6) catA - rice
                  >gi 1261858 dbj BAA06232 (D29966) catalase [Oryza sativa]
Seq. No.
                  415391
Seq. ID
                  uC-osflcyp174c03a1
Method
                  BLASTX
NCBI GI
                  g1136120
BLAST score
                  266
E value
                  5.0e-27
Match length
                  69
                  97
% identity
NCBI Description (X91806) alpha-tubulin [Oryza sativa]
```

```
415392
Seq. No.
Seq. ID
                  uC-osflcyp174c03b1
Method
                  BLASTX
NCBI GI
                  g542179
BLAST score
                  845
E value
                  5.0e-91
Match length
                  161
                  99
% identity
                  alpha tubulin - maize >qi 629837 pir S39998 tubulin alpha
NCBI Description
                  chain - maize (fragment) >gi 393401 emb CAA52158 (X73980)
                  alpha tubulin [Zea mays]
                  415393
Seq. No.
Seq. ID
                  uC-osflcyp174c04a1
Method
                  BLASTX
NCBI GI
                  g2952328
BLAST score
                  760
                  4.0e-81
E value
Match length
                  148
% identity
                  98
                  (AF049889) 1-aminocyclopropane-1-carboxylate oxidase [Oryza
NCBI Description
                  sativa]
                  415394
Seq. No.
Seq. ID
                  uC-osflcyp174c04b1
Method
                  BLASTX
                  q2952328
NCBI GI
BLAST score
                  758
E value
                  8.0e-81
Match length
                  147
% identity
                  99
                  (AF049889) 1-aminocyclopropane-1-carboxylate oxidase [Oryza
NCBI Description
                  sativa]
                   415395
Seq. No.
                  uC-osflcyp174c05b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4469023
BLAST score
                   631
E value
                   6.0e-66
Match length
                  157
% identity
                  78
                  (AL035602) putative protein [Arabidopsis thaliana]
NCBI Description
                   415396
Seq. No.
                  uC-osflcyp174c06b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4522004
BLAST score
                  155
                   3.0e-10
E value
Match length
                  132
                   33
% identity
                  (AC007069) putative histidine kinase, sensory transduction
NCBI Description
                   [Arabidopsis thaliana]
                   415397
Seq. No.
                  uC-osflcyp174c07b1
Seq. ID
```

```
BLASTX
Method
                  g4337175
NCBI GI
                  359
BLAST score
                  5.0e-34
E value
                  132
Match length
                  54
% identity
                  (AC006416) ESTs gb T20589, gb T04648, gb AA597906,
NCBI Description
                  gb T04111, gb R84180, gb R65428, gb T44439, gb T76570,
                  gb R90004, gb T45020, gb T42457, gb T20921, gb AA042762 and
                  gb_AA720210 come from this gene. [Arabidopsis thaliana]
                  415398
Seq. No.
                  uC-osflcyp174c08b1
Seq. ID
                  BLASTX
Method
                  g974782
NCBI GI
                  942
BLAST score
                  1.0e-102
E value
                  187
Match length
                  94
% identity
                  (Z49150) cobalamine-independent methionine synthase
NCBI Description
                  [Solenostemon scutellarioides]
                  415399
Seq. No.
Seq. ID
                  uC-osflcyp174c09b1
                  BLASTX
Method
                  q480737
NCBI GI
                  428
BLAST score
                  4.0e-42
E value
                  101
Match length
% identity
                  triose phosphate/3-phosphoglycerate/phosphate translocator
NCBI Description
                   - common tobacco >gi 629694 pir S42583 phosphate
                  translocator - common tobacco >qi 403023 emb CAA52979.1
                   (X75088) phosphate translocator [Nicotiana tabacum]
                  415400
Seq. No.
                  uC-osflcyp174c11b1
Seq. ID
                  BLASTX
Method
                  q4678208
NCBI GI
BLAST score
                  284
                   3.0e-25
E value
Match length
                  73
                  71
% identity
                  (AC007134) putative sugar transporter [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                   415401
Seq. ID
                   uC-osflcyp174c12b1
                  BLASTX
Method
NCBI GI
                  g2286153
BLAST score
                   862
                   6.0e-93
E value
Match length
                  179
% identity
                   92
                  (AF007581) cytoplasmic malate dehydrogenase [Zea mays]
NCBI Description
```

415402

Seq. No.

Seq. ID

uC-osflcyp174d02a1 Seq. ID Method BLASTX q464981 NCBI GI BLAST score 260 2.0e-22 E value Match length 59 86 % identity UBIQUITIN-CONJUGATING ENZYME E2-17 KD (UBIQUITIN-PROTEIN NCBI Description LIGASE) (UBIQUITIN CARRIER PROTEIN) >gi 388207 (L23762) ubiquitin carrier protein [Lycopersicon esculentum] 415403 Seq. No. Seq. ID uC-osflcyp174d02b1 BLASTX Method q2668744 NCBI GI 765 BLAST score E value 1.0e-81 145 Match length % identity 97 (AF034946) ubiquitin conjugating enzyme [Zea mays] NCBI Description 415404 Seq. No. uC-osflcyp174d03b1 Seq. ID Method BLASTX q3367520 NCBI GI 621 BLAST score 1.0e-64 E value 172 Match length % identity 68 (AC004392) Similar to protein kinase APK1A, NCBI Description tyrosine-serine-threonine kinase gb_D12522 from A. thaliana. [Arabidopsis thaliana] Seq. No. 415405 uC-osflcyp174d04b1 Seq. ID BLASTX Method g4559339 NCBI GI BLAST score 533 E value 2.0e-54 111 Match length 90 % identity (AC007087) putative ATP-dependent RNA helicase [Arabidopsis NCBI Description thaliana] 415406 Seq. No. uC-osflcyp174d06b1 Seq. ID BLASTX Method g4249409 NCBI GI 413 BLAST score 3.0e-40E value 132 Match length % identity NCBI Description (AC006072) putative sugar transporter [Arabidopsis thaliana] 415407 Seq. No. uC-osflcyp174d08a1

```
BLASTX
Method
                  g3935185
NCBI GI
                  148
BLAST score
                   2.0e-09
E value
                   91
Match length
                   37
% identity
                  (AC004557) F17L21.28 [Arabidopsis thaliana]
NCBI Description
                   415408
Seq. No.
                  uC-osflcyp174d08b1
Seq. ID
                  BLASTX
Method
                   g3935185
NCBI GI
                   196
BLAST score
                   6.0e-15
E value
                   90
Match length
% identity
                   43
                  (AC004557) F17L21.28 [Arabidopsis thaliana]
NCBI Description
                   415409
Seq. No.
Seq. ID
                   uC-osflcyp174d09a1
Method
                   BLASTN
                   g5478796
NCBI GI
                   457
BLAST score
                   0.0e + 00
E value
                   499
Match length
                   98
% identity
                   Oryza sativa CAO mRNA for chlorophyll b synthase, partial
NCBI Description
                   cds
                   415410
Seq. No.
Seq. ID
                   uC-osflcyp174d09b1
                   BLASTX
Method
                   g5478807
NCBI GI
BLAST score
                   462
                   5.0e-46
E value
                   172
Match length
                   58
% identity
NCBI Description (AB021316) chlorophyll b synthase [Arabidopsis thaliana]
                   415411
Seq. No.
Seq. ID
                   uC-osflcyp174d11a1
                   BLASTX
Method
                   q4874285
NCBI GI
                   486
BLAST score
                   7.0e-49
E value
Match length
                   119
                   71
% identity
                  (AC007212) putative phosphatidylinositol/phophatidylcholine
NCBI Description
                   transfer protein [Arabidopsis thaliana]
Seq. No.
                   415412
                   uC-osflcyp174d12a1
Seq. ID
                   BLASTX
Method
                   g4769012
NCBI GI
                   169
BLAST score
E value
                   2.0e-23
Match length
                   67
```

```
% identity
NCBI Description (AF143746) CER1 [Oryza sativa]
                  415413
Seq. No.
Seq. ID
                  uC-osflcyp174d12b1
                  BLASTX
Method
                  q4769012
NCBI GI
BLAST score
                  703
                  2.0e-74
E value
                  134
Match length
                  99
% identity
NCBI Description (AF14:/40, "Oryza sativa]
                  415414
Seq. No.
                  uC-osflcyp174e02b1
Seq. ID
                  BLASTX
Method
                  g1703380
NCBI GI
BLAST score
                  486
                  6.0e-49
E value
Match length
                  107
                  93
% identity
NCBI Description ADP-RIBOSYLATION FACTOR >gi 1132483 dbj BAA04607 (D17760)
                  ADP-ribosylation factor [Oryza sativa]
Seq.
Seq. 1
                  BLASTX
Method
                  g5262156
NCBI GI
                  499
BLAUI score
E value
                  2 00-50
Match 1
% iden
                                                                   a]
NCBI Descri_ ..
                  , . . . . . .
Seq. No.
                  415416
Seq. ID
                  uC-osflcyp174e03b1
                  BLASTX
Method
                  g5262156
NCBI GI
BLAST score
                  355
                  2.0e-33
E value
Match length
                  149
% identity
                  42
NCBI Description (AL080237) putative protein [Arabidopsis ta iana]
                  415417
Seq. No.
Seq. ID
                  uC-osflcyp174e04a1
Method
                  BLASTX
                  q1076746
NCBI GI
                  172
BLAST score
E value
                  4.0e-12
Match length
                  43
% identity
                  heat shock protein 70 - rice (fragment)
NCBI Description
                  >gi_763160_emb_CAA47948_ (X67711) heat shock protein 70
                  [Oryza sativa]
Seq. No.
                  415418
```

```
uC-osflcyp174e04b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2827002
                   629
BLAST score
                   1.0e-65
E value
                  124
Match length
                   97
% identity
                  (AF005993) HSP70 [Triticum aestivum]
NCBI Description
                   415419
Seq. No.
                  uC-osflcyp174e05b1
Seq. ID
Method
                  BLASTX
                   g3297816
NCBI GI
BLAST score
                   533
                   2.0e-54
E value
Match length
                   162
                   65
% identity
                  (AL031032) putative protein [Arabidopsis thaliana]
NCBI Description
                   415420
Seq. No.
                   uC-osflcyp174e06b1
Seq. ID
Method
                   BLASTX
                   g1171008
NCBI GI
BLAST score
                   458
                   1.0e-45
E value
Match length
                   117
% identity
                   67
                   POLLEN ALLERGEN PHL P 1 PRECURSOR (PHL P I)
NCBI Description
                   >gi 629812 pir S44182 allergen Phl p I - common timothy
                   >gi 473360 emb CAA55390 (X78813) Phl p I allergen [Phleum
                   pratense]
Seq. No.
                   415421
                   uC-osflcyp174e07b1
Seq. ID
                   BLASTX
Method
                   g4753658
NCBI GI
BLAST score
                   281
E value
                   5.0e-25
                   117
Match length
% identity
                   57
                  (AL049751) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   415422
                   uC-osflcyp174e09b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2826884
BLAST score
                   178
E value
                   1.0e-12
Match length
                   147
% identity
                   39
                   (AJ223635) transcription factor IIA large subunit
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                   415423
                   uC-osflcyp174e10b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   q451193
```

```
279
BLAST score
                  1.0e-24
E value
Match length
                  85
% identity
                  66
                   (L28008) wali7 [Triticum aestivum]
NCBI Description
                  >gi 1090845_prf__2019486B wali7 gene [Triticum aestivum]
                  415424
Seq. No.
                  uC-osflcyp174f01b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1213460
BLAST score
                  423
E value
                  1.0e-41
Match length
                  166
                  51
% identity
NCBI Description
                  (U03374) C subunit of V-ATPase [Amblyomma americanum]
Seq. No.
                  415425
Seq. ID
                  uC-osflcyp174f02a1
Method
                  BLASTX
NCBI GI
                  q439879
BLAST score
                  192
                  1.0e-14
E value
Match length
                   43
                   81
% identity
                  (L15194) [Golden delicious apple fruit expressed mRNA,
NCBI Description
                   complete cds.], gene product [Malus domestica]
Seq. No.
                   415426
                   uC-osflcyp174f02b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2995990
BLAST score
                   298
E value
                   6.0e-27
Match length
                   125
                   50
% identity
                   (AF053746) dormancy-associated protein [Arabidopsis
NCBI Description
                   thaliana] >gi 2995992 (AF053747) dormancy-associated
                  protein [Arabidopsis thaliana]
                   415427
Seq. No.
                   uC-osflcyp174f03b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   q3885892
BLAST score
                   224
                   5.0e-26
E value
                   115
Match length
                   61
% identity
                   (AF093634) photosystem-1 F subunit precursor [Oryza sativa]
NCBI Description
Seq. No.
                   415428
                   uC-osflcyp174f04a1
Seq. ID
Method
                  BLASTX
                   g3193301
NCBI GI
                   278
BLAST score
                   2.0e-24
E value
                   91
Match length
```

```
% identity
                  (AF069298) Arabidopsis putative chloroplast outer envelope
NCBI Description
                  86-like protein T10P11.19 (GB: AC002330) [Arabidopsis
                  thaliana]
                  415429
Seq. No.
Seq. ID
                  uC-osflcyp174f04b1
Method
                  BLASTX
NCBI GI
                  a710465
                  173
BLAST score
E value
                  6.0e-13
                  64
Match length
                  55
% identity
                  OEP86=outer envelope protein [Peas, Peptide Chloroplast,
NCBI Description
                  878 aa]
                  415430
Seq. No.
                  uC-osflcyp174f05b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4262154
                  230
BLAST score
                  7.0e-19
E value
                  72
Match length
                  62
% identity
                  (AC005275) putative protein phosphatase regulatory subunit
NCBI Description
                   [Arabidopsis thaliana]
                  415431
Seq. No.
Seq. ID
                  uC-osflcyp174f06b1
Method
                  BLASTX
                  q3334320
NCBI GI
                  455
BLAST score
                  3.0e-45
E value
                  135
Match length
% identity
                  73
NCBI Description 40S RIBOSOMAL PROTEIN SA (P40) >gi 2444420 (AF020553)
                  ribosome-associated protein p40 [Glycine max]
Seq. No.
                   415432
Seq. ID
                   uC-osflcyp174f08a1
                   BLASTX
Method
NCBI GI
                  q133898
BLAST score
                   203
                  8.0e-16
E value
Match length
                  54
% identity
                  76
NCBI Description 40S RIBOSOMAL PROTEIN S27A
Seq. No.
                   415433
Seq. ID
                  uC-osflcyp174f08b1
Method
                  BLASTX
NCBI GI
                  q82733
BLAST score
                  432
                  2.0e-43
E value
                  113
Match length
% identity
                   81
NCBI Description ubiquitin fusion protein UBF9 - maize >gi_168651 (M68937)
```

```
ubiquitin fusion protein [Zea mays]
                  >qi 1589388 prf 2211240B ubiquitin fusion protein [Zea
                  mays]
                  415434
Seq. No.
                  uC-osflcyp174f10b1
Seq. ID
Method
                  BLASTX
                  g2829887
NCBI GI
BLAST score
                  174
                  3.0e-12
E value
Match length
                  170
% identity
                  30
                  (AC002396) Hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   415435
Seq. No.
                  uC-osflcyp174f12b1
Seq. ID
                  BLASTX
Method
NCBI GI
                   q3281853
BLAST score
                   261
                   2.0e-22
E value
                   72
Match length
                   72
% identity
                   (AL031004) putative protein [Arabidopsis thaliana]
NCBI Description
                   415436
Seq. No.
                   uC-osflcyp174g02b1
Seq. ID
                   BLASTX
Method
NCBI GI
                   q3702321
BLAST score
                   467
                   1.0e-46
E value
                   113
Match length
                   80
% identity
                   (AC005397) putative TGF-beta receptor interacting protein
NCBI Description
                   [Arabidopsis thaliana]
                   415437
Seq. No.
                   uC-osflcyp174g03b1
Seq. ID
Method
                   BLASTN
                   g5852170
NCBI GI
                   86
BLAST score
                   2.0e-40
E value
                   165
Match length
                   88
% identity
                   Oryza sativa indica(GLA4) genomic DNA, chromosome 4, BAC
NCBI Description
                   clone:t17804
                   415438
Seq. No.
                   uC-osflcyp174g05a1
Seq. ID
Method
                   BLASTX
                   g3777602
NCBI GI
BLAST score
                   268
                   2.0e-23
E value
                   104
Match length
                   59
% identity
NCBI Description (AF095709) 50S ribosomal protein L10 [Oryza sativa]
```

ubiquitin fusion protein [Zea mays] >gi_902527 (U29161)

Seq. ID

Method

Seq. No. 415439 uC-osflcyp174g05b1 Seq. ID Method BLASTX q3777602 NCBI GI BLAST score 778 4.0e-83 E value Match length 169 % identity 92 (AF095709) 50S ribosomal protein L10 [Oryza sativa] NCBI Description Seq. No. 415440 Seq. ID uC-osflcyp174g08b1 Method BLASTX NCBI GI q3757521 BLAST score 452 7.0e-45E value Match length 157 % identity 54 NCBI Description (AC005167) unknown protein [Arabidopsis thaliana] Seq. No. 415441 Seq. ID uC-osflcyp174g11a1 Method BLASTX NCBI GI g729944 BLAST score 172 1.0e-17 E value 58 Match length 78 % identity NCBI Description POLLEN ALLERGEN ZEA M 1 (ZEA M I) >qi 478272 pir JC1524 major allergen mI protein - maize >gi 293902 (L14271) Zea mI [Zea mays] Seq. No. 415442 Seq. ID uC-osflcyp174g11b1 Method BLASTX NCBI GI g1167836 BLAST score 431 2.0e-42 E value Match length 110 % identity 65 NCBI Description (Z68893) protein with incomplete signal sequence [Holcus lanatus] 415443 Seq. No. Seq. ID uC-osflcyp174g12b1 Method BLASTX NCBI GI g5019464 BLAST score 235 8.0e-20 E value Match length 83 55 % identity (AJ132219) putative MADS domain transcription factor GGM13 NCBI Description [Gnetum gnemon] Seq. No. 415444

54236

uC-osflcyp174h01b1

BLASTX

```
NCBI GI
                  g4585908
                  307
BLAST score
E value
                  7.0e-28
Match length
                  85
% identity
                  65
NCBI Description
                  (AC006298) putative lysosomal acid lipase [Arabidopsis
                  thaliana]
Seq. No.
                  415445
                  uC-osflcyp174h02a1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g1532047
BLAST score
                  335
                  0.0e+00
E value
Match length
                  343
                  99
% identity
NCBI Description O.sativa mRNA for S-adenosylmethionine decarboxylase
Seq. No.
                  415446
Seq. ID
                  uC-osflcyp174h02b1
Method
                  BLASTX
NCBI GI
                  g2129921
BLAST score
                  179
E value
                  6.0e-13
Match length
                  51
                  67
% identity
NCBI Description
                  hypothetical protein 1 - Madagascar periwinkle >gi 758694
                  (U12573) putative [Catharanthus roseus]
Seq. No.
                  415447
                  uC-osflcyp174h03b1
Seq. ID
Method
                  BLASTX
                  g1352613
NCBI GI
BLAST score
                  396
                  3.0e-38
E value
                  90
Match length
                  91
% identity
                  OCS-ELEMENT BINDING FACTOR 1 (OCSBF-1)
NCBI Description
                  >gi 444047 emb CAA44607 (X62745) ocs-binding factor 1 [Zea
                  mays]
                  415448
Seq. No.
Seq. ID
                  uC-osflcyp174h04b1
Method
                  BLASTX
NCBI GI
                  q6094553
BLAST score
                  577
                  2.0e-59
E value
Match length
                  188
                  63
% identity
                  (AC010676) unknown protein [Arabidopsis thaliana]
NCBI Description
                  415449
Seq. No.
Seq. ID
                  uC-osflcyp174h05a1
Method
                  BLASTX
NCBI GI
                  g129591
BLAST score
                  215
E value
                  3.0e-17
```

```
Match length
                  39
% identity
                  PHENYLALANINE AMMONIA-LYASE >qi 295824 emb CAA34226
NCBI Description
                  (X16099) phenylalanine ammonia-lyase [Oryza sativa]
                  415450
Seq. No.
                  uC-osflcyp174h05b1
Seq. ID
Method
                  BLASTX
                  a129591
NCBI GI
                  905
BLAST score
                  5.0e-98
E value
                  182
Match length
% identity
                  98
NCBI Description PHENYLALANINE AMMONIA-LYASE >gi 295824 emb CAA34226
                  (X16099) phenylalanine ammonia-Tyase [Oryza sativa]
                  415451
Seq. No.
Seq. ID
                  uC-osflcyp174h06b1
Method
                  BLASTX
                  q1769887
NCBI GI
                  492
BLAST score
                  1.0e-49
E value
                  127
Match length
% identity
                 (X95736) amino acid permease 6 [Arabidopsis thaliana]
NCBI Description
                  415452
Seq. No.
                  uC-osflcyp174h07b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2316016
BLAST score
                  684
                  4.0e-72
E value
Match length
                  174
                  69
% identity
NCBI Description (U92650) MRP-like ABC transporter [Arabidopsis thaliana]
Seq. No.
                  415453
                  uC-osflcyp174h08b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3264611
BLAST score
                  526
                  1.0e-53
E value
Match length
                  104
% identity
                  94
NCBI Description (AF061511) seven in absentia homolog [Zea mays]
                  415454
Seq. No.
                  uC-osflcyp174h09b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g480618
BLAST score
                  217
E value
                  2.0e-17
                  115
Match length
                  49
% identity
NCBI Description ATAF1 protein - Arabidopsis thaliana (fragment)
                  >gi 1345506 emb CAA52771 (X74755) ATAF1 [Arabidopsis
```

thaliana]

415455 Seq. No. Seq. ID uC-osflcyp174h10b1 Method BLASTX NCBI GI g3953458 BLAST score 760 5.0e-81 E value Match length 170 88 % identity (AC002328) F20N2.3 [Arabidopsis thaliana] NCBI Description 415456 Seq. No. Seq. ID uC-osflcyp174h11b1 BLASTX Method q5919219 NCBI GI BLAST score 261 E value 2.0e-22 161 Match length % identity (AF186273) leucine-rich repeats containing F-box protein NCBI Description FBL3 [Homo sapiens] 415457 Seq. No. Seq. ID uC-osflcyp174h12a1 Method BLASTX q3875708 NCBI GI 143 BLAST score 8.0e-09 E value Match length 137 % identity (Z35598) Asparagine, Serine and Glycine rich predicted NCBI Description protein [Caenorhabditis elegans] >gi_3880108_emb_CAA86461.1_ (Z46343) Asparagine, Serine and Glycine rich predicted protein [Caenorhabditis elegans] 415458 Seq. No. uC-osflcyp175a02b1 Seq. ID Method BLASTX NCBI GI q4803944 BLAST score 619 E value 2.0e-64 182 Match length 66 % identity (ACO06264) putative C2-domain protein (prosite: PD0C00380) NCBI Description [Arabidopsis thaliana] 415459 Seq. No. uC-osflcyp175a03b1 Seq. ID BLASTX Method g2829902 NCBI GI 490 BLAST score 2.0e-49E value 132 Match length 71 % identity (AC002311) Putative sulphate transporter protein#protein NCBI Description

[Arabidopsis thaliana]

415460 Seq. No. Seq. ID uC-osflcyp175a04b1 Method BLASTN g607894 NCBI GI BLAST score 194 E value 1.0e-105 416 Match length 99 % identity NCBI Description Oryza sativa IR54 anther specific (RTS2) gene, complete cds 415461 Seq. No. Seq. ID uC-osflcyp175a05b1 BLASTX Method g1170937 NCBI GI BLAST score 645 1.0e-67 E value 124 Match length 99 % identity S-ADENOSYLMETHIONINE SYNTHETASE 1 (METHIONINE NCBI Description ADENOSYLTRANSFERASE 1) (ADOMET SYNTHETASE 1) >gi 450549 emb CAA81481 (Z26867) S-adenosyl methionine synthetase [Oryza sativa] 415462 Seq. No. Seq. ID uC-osflcyp175a06b1 Method BLASTX NCBI GI g1707412 406 BLAST score 1.0e-39 E value Match length 157 % identity 54 (X95906) Cleavage and Polyadenylation Specifity Factor NCBI Description protein [Bos taurus] Seq. No. 415463 Seq. ID uC-osflcyp175a07b1 Method BLASTX NCBI GI q2500353 BLAST score 680 E value 9.0e-72 Match length 127 % identity 99 60S RIBOSOMAL PROTEIN L10-3 (QM/R22) >qi 1293784 (U55048) NCBI Description similar to human QM protein, a putative tumor supressor, and to maize ubiquinol-cytochrome C reductase complex subunit VI requiring protein SC34 [Oryza sativa] Seq. No. 415464 Seq. ID uC-osflcyp175a08b1 BLASTN Method NCBI GI g2463510 BLAST score 69 E value 3.0e-30 Match length 151 25 % identity NCBI Description Z.mays small nuclear RNA genes snoR1.1, snoR2.2, snoR3.2, U14.1a, U14.1b, U14.1c and U14.1d

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415465
Seq. No.
                  uC-osflcyp175a09b1
Seq. ID
Method
                  BLASTX
                  g4467147
NCBI GI
                  353
BLAST score
E value
                  2.0e-33
                  142
Match length
                  55
% identity
                  (AL035540) putative protein [Arabidopsis thaliana]
NCBI Description
                  415466
Seq. No.
                  uC-osflcyp175a10b1
Seq. ID
                  BLASTX
Method
NCBI GI
                  g2895866
BLAST score
                   454
E value
                   4.0e-45
Match length
                   123
% identity
                   76
                   (AF045770) methylmalonate semi-aldehyde dehydrogenase
NCBI Description
                   [Oryza sativa]
                   415467
Seq. No.
                   uC-osflcyp175a12b1
Seq. ID
                   BLASTX
Method
                   g4432839
NCBI GI
BLAST score
                   228
                   9.0e-19
E value
Match length
                   136
% identity
                   43
                   (AC006283) unknown protein [Arabidopsis thaliana]
NCBI Description
                   415468
Seq. No.
                   uC-osflcyp175b01b1
Seq. ID
Method
                   BLASTX
                   g417154
NCBI GI
                   788
BLAST score
                   2.0e-84
E value
Match length
                   159
                   97
% identity
                   HEAT SHOCK PROTEIN 82 >gi_100685_pir__S25541 heat shock
NCBI Description
                   protein 82 - rice (strain Taichung Native One)
                   >gi_20256_emb_CAA77978_ (Z11920) heat shock protein 82
                   (HSP82) [Oryza sativa]
                   415469
Seq. No.
                   uC-osflcyp175b02b1
Seq. ID
                   BLASTX
Method
                   g544242
NCBI GI
                   870
BLAST score
E value
                   7.0e-94
Match length
                   178
                   94
% identity
                  ENDOPLASMIN HOMOLOG PRECURSOR (GRP94 HOMOLOG)
NCBI Description
                   >gi_485498_pir__S33533 heat shock protein 90 homolog
                   precursor - barley >gi_22652_emb_CAA48143_ (X67960) GRP94
                   homologue [Hordeum vulgare]
```

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Seq. No.
                  415470
                  uC-osflcyp175b04b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2244831
                  228
BLAST score
                  1.0e-18
E value
Match length
                  167
                  38
% identity
                  (Z97337) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                  415471
Seq. No.
Seq. ID
                  uC-osflcyp175b06b1
Method
                  BLASTX
                  q2498077
NCBI GI
                   651
BLAST score
E value
                   3.0e-68
                   140
Match length
% identity
                   84
                  NUCLEOSIDE DIPHOSPHATE KINASE I (NDK I) (NDP KINASE I)
NCBI Description
                   (PP18) >qi 1777930 (U55019) nucleoside diphosphate kinase
                   [Saccharum officinarum]
                   415472
Seq. No.
Seq. ID
                   uC-osflcyp175b07b1
Method
                   BLASTX
                   g417260
NCBI GI
                   416
BLAST score
E value
                   1.0e-40
Match length
                   127
% identity
                   67
                   LIGHT REGULATED PROTEIN PRECURSOR >gi 422003 pir_ S33632
NCBI Description
                   lir1 protein - rice >gi 20263 emb CAA48706 (X68807)
                   light-regulated gene [Oryza sativa]
                   415473
Seq. No.
                   uC-osflcyp175b08b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g4415931
BLAST score
                   482
E value
                   2.0e-48
                   130
Match length
                   66
% identity
                   (AC006418) unknown protein [Arabidopsis thaliana]
NCBI Description
                   >qi 4559393 qb AAD23053.1 AC006526 18 (AC006526) unknown
                   protein [Arabidopsis thaliana]
                   415474
Seq. No.
                   uC-osflcyp175b09b1
Seq. ID
Method
                   BLASTX
                   g4567286
NCBI GI
                   480
BLAST score
                   4.0e-48
E value
Match length
                   126
                   71
% identity
                   (AC006841) putative coatomer alpha subunit [Arabidopsis
NCBI Description
                   thaliana]
```

Seq. No. 415475 Seq. ID uC-osflcyp175b11b1 BLASTX Method NCBI GI q3643602 BLAST score 175 1.0e-12 E value Match length 51 69 % identity (AC005395) putative tonoplast intrinsic protein NCBI Description [Arabidopsis thaliana] Seq. No. 415476 Seq. ID uC-osflcyp175c01b1 Method BLASTX NCBI GI q439586 BLAST score 889 4.0e-96 E value Match length 171 94 % identity (L27348) calreticulin [Hordeum vulgare] NCBI Description 415477 Seq. No. Seq. ID uC-osflcyp175c02b1 BLASTX Method NCBI GI g2583133 BLAST score 158 E value 2.0e-10 Match length 117 % identity NCBI Description (AC002387) unknown protein [Arabidopsis thaliana] Seq. No. 415478 Seq. ID uC-osflcyp175c03b1 Method BLASTN NCBI GI g20163 BLAST score 82 9.0e-39 E value Match length 82 % identity 100 NCBI Description O.sativa Rrl5 mRNA for 5S ribosomal RNA 415479 Seq. No. uC-osflcyp175c04b1 Seq. ID Method BLASTX NCBI GI g2827552 BLAST score 224 3.0e-18 E value Match length 143 % identity 34 NCBI Description (AL021635) predicted protein [Arabidopsis thaliana] 415480 Seq. No. uC-osflcyp175c07b1 Seq. ID Method BLASTX g2506826 NCBI GI BLAST score 349

E value 9.0e-33 Match length 116 62 % identity NONSPECIFIC LIPID-TRANSFER PROTEIN 1 PRECURSOR (LTP 1) NCBI Description (PAPI) >gi 1619604_emb CAA69949.1_ (Y08691) lipid transfer protein [Oryza satīva] >gi 1667590 (U77295) lipid transfer protein [Oryza sativa] 415481 Seq. No. uC-osflcyp175c08b1 Seq. ID BLASTX Method q3023816 NCBI GI BLAST score 598 4.0e-62 E value 117 Match length 97 % identity GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC NCBI Description >qi 968996 (U31676) qlyceraldehyde-3-phosphate dehydrogenase [Oryza sativa] 415482 Seq. No. uC-osflcyp175c09b1 Seq. ID BLASTX Method NCBI GI q6015065 844 BLAST score 4.0e-91 E value 177 Match length 92 % identity ELONGATION FACTOR 2 (EF-2) >gi_2369714 emb_CAB09900_ NCBI Description (Z97178) elongation factor 2 [Beta vulgaris] 415483 Seq. No. Seq. ID uC-osflcyp175c10b1 BLASTX Method NCBI GI g733454 BLAST score 301 5.0e-49E value Match length 129 % identity 78 (U23188) chlorophyll a/b-binding apoprotein CP26 precursor NCBI Description [Zea mays] 415484 Seq. No. uC-osflcyp175c11b1 Seq. ID Method BLASTX g3170570 NCBI GI BLAST score 166 2.0e-11 E value 137 Match length 33 % identity (AF058302) FrnE [Streptomyces roseofulvus] NCBI Description

Seq. No. 415485

Seq. ID uC-osflcyp175c12b1

Method BLASTX NCBI GI g2493130 BLAST score 745

E value

```
3.0e-79
E value
                  154
Match length
                  94
% identity
                  VACUOLAR ATP SYNTHASE SUBUNIT B ISOFORM 2 (V-ATPASE B
NCBI Description
                  SUBUNIT) >gi_459200 (U07053) vacuolar H+-ATPase subunit B
                  [Gossypium hirsutum]
                  415486
Seq. No.
                  uC-osflcyp175d01b1
Seq. ID
                  BLASTX
Method
                  g1729971
NCBI GI
                  529
BLAST score
                  6.0e-54
E value
                  150
Match length
                  73
% identity
                  TONOPLAST INTRINSIC PROTEIN, GAMMA (GAMMA TIP)
NCBI Description
                  (AQUAPORIN-TIP) >gi 1076745_pir__S52004 gamma-Tip protein -
                  rice >gi 473997_dbj_BAA05017_ (D25534) gamma-Tip [Oryza
                  sativa]
                  415487
Seq. No.
                  uC-osflcyp175d03b1
Seq. ID
                  BLASTX
Method
                  g3201627
NCBI GI
                  540
BLAST score
                  3.0e-55
E value
                  122
Match length
                  77
% identity
                  (AC004669) putative SWH1 protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   415488
Seq. ID
                  uC-osflcyp175d04b1
                  BLASTX
Method
                  q5080762
NCBI GI
BLAST score
                   382
                   1.0e-36
E value
                   179
Match length
                   44
% identity
                   (AC007203) Similar to retrotransposon polyprotein
NCBI Description
                   [Arabidopsis thaliana]
                   415489
Seq. No.
Seq. ID
                   uC-osflcyp175d08b1
                   BLASTX
Method
                   q4263775
NCBI GI
BLAST score
                   348
                   1.0e-32
E value
                   82
Match length
                   79
% identity
NCBI Description (AC006068) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   415490
                   uC-osflcyp175d09b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g4262242
BLAST score
                   468
                   9.0e-47
```

```
129
Match length
                  67
% identity
                  (AC006200) NADC homolog [Arabidopsis thaliana]
NCBI Description
                  415491
Seq. No.
Seq. ID
                  uC-osflcyp175d12b1
                  BLASTX
Method
NCBI GI
                  g82669
BLAST score
                  753
                  3.0e-80
E value
                  148
Match length
                  94
% identity
                  alcohol dehydrogenase (EC 1.1.1.1) 1 - maize
NCBI Description
                  >gi 22124_emb_CAA27681_ (X04049) alcohol dehydrogenase 1
                   [Zea mays]
                  415492
Seq. No.
                  uC-osflcyp175e01b1
Seq. ID
                  {\tt BLASTX}
Method
NCBI GI
                  g3980412
                  698
BLAST score
                  1.0e-73
E value
                  165
Match length
                  29
% identity
                  (AC004561) pumilio-like protein [Arabidopsis thaliana]
NCBI Description
                  415493
Seq. No.
Seq. ID
                  uC-osflcyp175e05b1
                  BLASTX
Method
                  g3236248
NCBI GI
BLAST score
                   417
                   8.0e-41
E value
                   96
Match length
                   81
% identity
                 (AC004684) unknown protein [Arabidopsis thaliana]
NCBI Description
                   415494
Seq. No.
Seq. ID
                  uC-osflcyp175e06b1
                  BLASTX
Method
NCBI GI
                  g1136122
BLAST score
                   666
                   4.0e-70
E value
                   125
Match length
% identity
NCBI Description (X91807) alfa-tubulin [Oryza sativa]
Seq. No.
                   415495
Seq. ID
                   uC-osflcyp175e07b1
Method
                   BLASTX
                   q5915821
NCBI GI
BLAST score
                   455
                   2.0e-45
E value
Match length
                   127
% identity
NCBI Description
                  CYTOCHROME P450 77A3 >gi 2739010 gb AAB94593 (AF022464)
                   CYP77A3p [Glycine max]
```

```
Seq. No.
                  415496
Seq. ID
                  uC-osflcyp175e10b1
Method
                  BLASTX
NCBI GI
                  q5912299
BLAST score
                  781
E value
                  1.0e-83
Match length
                  155
                  99
% identity
NCBI Description
                  (AJ133787) gigantea homologue [Oryza sativa]
                  415497
Seq. No.
Seq. ID
                  uC-osflcyp175e12b1
Method
                  BLASTX
NCBI GI
                  g3023713
BLAST score
                  455
E value
                  8.0e-59
Match length
                  123
% identity
                  91
NCBI Description
                  ENOLASE (2-PHOSPHOGLYCERATE DEHYDRATASE)
                   (2-PHOSPHO-D-GLYCERATE HYDRO-LYASE) (OSE1) >qi 780372
                   (U09450) enolase [Oryza sativa]
Seq. No.
                  415498
                  uC-osflcyp175f01b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2642213
BLAST score
                  223
E value
                  5.0e-18
Match length
                  89
% identity
                  52
                  (AF030385) nitrate-induced NOI protein [Zea mays]
NCBI Description
                  >gi_2895781 (AF045033) nitrate-induced NOI protein [Zea
                  mays]
                  415499
Seq. No.
Seq. ID
                  uC-osflcyp175f06b1
Method
                  BLASTX
NCBI GI
                  g5915857
BLAST score
                  581
E value
                  2.0e-66
Match length
                  149
                  87
% identity
                  CYTOCHROME P450 98A1 >gi 2766448 (AF029856) cytochrome P450
NCBI Description
                  CYP98A1 [Sorghum bicolor]
Seq. No.
                  415500
Seq. ID
                  uC-osflcyp175f07b1
Method
                  BLASTX
NCBI GI
                  g2224925
BLAST score
                  307
E value
                  5.0e-28
Match length
                  145
                  48
% identity
NCBI Description
                  (AF002678) kinesin-like protein [Arabidopsis thaliana]
Seq. No.
                  415501
Seq. ID
                  uC-osflcyp175f08b1
```

Method BLASTX NCBI GI q4582468 BLAST score 348 E value 1.0e-32 Match length 87 % identity 77 (AC007071) putative 40S ribosomal protein; contains NCBI Description C-terminal domain [Arabidopsis thaliana] 415502 Seq. No. uC-osflcyp175f09b1 Seq. ID BLASTX Method NCBI GI g115787 BLAST score 541 1.0e-55 E value 120 Match length 86 % identity CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I NCBI Description CAB-2) (LHCP) >gi_82461_pir__S03706 chlorophyll a/b-binding protein 2R precursor - rice >gi_20182_emb_CAA32109 (X13909) chlorophyll a/b-binding preprotein (AA -28 to 235) [Oryza sativa] 415503 Seq. No. Seq. ID uC-osflcyp175f10b1 BLASTX Method NCBI GI g2431769 BLAST score 279 E value 1.0e-24 Match length 110 % identity 56 (U62752) acidic ribosomal protein Pla [Zea mays] NCBI Description 415504 Seq. No. Seq. ID uC-osflcyp175f11b1 BLASTX Method NCBI GI q4417280 BLAST score 393 5.0e-38 E value Match length 133 58 % identity NCBI Description (AC007019) putative ATP synthase [Arabidopsis thaliana] Seq. No. 415505 Seq. ID uC-osflcyp175g04b1 Method BLASTX NCBI GI g2827529 BLAST score 431 2.0e-42 E value Match length 156 % identity 50 NCBI Description (AL021633) putative protein [Arabidopsis thaliana]

54248

415506

BLASTX

q5823570

uC-osflcyp175g06b1

Seq. No.

Seq. ID Method

NCBI GI

```
675
BLAST score
                  5.0e-71
E value
Match length
                  177
% identity
                  74
                  (AL049730) putative protein [Arabidopsis thaliana]
NCBI Description
                  415507
Seq. No.
Seq. ID
                  uC-osflcyp175g07b1
                  BLASTX
Method
NCBI GI
                  g4506891
BLAST score
                  214
                  4.0e-17
E value
                  72
Match length
                  47
% identity
                  SET translocation (myeloid leukemia-associated)
NCBI Description
                  >gi 346361 pir A45018 template activating factor-I, splice
                  form beta - human >gi 338039 (M93651) set [Homo sapiens]
                  415508
Seq. No.
Seq. ID
                  uC-osflcyp175g08b1
Method
                  BLASTX
NCBI GI
                  q4504909
                  373
BLAST score
                  1.0e-35
E value
Match length
                  160
                  49
% identity
                  karyopherin (importin) beta 3 >gi 2102696 (U72761)
NCBI Description
                  karyopherin beta 3 [Homo sapiens]
                  415509
Seq. No.
Seq. ID
                  uC-osflcyp175g11b1
                  BLASTX
Method
                  g2286153
NCBI GI
                  598
BLAST score
                  7.0e-80
E value
Match length
                  176
                  85
% identity
NCBI Description (AF007581) cytoplasmic malate dehydrogenase [Zea mays]
                  415510
Seq. No.
Seq. ID
                  uC-osflcyp175g12b1
Method
                  BLASTN
NCBI GI
                  q5410347
BLAST score
                  78
                  1.0e-35
E value
Match length
                  340
% identity
                  83
NCBI Description Sorghum bicolor BAC clone 110K5, partial sequence
                  415511
Seq. No.
Seq. ID
                  uC-osflcyp175h01b1
Method
                  BLASTX
NCBI GI
                  g118170
BLAST score
                  304
E value
                  1.0e-27
Match length
                  77
% identity
                  83
```

```
CYSTEINE PROTEINASE INHIBITOR-I (ORYZACYSTATIN-I)
NCBI Description
                  >gi 82491 pir A28464 oryzacystatin - rice >gi 169784
                  (J03469) oryzacystatin [Oryza sativa] >gi_169807 (M29259)
                  oryzastatin [Oryza sativa] >gi_259137_bbs_120195 (S49967)
                  oryzacystatin=cysteine protease inhibitor [Oryza=rice,
                  Peptide, 102 aa] [Oryza] >gi 1280613 (U54702) oryzacystatin
                  [Oryza sativa]
Seq. No.
                  415512
Seq. ID
                  uC-osflcyp175h05b1
                  BLASTX
Method
NCBI GI
                  q464988
                  325
BLAST score
E value
                  3.0e-30
                  63
Match length
                  97
% identity
                  UBIQUITIN-CONJUGATING ENZYME E2-17 KD 11 (UBIQUITIN-PROTEIN
NCBI Description
                  LIGASE 11) (UBIQUITIN CARRIER PROTEIN 11)
                  >gi_421856_pir__S32673 ubiquitin--protein ligase (EC
                  6.3.2.19) UBC11 - Arabidopsis thaliana (fragment)
                  >gi 297880 emb CAA78716 (Z14992) ubiquitin conjugating
                  enzyme [Arabidopsis thaliana] >gi 349215 (L00641) ubiquitin
                  conjugating enzyme [Arabidopsis thaliana]
                  415513
Seq. No.
                  uC-osflcyp175h07b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g129591
BLAST score
                  359
E value
                  3.0e-34
                  99
Match length
                  73
% identity
                  PHENYLALANINE AMMONIA-LYASE >qi 295824 emb CAA34226
NCBI Description
                  (X16099) phenylalanine ammonia-lyase [Oryza sativa]
Seq. No.
                  415514
                  uC-osflcyp175h08b1
Seq. ID
                  BLASTX
Method
NCBI GI
                  g3023816
BLAST score
                  466
                  7.0e-47
E value
Match length
                  108
                  90
% identity
                  GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC
NCBI Description
                  >gi 968996 (U31676) glyceraldehyde-3-phosphate
                  dehydrogenase [Oryza sativa]
Seq. No.
                  415515
                  uC-osflcyp176a02b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2119927
BLAST score
                  339
E value
                  1.0e-31
                  76
Match length
                  86
% identity
NCBI Description translation elongation factor G, chloroplast - soybean
```

415516 Seq. No. uC-osflcyp176a03b1 Seq. ID BLASTX Method g1174613 NCBI GI BLAST score 861 8.0e-93 E value 172 Match length 100 % identity 26S PROTEASE REGULATORY SUBUNIT 6A HOMOLOG (TAT-BINDING NCBI Description PROTEIN HOMOLOG 1) (TBP-1) >gi 556560 dbj BAA04614 (D17788) rice homologue of Tat binding protein [Oryza sativa] 415517 Seq. No. uC-osflcyp176a04b1 Seq. ID Method BLASTX g1076746 NCBI GI 675 BLAST score 4.0e-71 E value Match length 164 % identity 82 heat shock protein 70 - rice (fragment) NCBI Description >gi 763160 emb CAA47948 (X67711) heat shock protein 70 [Oryza sativa] 415518 Seq. No. Seq. ID uC-osflcyp176a05b1 BLASTX Method g5430752 NCBI GI 162 BLAST score 5.0e-11 E value Match length 125 39 % identity NCBI Description (AC007504) Hypothetical Protein [Arabidopsis thaliana] 415519 Seq. No. Seq. ID uC-osflcyp176a06b1 BLASTN Method g3550984 NCBI GI 33 BLAST score 2.0e-09 E value 73 Match length 86 % identity NCBI Description Oryza sativa mRNA for OsS5a, complete cds 415520 Seq. No. Seq. ID uC-osflcyp176a08b1 BLASTX Method g6006363 NCBI GI BLAST score 317 3.0e-29 E value Match length 66 92 % identity (AP000559) ESTs AU078183(C62904), C73912(E21020) correspond NCBI Description to a region of the predicted gene.; Similar to water stress inducible protein (U74296) [Oryza sativa]

```
415521
Seq. No.
Seq. ID
                  uC-osflcyp176a09b1
                  BLASTX
Method
NCBI GI
                  g2130069
                  327
BLAST score
                  3.0e-30
E value
                  73
Match length
                  88
% identity
                  catalase (EC 1.11.1.6) catA - rice
NCBI Description
                  >gi 1261858_dbj_BAA06232_ (D29966) catalase [Oryza sativa]
                  415522
Seq. No.
Seq. ID
                  uC-osflcyp176a12b1
                  BLASTX
Method
                  g3550985
NCBI GI
                  491
BLAST score
                  2.0e-49
E value
                  135
Match length
                  76
% identity
NCBI Description (AB010740) OsS5a [Oryza sativa]
                  415523
Seq. No.
Seq. ID
                  uC-osflcyp176b01b1
                  BLASTX
Method
NCBI GI
                  g4512667
                   345
BLAST score
                   2.0e-32
E value
                  172
Match length
                   47
% identity
NCBI Description (AC006931) putative MAP kinase [Arabidopsis thaliana]
                   415524
Seq. No.
                  uC-osflcyp176b03b1
Seq. ID
                  BLASTX
Method
NCBI GI
                   g2493147
                   527
BLAST score
                   1.0e-53
E value
                   126
Match length
                   86
% identity
NCBI Description VACUOLAR ATP SYNTHASE 16 KD PROTEOLIPID SUBUNIT >gi 857574
                   (U27098) H+-ATPase [Oryza sativa]
                   415525
Seq. No.
                   uC-osflcyp176b05b1
Seq. ID
                   BLASTX
Method
NCBI GI
                   q4468814
BLAST score
                   412
                   3.0e-40
E value
Match length
                   142
                   60
% identity
                  (AL035601) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   415526
                   uC-osflcyp176b06b1
Seq. ID
Method
                   BLASTX
                   g3834321
NCBI GI
                   698
BLAST score
```

NCBI GI

E value 8.0e-74Match length 156 83 % identity NCBI Description (AC005679) Strong similarity to F13P17.9 gi 3337356 transport protein SEC61 alpha subunit homolog from Arabidopsis thaliana BAC gb AC004481. [Arabidopsis thaliana] Seq. No. 415527 Seq. ID uC-osflcyp176b08b1 Method BLASTX NCBI GI q3935138 BLAST score 489 3.0e-49E value 189 Match length % identity 50 NCBI Description (AC005106) T25N20.2 [Arabidopsis thaliana] Seq. No. 415528 Seq. ID uC-osflcyp176b10b1 Method BLASTX NCBI GI g2829916 BLAST score 183 E value 5.0e-15 61 Match length 79 % identity (AC002291) Unknown protein [Arabidopsis thaliana] NCBI Description Seq. No. 415529 Seq. ID uC-osflcyp176b11b1 Method BLASTX NCBI GI g1706260 BLAST score 526 E value 1.0e-53 Match length 116 % identity 89 CYSTEINE PROTEINASE 1 PRECURSOR >gi 2118131 pir S59597 NCBI Description cysteine proteinase 1 precursor - maize >gi 643597 dbj BAA08244 (D45402) cysteine proteinase [Zea mays] 415530 Seq. No. uC-osflcyp176b12b1 Seq. ID Method BLASTX NCBI GI q1778095 317 BLAST score 4.0e-29 E value 88 Match length % identity 69 (U64903) putative sugar transporter; member of major NCBI Description facilitative superfamily; integral membrane protein [Beta vulgaris] 415531 Seq. No. Seq. ID uC-osflcyp176c04b1 Method BLASTX

54253

g3345477

```
BLAST score
                  664
                  9.0e-70
E value
Match length
                  126
% identity
                  100
NCBI Description (AB016283) carbonic anhydrase [Oryza sativa]
                  415532
Seq. No.
Seq. ID
                  uC-osflcyp176c06b1
Method
                  BLASTN
                  g4097337
NCBI GI
BLAST score
                  267
E value
                  1.0e-148
                  333
Match length
                  100
% identity
NCBI Description
                  Oryza sativa metallothionein-like protein mRNA, complete
                  cds
                  415533
Seq. No.
Seq. ID
                  uC-osflcyp176c07b1
Method
                  BLASTN
NCBI GI
                  g218141
BLAST score
                  96
E value
                  2.0e-46
Match length
                  263
                  92
% identity
NCBI Description Rice mRNA abundantly expressed at microspore stage
                  415534
Seq. No.
Seq. ID
                  uC-osflcyp176c08b1
Method
                  BLASTX
NCBI GI
                  g4666287
BLAST score
                  810
E value
                  8.0e-87
Match length
                  162
% identity
                  100
NCBI Description
                  (D85764) cytosolic monodehydroascorbate reductase [Oryza
                  sativa]
Seq. No.
                  415535
Seq. ID
                  uC-osflcyp176c09b1
Method
                  BLASTX
NCBI GI
                  g2244847
BLAST score
                  150
E value
                  2.0e-09
Match length
                  95
% identity
                  41
NCBI Description
                  (Z97337) hydroxyproline-rich glycoprotein homolog
                   [Arabidopsis thaliana]
Seq. No.
                  415536
Seq. ID
                  uC-osflcyp176c11b1
Method
                  BLASTX
NCBI GI
                  g2827544
BLAST score
                  358
                  7.0e - 34
E value
Match length
                  109
% identity
                  72
```

```
NCBI Description
                  (AL021635) HSP associated protein like [Arabidopsis
                  thaliana]
Seq. No.
                  415537
Seq. ID
                  uC-osflcyp176d01b1
                  BLASTX
Method
NCBI GI
                  q4586308
BLAST score
                  375
                  6.0e-44
E value
                  180
Match length
% identity
                  55
                  (AB025102) protoporphyrinogen IX oxidase [Glycine max]
NCBI Description
Seq. No.
                  415538
                  uC-osflcyp176d03b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g132105
                  769
BLAST score
E value
                  5.0e-82
Match length
                  163
                  90
% identity
                  RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
NCBI Description
                  (RUBISCO SMALL SUBUNIT C) >gi 68094 pir RKRZS9
                  ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                  precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_
                  (D00643) small subunit of ribulose-1,5-bisphosphate
                  carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364)
                  ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
                  sativa] >gi 226375 prf 1508256A ribulose bisphosphate
                  carboxylase S [Oryza sativa]
                  415539
Seq. No.
                  uC-osflcyp176d04b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2281633
BLAST score
                  288
                  2.0e-32
E value
Match length
                  114
                  62
% identity
NCBI Description
                  (AF003097) AP2 domain containing protein RAP2.4
                  [Arabidopsis thaliana]
Seq. No.
                  415540
Seq. ID
                  uC-osflcyp176d06b1
Method
                  BLASTX
NCBI GI
                  q2570515
BLAST score
                  479
E value
                  3.0e-48
Match length
                  111
% identity
                  83
NCBI Description
                  (AF022740) glycolate oxidase [Oryza sativa]
Seq. No.
                  415541
Seq. ID
                  uC-osflcyp176d07b1
Method
                  BLASTX
```

g5295966

162

NCBI GI BLAST score

6.0e-11 E value Match length 60 57 % identity (AB026295) Similar to Glycine max gmsti mRNA.(X79770) NCBI Description [Oryza sativa] 415542 Seq. No. Seq. ID uC-osflcyp176d09b1 Method BLASTX NCBI GI q1449179 673 BLAST score 9.0e-71 E value 179 Match length 74 % identity (D86506) N-ethylmaleimide sensitive fusion protein NCBI Description [Nicotiana tabacum] 415543 Seq. No. Seq. ID uC-osflcyp176d11b1 Method BLASTX NCBI GI q3511128 153 BLAST score 8.0e-10 E value 104 Match length 39 % identity (AF060858) unknown [Salmonella dublin] NCBI Description 415544 Seq. No. Seq. ID uC-osflcyp176e04b1 Method BLASTX q2499819 NCBI GI 748 BLAST score E value 1.0e-79 166 Match length % identity 87 ASPARTIC PROTEINASE ORYZASIN 1 PRECURSOR NCBI Description >gi_2130068_pir__S66516 aspartic proteinase 1 precursor rice >gi_1030715_dbj_BAA06876_ (D32165) aspartic protease [Oryza sativa] >gi 1711289 dbj BAA06875 (D32144) aspartic protease [Oryza sativa] Seq. No. 415545 Seq. ID uC-osflcyp176e07b1 BLASTX Method NCBI GI q5880464 BLAST score 641 4.0e-67 E value Match length 165 71 % identity (AF088901) actin bundling protein ABP135 [Lilium NCBI Description longiflorum] Seq. No. 415546 uC-osflcyp176e08b1 Seq. ID Method BLASTX NCBI GI g2465151 221 BLAST score

```
7.0e-18
E value
Match length
                  118
                  44
% identity
                  (Z99753) hypothetical protein [Schizosaccharomyces pombe]
NCBI Description
                  415547
Seq. No.
Seq. ID
                  uC-osflcyp176e09b1
                  BLASTX
Method
                  q4006871
NCBI GI
                  488
BLAST score
                  4.0e-49
E value
                  164
Match length
                  59
% identity
                  (Z99707) patatin-like protein [Arabidopsis thaliana]
NCBI Description
                  415548
Seq. No.
                  uC-osflcyp176e10b1
Seq. ID
                  BLASTX
Method
NCBI GI
                  q3024122
                   765
BLAST score
                  1.0e-81
E value
                  144
Match length
                  100
% identity
                  S-ADENOSYLMETHIONINE SYNTHETASE 2 (METHIONINE
NCBI Description
                  ADENOSYLTRANSFERASE 2) (ADOMET SYNTHETASE 2) >gi_1778821
                   (U82833) S-adenosyl-L-methionine synthetase [Oryza sativa]
                   415549
Seq. No.
Seq. ID
                   uC-osflcyp176e11b1
Method
                   BLASTX
                   q6063542
NCBI GI
                   655
BLAST score
                   9.0e-69
E value
                   150
Match length
% identity
                  (AP000615) EST C74302(E30840) corresponds to a region of
NCBI Description
                   the predicted gene.; similar to glyceraldehyde-3-phosphate
                   dehydrogenase. (M64118) [Oryza sativa]
Seq. No.
                   415550
Seq. ID
                   uC-osflcyp176e12b1
                   BLASTX
Method
                   q1197461
NCBI GI
                   824
BLAST score
                   2.0e-88
E value
Match length
                   172
                   87
% identity
                  (X78819) casein kinase I [Arabidopsis thaliana]
NCBI Description
                   415551
Seq. No.
                   uC-osflcyp176f02b1
Seq. ID
                   BLASTX
Method
NCBI GI
                   g2662343
BLAST score
                   747
                   2.0e-79
E value
Match length
                   150
                   97
% identity
```

Method

```
NCBI Description (D63581) EF-1 alpha [Oryza sativa]
                  415552
Seq. No.
Seq. ID
                  uC-osflcyp176f03b1
                  BLASTX
Method
NCBI GI
                  g1495251
                . 482
BLAST score
E value
                  2.0e-48
                  120
Match length
                  73
% identity
                 (Z70314) heat-shock protein [Arabidopsis thaliana]
NCBI Description
                  415553
Seq. No.
Seq. ID
                  uC-osflcyp176f05b1
                  BLASTX
Method
NCBI GI
                  g6015058
                  873
BLAST score
                  3.0e-94
E value
Match length
                  174
% identity
                  97
NCBI Description ELONGATION FACTOR 1-ALPHA (EF-1-ALPHA) >gi 2791834
                  (AF041463) elongation factor 1-alpha [Manihot esculenta]
                  415554
Seq. No.
Seq. ID
                  uC-osflcyp176f08b1
                  BLASTX
Method
                  g2832617
NCBI GI
BLAST score
                  319
                  2.0e-29
E value
Match length
                  120
% identity
                  54
NCBI Description (AL021711) putative protein [Arabidopsis thaliana]
Seq. No.
                  415555
Seq. ID
                  uC-osflcyp176f09b1
                  BLASTX
Method
                  g1944573
NCBI GI
BLAST score
                  413
                  2.0e-40
E value
Match length
                  90
                  88
% identity
NCBI Description (Z49146) phenylalanine ammonia-lyase [Hordeum vulgare]
                   415556
Seq. No.
Seq. ID
                  uC-osflcyp176f10b1
Method
                  BLASTN
NCBI GI
                  g6041757
BLAST score
                  393
                  0.0e+00
E value
Match length
                  461
% identity
                  96
NCBI Description Genomic Sequence For Oryza sativa Clone 10P20, Lemont
                  Strain, Complete Sequence, complete sequence
                   415557
Seq. No.
                  uC-osflcyp176f11b1
Seq. ID
                  BLASTX
```

```
NCBI GI
                  g3367523
BLAST score
                  259
                  3.0e-22
E value
Match length
                  86
% identity
                  57
NCBI Description (AC004392) ESTs gb AA728658 and gb_N95943 come from this
                  gene. [Arabidopsis thaliana]
                  415558
Seq. No.
                  uC-osflcyp176f12b1
Seq. ID
                  BLASTX
Method
                  g1421730
NCBI GI
BLAST score
                  771
                  6.0e-91
E value
                  182
Match length
% identity
NCBI Description (U43082) RF2 [Zea mays]
Seq. No.
                  415559
                  uC-osflcyp176g01b1
Seq. ID
                  BLASTX
Method
                  q5921647
NCBI GI
BLAST score
                   387
                   3.0e - 37
E value
                  120
Match length
                   62
% identity
NCBI Description (AF155332) flavonoid 3'-hydroxylase [Petunia x hybrida]
                   415560
Seq. No.
Seq. ID
                   uC-osflcyp176g03b1
Method
                   BLASTX
                   q602292
NCBI GI
                   350
BLAST score
                   7.0e-33
E value
Match length
                   139
% identity
NCBI Description (U17987) RCH2 protein [Brassica napus]
Seq. No.
                   415561
Seq. ID
                   uC-osflcyp176g04b1
                   BLASTX
Method
NCBI GI
                   g5912299
BLAST score
                   426
                   7.0e-42
E value
Match length
                   97
% identity
                   86
NCBI Description (AJ133787) gigantea homologue [Oryza sativa]
                   415562
Seq. No.
Seq. ID
                   uC-osflcyp176g05b1
Method
                   BLASTX
                   g6016438
NCBI GI
BLAST score
                   300
                   5.0e-27
E value
                   152
Match length
% identity
                   40
NCBI Description KINESIN HEAVY CHAIN (SYNKIN) >gi_2879849_emb_CAA12647_
```

(AJ225894) kinesin [Syncephalastrum racemosum]

```
415563
Seq. No.
Seq. ID
                  uC-osflcyp176g09b1
Method
                  BLASTX
NCBI GI
                  g2499497
BLAST score
                  165
                  2.0e-11
E value
                  89
Match length
% identity
                  46
                  PHOSPHOGLYCERATE KINASE, CHLOROPLAST PRECURSOR
NCBI Description
                  >gi 1161600_emb_CAA88841_ (Z48977) phosphoglycerate kinase
                   [Nicotiana tabacum]
                  415564
Seq. No.
Seq. ID
                  uC-osflcyp176g10b1
Method
                  BLASTX
NCBI GI
                  g417154
BLAST score
                  743
E value
                  4.0e-79
                  153
Match length
                  97
% identity
                  HEAT SHOCK PROTEIN 82 >gi 100685 pir S25541 heat shock
NCBI Description
                  protein 82 - rice (strain Taichung Native One)
                  >gi_20256_emb_CAA77978_ (Z11920) heat shock protein 82
                   (HSP82) [Oryza sativa]
                  415565
Seq. No.
Seq. ID
                  uC-osflcyp176g11b1
Method
                  BLASTX
NCBI GI
                  q4680212
BLAST score
                  150
E value
                  2.0e-09
Match length
                  39
                  77
% identity
NCBI Description
                  (AF114171) hypothetical protein [Sorghum bicolor]
Seq. No.
                  415566
Seq. ID
                  uC-osflcyp176g12b1
Method
                  BLASTX
NCBI GI
                  g3668089
BLAST score
                  145
                  7.0e-09
E value
Match length
                  48
% identity
                  67
NCBI Description
                  (AC004667) unknown protein [Arabidopsis thaliana]
Seq. No.
                  415567
Seq. ID
                  uC-osflcyp176h01b1
Method
                  BLASTX
NCBI GI
                  g585551
BLAST score
                  186
E value
                  3.0e-14
Match length
                  78
% identity
                  55
NCBI Description
                  NUCLEOSIDE DIPHOSPHATE KINASE I (NDK I) (NDP KINASE I)
                  >gi 629798 pir S43330 nucleoside-diphosphate kinase (EC
```

```
nucleoside diphosphate kinase [Oryza sativa]
Seq. No.
                  415568
Seq. ID
                  uC-osflcyp176h02b1
Method
                  BLASTX
                  a2129840
NCBI GI
BLAST score
                  503
                  6.0e-51
E value
                  153
Match length
                  63
% identity
NCBI Description
                  nucleosome assembly protein 1 - soybean >gi 1161252
                   (L38856) nucleosome assembly protein 1 [Glycine max]
                  415569
Seq. No.
Seq. ID
                  uC-osflcyp176h04b1
Method
                  BLASTX
NCBI GI
                  q5042444
BLAST score
                  341
                  5.0e-32
E value
                   98
Match length
                  73
% identity
NCBI Description
                  (AC007789) putative low molecular early light-inducible
                  protein [Oryza sativa]
                  415570
Seq. No.
Seq. ID
                  uC-osflcyp176h05b1
Method
                  BLASTX
NCBI GI
                  g3123745
BLAST score
                   368
                   5.0e - 35
E value
                  170
Match length
                   46
% identity
                  (AB013447) aluminum-induced [Brassica napus]
NCBI Description
Seq. No.
                   415571
Seq. ID
                  uC-osflcyp176h06b1
Method
                  BLASTX
NCBI GI
                  g4218120
BLAST score
                   421
E value
                   3.0e-41
                   99
Match length
                   81
% identity
NCBI Description
                   (AL035353) Proline-rich APG-like protein [Arabidopsis
                   thaliana]
                   415572
Seq. No.
                  uC-osflcyp176h08b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g120510
BLAST score
                  334
                   4.0e-31
E value
Match length
                  92
                  74
% identity
                  FERRITIN 2 PRECURSOR >gi 82688 pir S24057 ferritin
NCBI Description
                  precursor (clone FM2) - maize >gi 22278 emb CAA43664
```

2.7.4.6) - rice >gi 303849 dbj BAA03798 (D16292)

(X61392) ferritin [Zea mays]

Method

BLASTX

```
Seq. No.
                  415573
Seq. ID
                  uC-osflcyp176h09b1
                  BLASTX
Method
NCBI GI
                  g2979554
                  358
BLAST score
                  7.0e - 34
E value
                  160
Match length
% identity
                  51
                  (AC003680) CDC4 like protein [Arabidopsis thaliana]
NCBI Description
                   415574
Seq. No.
Seq. ID
                  uC-osflcyp176h10b1
                  BLASTX
Method
                  g5915836
NCBI GI
BLAST score
                   449
                  2.0e-44
E value
Match length
                  134
                   60
% identity
NCBI Description
                  CYTOCHROME P450 71D7 >gi 1762144 (U48435) putative
                  cytochrome P450 [Solanum chacoense]
                   415575
Seq. No.
Seq. ID
                  uC-osflcyp176h12b1
Method
                  BLASTX
                  g2129921
NCBI GI
BLAST score
                  179
                   6.0e-13
E value
Match length
                   51
% identity
                   67
                  hypothetical protein 1 - Madagascar periwinkle >gi 758694
NCBI Description
                   (U12573) putative [Catharanthus roseus]
Seq. No.
                   415576
Seq. ID
                   uC-osflcyp177a02b1
Method
                   BLASTX
NCBI GI
                   g3789948
BLAST score
                   474
E value
                   1.0e-47
Match length
                   95
                   94
% identity
NCBI Description (AF094773) translation initiation factor 5A [Oryza sativa]
Seq. No.
                   415577
Seq. ID
                   uC-osflcyp177a03b1
Method
                   BLASTX
NCBI GI
                   g2454182
BLAST score
                   163
                   4.0e-11
E value
Match length
                   37
                   78
% identity
                  (U80185) pyruvate dehydrogenase E1 alpha subunit
NCBI Description
                   [Arabidopsis thaliana]
                   415578
Seq. No.
                   uC-osflcyp177a04b1
Seq. ID
```

```
NCBI GI
                  g2493147
BLAST score
                  185
E value
                  2.0e-14
                  44
Match length
                  86
% identity
                  VACUOLAR ATP SYNTHASE 16 KD PROTEOLIPID SUBUNIT >gi 857574
NCBI Description
                  (U27098) H+-ATPase [Oryza sativa]
                  415579
Seq. No.
Seq. ID
                  uC-osflcyp177a05a1
                  BLASTN
Method
                  g1173556
NCBI GI
                  207
BLAST score
                  1.0e-113
E value
                  223
Match length
                  99
% identity
NCBI Description Oryza sativa Ory s 1 mRNA, complete cds
                  415580
Seq. No.
Seq. ID
                  uC-osflcyp177a05b1
Method
                  BLASTX
                  g1171008
NCBI GI
                  242
BLAST score
                  8.0e-21
E value
                  71
Match length
                  63
% identity
                  POLLEN ALLERGEN PHL P 1 PRECURSOR (PHL P I)
NCBI Description
                  >gi_629812_pir__S44182 allergen Phl p I - common timothy
                  >gi_473360_emb_CAA55390_ (X78813) Phl p I allergen [Phleum
                  pratense]
                  415581
Seq. No.
                  uC-osflcyp177a08b1
Seq. ID
                  BLASTX
Method
NCBI GI
                  q4126809
BLAST score
                  234
E value
                  3.0e-19
                  47
Match length
% identity
                  96
NCBI Description (AB017042) glyoxalase I [Oryza sativa]
Seq. No.
                  415582
                  uC-osflcyp177a09b1
Seq. ID
                  BLASTX
Method
NCBI GI
                  q445605
BLAST score
                  148
                  2.0e-09
E value
                  72
Match length
                   46
% identity
NCBI Description heat shock protein hsp70 [Pisum sativum]
Seq. No.
                   415583
Seq. ID
                  uC-osflcyp177a11a1
Method
                  BLASTN
NCBI GI
                  g218144
                  207
BLAST score
                  1.0e-113
E value
```

```
218
Match length
                  99
% identity
NCBI Description Rice mRNA for ATP/ADP translocator, complete cds
                  415584
Seq. No.
Seq. ID
                  uC-osflcyp177b04b1
Method
                  BLASTX
NCBI GI
                  g5640111
                  294
BLAST score
E value
                  3.0e-26
Match length
                  74
% identity
                  80
NCBI Description (AJ243875) RAD23 protein [Lycopersicon esculentum]
                  415585
Seq. No.
                  uC-osflcyp177b05b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3821793
BLAST score
                  707
                  7.0e-75
E value
Match length
                  158
% identity
                  84
NCBI Description (Y11526) casein kinase II alpha subunit [Zea mays]
                  415586
Seq. No.
                  uC-osflcyp177b06a1
Seq. ID
Method
                  BLASTN
NCBI GI
                  q4079797
BLAST score
                  125
                  7.0e-64
E value
Match length
                  199
% identity
                  99
                  Oryza sativa 23 kDa polypeptide of photosystem II mRNA,
NCBI Description
                  complete cds
                   415587
Seq. No.
Seq. ID
                  uC-osflcyp177b06b1
                  BLASTX
Method
                  g2570499
NCBI GI
BLAST score
                  143
                   3.0e-09
E value
                   40
Match length
                   70
% identity
                  (AF022732) 23kDa polypeptide of photosystem II [Oryza
NCBI Description
                   sativa]
                   415588
Seq. No.
                   uC-osflcyp177b07b1
Seq. ID
                  BLASTX
Method
                   g132819
NCBI GI
BLAST score
                   369
                   7.0e-39
E value
                   149
Match length
                   61
% identity
                   50S RIBOSOMAL PROTEIN L24, CHLOROPLAST PRECURSOR (CL24)
NCBI Description
                   >gi_71307_pir__R5PM24 ribosomal protein L24 precursor,
                   chloroplast - garden pea >gi_20873_emb_CAA32185_ (X14020)
```

Seq. No.

Seq. ID Method 415594

BLASTX

uC-osflcyp177c03b1

```
CL24 ribosomal preprotein (AA -39 to 155) [Pisum sativum]
                  415589
Seq. No.
                  uC-osflcyp177b08a1
Seq. ID
Method
                  BLASTN
                  g218144
NCBI GI
                  272
BLAST score
                  1.0e-151
E value
                  283
Match length
                  99
% identity
NCBI Description Rice mRNA for ATP/ADP translocator, complete cds
                  415590
Seq. No.
                  uC-osflcyp177b08b1
Seq. ID
                  BLASTX
Method
NCBI GI
                  g485517
                  666
BLAST score
                  5.0e-70
E value
                  131
Match length
                  100
% identity
NCBI Description ADP, ATP carrier protein - rice
                   415591
Seq. No.
                  uC-osflcyp177b12b1
Seq. ID
                  BLASTX
Method
                   q4185515
NCBI GI
                   300
BLAST score
                   4.0e-27
E value
                  85
Match length
                   68
% identity
                   (AF102824) actin depolymerizing factor 6 [Arabidopsis
NCBI Description
                   thaliana] >gi_6007773 gb_AAF01035.1 AF183576 1 (AF183576)
                   actin depolymerizing factor 6 [Arabidopsis thaliana]
                   415592
Seq. No.
Seq. ID
                   uC-osflcyp177c01b1
                   BLASTX
Method
                   g1164988
NCBI GI
                   401
BLAST score
                   7.0e-39
E value
                   137
Match length
                   60
% identity
                  (X94335) YOR3513c [Saccharomyces cerevisiae]
NCBI Description
                   415593
Seq. No.
Seq. ID
                   uC-osflcyp177c02b1
                   BLASTX
Method
                   q6014701
NCBI GI
                   360
BLAST score
                   3.0e-41
E value
Match length
                   152
% identity
                  (AF190450) enoyl-CoA-hydratase [Avicennia marina]
NCBI Description
```

```
NCBI GI
                   g633110
                   645
BLAST score
                   2.0e-67
E value
                   189
Match length
                   72
% identity
                  (D31843) plasma membrane H+-ATPase [Oryza sativa]
NCBI Description
                   415595
Seq. No.
Seq. ID
                   uC-osflcyp177c04b1
Method
                   BLASTX
                   g2982459
NCBI GI
BLAST score
                   300
                   4.0e-33
E value
                   133
Match length
                   57
% identity
                  (AL022223) putative protein [Arabidopsis thaliana]
NCBI Description
                   415596
Seq. No.
Seq. ID
                   uC-osflcyp177c05b1
                   BLASTN
Method
                   g2618602
NCBI GI
                   45
BLAST score
                   7.0e-16
E value
                   85
Match length
                   88
% identity
                   Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                   MSJ1, complete sequence
                   415597
Seq. No.
Seq. ID
                   uC-osflcyp177c07b1
Method
                   BLASTX
NCBI GI
                   q4567246
BLAST score
                   336
E value
                   3.0e-31
                   107
Match length
% identity
                   64
                   (AC007070) unknown protein [Arabidopsis thaliana]
NCBI Description
                   415598
Seq. No.
Seq. ID
                   uC-osflcyp177c10b1
Method
                   BLASTX
NCBI GI
                   q4337177
BLAST score
                   545
                   8.0e-56
E value
                   154
Match length
% identity
                   (AC006416) Identical to gb Y10557 g5bf gene from
NCBI Description
                   Arabidopsis thaliana. ESTs gb R30578, gb R90475,
                   gb T22384, gb T22425, gb N6493\overline{4} and gb T4\overline{67}67 come from
                   this gene. [Arabidopsis thaliana]
                   415599
Seq. No.
Seq. ID
                   uC-osflcyp177c12b1
Method
                   BLASTX
                   g2495180
NCBI GI
BLAST score
                   475
                   1.0e-47
E value
```

```
Match length
                  122
% identity
                  71
                  PORPHOBILINOGEN DEAMINASE PRECURSOR (PBG)
NCBI Description
                   (HYDROXYMETHYLBILANE SYNTHASE) (HMBS) (PRE-UROPORPHYRINOGEN
                  SYNTHASE) >gi_421882_pir__S35873 hydroxymethylbilane
                  synthase (EC 4.3.1.8) - garden pea >gi_541971_pir__JQ2278
                  hydroxymethylbilane synthase (EC 4.3.1.8) precursor -
                  garden pea chloroplast >gi_313724_emb_CAA51820_ (X73418)
                  hydroxymethylbilane synthase [Pisum sativum]
                  415600
Seq. No.
Seq. ID
                  uC-osflcyp177d01b1
Method
                  BLASTX
                  g2642648
NCBI GI
                  846
BLAST score
                   5.0e-91
E value
                  187
Match length
                   89
% identity
                   (AF033852) cytosolic heat shock 70 protein; HSC70-3
NCBI Description
                   [Spinacia oleracea] >gi_2660768 (AF034616) cytosolic heat
                   shock 70 protein [Spinacia oleracea] >gi_2660770 (AF034617)
                   cytosolic heat shock 70 protein [Spinacia oleracea]
                   415601
Seq. No.
                   uC-osflcyp177d02b1
Seq. ID
                   BLASTX
Method
                   g2829887
NCBI GI
                   247
BLAST score
                   4.0e-21
E value
Match length
                   74
                   58
% identity
                  (AC002396) Hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   415602
Seq. No.
Seq. ID
                   uC-osflcyp177d07b1
                   BLASTX
Method
                   g5668770
NCBI GI
BLAST score
                   146
                   4.0e-09
E value
Match length
                   118
                   43
% identity
                  (AC005916) T17H3.9 [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   415603
Seq. ID
                   uC-osflcyp177d08b1
Method
                   BLASTX
                   g5915857
NCBI GI
BLAST score
                   498
                   2.0e-50
E value
Match length
                   137
                   71
% identity
NCBI Description CYTOCHROME P450 98A1 >gi_2766448 (AF029856) cytochrome P450
                   CYP98A1 [Sorghum bicolor]
                   415604
Seq. No.
                   uC-osflcyp177d09b1
Seq. ID
```

BLASTX

Method

Seq. ID

```
NCBI GI
                  g2440029
BLAST score
                  207
                  2.0e-16
E value
Match length
                  59
% identity
                  64
                  (Y14851) DAL1 protein [Arabidopsis thaliana]
NCBI Description
                  >gi 2440031 emb CAA75115 (Y14850) DAL1 protein
                  [Arabidopsis thaliana]
                  415605
Seq. No.
                  uC-osflcyp177d10b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2493318
                  323
BLAST score
E value
                  8.0e-30
                  116
Match length
% identity
                  53
                  BLUE COPPER PROTEIN PRECURSOR >qi 562779 emb CAA80963
NCBI Description
                  (Z25471) blue copper protein [Pisum sativum]
                  >gi 1098264 prf 2115352A blue Cu protein [Pisum sativum]
                  415606
Seq. No.
                  uC-osflcyp177d12b1
Seq. ID
Method
                  BLASTX
                  q1085650
NCBI GI
BLAST score
                  206
                  3.0e-16
E value
                  54
Match length
% identity
                  78
                  aspartate transcarbomoylase - wheat >gi 688218 bbs 156442
NCBI Description
                  aspartate carbamoyltransferase {C-terminal} {EC 2.1.3.2}
                   [Triticum aestivum=wheat, avalon, seedlings, Peptide
                  Partial, 233 aa]
                  415607
Seq. No.
                  uC-osflcyp177e03b1
Seq. ID
Method
                  BLASTX
                  q1698548
NCBI GI
                  204
BLAST score
                  8.0e-16
E value
Match length
                  144
                  33
% identity
                  (U58971) calmodulin-binding protein [Nicotiana tabacum]
NCBI Description
Seq. No.
                  415608
                  uC-osflcyp177e04b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3334138
BLAST score
                  173
                  1.0e-12
E value
Match length
                  91
                  43
% identity
NCBI Description
                  CALNEXIN HOMOLOG PRECURSOR >gi 669003 (U20502) calnexin
                  [Glycine max]
                   415609
Seq. No.
```

54268

uC-osflcyp177e10b1

BLASTX Method g4582787 NCBI GI BLAST score 284 2.0e-25 E value 76 Match length 75 % identity NCBI Description (AJ012281) adenosine kinase [Zea mays] 415610 Seq. No. uC-osflcyp177e11b1 Seq. ID BLASTX Method g3258570 NCBI GI 263 BLAST score 6.0e-23 E value 64 Match length 75 % identity NCBI Description (U89959) Unknown protein [Arabidopsis thaliana] 415611 Seq. No. uC-osflcyp177f02a1 Seq. ID Method BLASTN NCBI GI q3986152 298 BLAST score 1.0e-167 E value 346 Match length 98 % identity NCBI Description Oryza sativa gene for plastidic ATP sulfurylase, complete cds 415612 Seq. No. Seq. ID uC-osflcyp177f02b1 BLASTX Method q4063821 NCBI GI 469 BLAST score E value 4.0e-47 Match length 104 87 % identity NCBI Description (AB015204) plastidic ATP sulfurylase [Oryza sativa] 415613 Seq. No. Seq. ID uC-osflcyp177f04b1 BLASTX Method NCBI GI q2407281 562 BLAST score 6.0e-58 E value 130 Match length 82 % identity NCBI Description (AF017363) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa] Seq. No. 415614 Seq. ID uC-osflcyp177f05b1 BLASTX Method NCBI GI q3901094 BLAST score 302 1.0e-27 E value Match length 96

```
% identity
                  (Z27090) pollen allergen Phl pI [Phleum pratense]
NCBI Description
                  415615
Seq. No.
Seq. ID
                  uC-osflcyp177f07a1
Method
                  BLASTN
                  q1574943
NCBI GI
BLAST score
                  287
                  1.0e-160
E value
                  326
Match length
                  47
% identity
NCBI Description Oryza sativa polyubiquitin (Rubq1) mRNA, complete cds
                  415616
Seq. No.
Seq. ID
                  uC-osflcyp177f07b1
                  BLASTX
Method
                  g1332579
NCBI GI
BLAST score
                  554
E value
                  7.0e-57
Match length
                  111
                  10
% identity
                  (X98063) polyubiquitin [Pinus sylvestris]
NCBI Description
                  415617
Seq. No.
Seq. ID
                  uC-osflcyp177f11b1
                  BLASTX
Method
NCBI GI
                  g1362009
BLAST score
                  400
                  6.0e-39
E value
Match length
                  93
% identity
                  52
NCBI Description ubiquitin-like protein 7 - Arabidopsis thaliana
                  415618
Seq. No.
Seq. ID
                  uC-osflcyp177g01a1
Method
                  BLASTX
                  q4884864
NCBI GI
                  171
BLAST score
                  4.0e-12
E value
Match length
                  43
                  74
% identity
NCBI Description
                  (AF133530) water channel protein MipH [Mesembryanthemum
                  crystallinum]
Seq. No.
                  415619
Seq. ID
                  uC-osflcyp177g02b1
                  BLASTX
Method
NCBI GI
                  g4678933
BLAST score
                  240
                  5.0e-20
E value
Match length
                  70
% identity
                  (AL049711) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  415620
Seq. ID
                  uC-osflcyp177g06a1
Method
                  BLASTX
```

```
g444790
NCBI GI
BLAST score
                  166
                  1.0e-11
E value
                  50
Match length
                  70
% identity
                  nucleotide translocator [Arabidopsis thaliana]
NCBI Description
                  415621
Seq. No.
                  uC-osflcyp177g07b1
Seq. ID
                  BLASTX
Method
                  q4567201
NCBI GI
                   374
BLAST score
                  8.0e-36
E value
                  102
Match length
                   70
% identity
                   (AC007168) putative aspartate aminotransferase [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   415622
                   uC-osflcyp177g10b1
Seq. ID
                   BLASTX
Method
                   q1171008
NCBI GI
                   232
BLAST score
E value
                   2.0e-19
Match length
                   76
                   54
% identity
                   POLLEN ALLERGEN PHL P 1 PRECURSOR (PHL P I)
NCBI Description
                   >gi 629812 pir S44182 allergen Phl p I - common timothy
                   >gi 473360 emb CAA55390 (X78813) Phl p I allergen [Phleum
                   pratense]
Seq. No.
                   415623
                   uC-osflcyp177g11b1
Seq. ID
                   BLASTX
Method
NCBI GI
                   g5912299
BLAST score
                   487
                   2.0e-49
E value
                   101
Match length
                   97
% identity
                  (AJ133787) gigantea homologue [Oryza sativa]
NCBI Description
Seq. No.
                   415624
                   uC-osflcyp177g12a1
Seq. ID
                   BLASTN
Method
NCBI GI
                   g5360229
BLAST score
                   170
                   9.0e-91
E value
Match length
                   230
                   93
% identity
NCBI Description Oryza sativa mRNA for Ran, complete cds
                   415625
Seq. No.
                   uC-osflcyp177g12b1
Seq. ID
                   BLASTN
Method
                   g2407280
NCBI GI
                   62
BLAST score
                   3.0e-26
E value
```

```
214
Match length
% identity
                  Oryza sativa ribulose 1,5-bisphosphate carboxylase small
NCBI Description
                  subunit mRNA, complete cds
Seq. No.
                  415626
Seq. ID
                  uC-osflcyp177h01b1
                  BLASTX
Method
NCBI GI
                  q3075488
BLAST score
                  430
                  7.0e-64
E value
                  139
Match length
                  92
% identity
                  (AF058796) chlorophyll a/b-binding protein [Oryza sativa]
NCBI Description
                  415627
Seq. No.
Seq. ID
                  uC-osflcyp177h06b1
                  BLASTX
Method
NCBI GI
                  g1173218
BLAST score
                  287
                  4.0e-26
E value
                  59
Match length
                  93
% identity
                  40S RIBOSOMAL PROTEIN S15A >gi 440824 (L27461) ribosomal
NCBI Description
                  protein S15 [Arabidopsis thaliana] >gi 2150130 (AF001412)
                  cytoplasmic ribosomal protein S15a [Arabidopsis thaliana]
                  415628
Seq. No.
Seq. ID
                  uC-osflcyp177h08b1
Method
                  BLASTX
NCBI GI
                  q549063
                   305
BLAST score
                   4.0e-28
E value
                   58
Match length
% identity
                   98
                  TRANSLATIONALLY CONTROLLED TUMOR PROTEIN HOMOLOG (TCTP)
NCBI Description
                   >gi 1072464 pir A38958 IgE-dependent histamine-releasing
                   factor homolog - rice >gi 303835 dbj BAA02151 (D12626)
                   21kd polypeptide [Oryza sativa]
                   415629
Seq. No.
Seq. ID
                   uC-osflcyp177h09a1
                   BLASTX
Method
NCBI GI
                   q4895194
BLAST score
                   188
E value
                   4.0e-14
Match length
                   84
                   43
% identity
NCBI Description
                   (AC007661) putative peptide transporter protein
                   [Arabidopsis thaliana]
Seq. No.
                   415630
Seq. ID
                   uC-osflcyp177h09b1
Method
                   BLASTX
                   q2160144
NCBI GI
BLAST score
                   359
                   5.0e - 34
E value
```

```
161
Match length
                 41
% identity
                 (AC000375) Strong similarity to Arabidopsis oligopeptide
NCBI Description
                 transporter (gb_X77503). [Arabidopsis thaliana]
                 415631
Seq. No.
                 uC-osflcyp177h10a1
Seq. ID
Method
                 BLASTN
                 g2613142
NCBI GI
                 257
BLAST score
E value
                 1.0e-142
                 273
Match length
                 99
% identity
NCBI Description Oryza sativa tubulin (RiP3) mRNA, complete cds
                  415632
Seq. No.
                 uC-osflcyp177h10b1
Seq. ID
                 BLASTX
Method
                  g1136120
NCBI GI
                  684
BLAST score
E value
                  4.0e-72
Match length
                  130
% identity
                  98
NCBI Description (X91806) alpha-tubulin [Oryza sativa]
                  415633
Seq. No.
                  uC-osflcyp177h11b1
Seq. ID
Method
                  BLASTX
                  q1706260
NCBI GI
                  606
BLAST score
                  6.0e-63
E value
Match length
                  130
                  89
% identity
                 CYSTEINE PROTEINASE 1 PRECURSOR >gi_2118131_pir __S59597
NCBI Description
                  cysteine proteinase 1 precursor - maize
                  >gi_643597_dbj_BAA08244_ (D45402) cysteine proteinase [Zea
                  mays]
                  415634
 Seq. No.
                  uC-osflcyp178a01b1
 Seq. ID
                  BLASTX
Method
                  g2431767
NCBI GI
                  357
BLAST score
                  7.0e-34
E value
                  120
Match length
 % identity
NCBI Description (U62751) acidic ribosomal protein P3a [7ea ma ]
                  415635
 Seq. No.
                  uC-osflcyp178a02a1
 Seq. ID
                  BLASTX
 Method
                  g2754849
 NCBI GI
                  217
 BLAST score
                  2.0e-17
 E value
                  51
 Match length
                  82
 % identity
```

[Fritillaria agrestis]

Seq. No. 415636 uC-osflcyp178a04a1 Seq. ID Method BLASTN NCBI GI g409782 BLAST score 106 1.0e-52 E value Match length 235 87 % identity NCBI Description Rice mRNA for ferredoxin-NADP+ reductase, complete cds 415637 Seq. No. uC-osflcyp178a04b1 Seq. ID Method BLASTX NCBI GI g6091723 BLAST score 436 4.0e-43 E value Match length 154 57 % identity NCBI Description (AC010797) hypothetical protein [Arabidopsis thaliana] Seq. No. 415638 uC-osflcyp178a05b1 Seq. ID BLASTX Method g2832618 NCBI GI 341 BLAST score 4.0e-32 E value 102 Match length 35 % identity NCBI Description (AL021711) putative protein [Arabidopsis thaliana] 415639 Seq. No. uC-osflcyp178a07b1 Seq. ID BLASTX Method g3878874 NCBI GI 303 BLAST score 2.0e-27 E value 147 Match length 44% identity NCBI Description (Z69793) R03A10.3 [Caenorhabditis elegans] 415640 Seq. No. uC-osflcyp178a08b1 Seq. ID BLASTN Method g3341647 NCBI GI 39 BLAST score 2.0e-12 E value 145 Match length 88 % identity NCBI Description Zea mays Ama gene encoding single-subunit RNA polymerase 415641 Seq. No. Seq. ID uC-osflcyp178a09b1 BLASTX Method NCBI GI q2565305 BLAST score 454

Seq. ID

Method

```
4.0e-45
E value
                   93
Match length
                   91
% identity
                   (AF024589) glycine decarboxylase P subunit [Hordeum sp. x
NCBI Description
                   Triticum sp.]
                   415642
Seq. No.
                   uC-osflcyp178a10a1
Seq. ID
Method
                   BLASTX
                   q729478
NCBI GI
BLAST score
                   401
                   5.0e-39
E value
                   87
Match length
                   90
% identity
                   FERREDOXIN--NADP REDUCTASE, LEAF ISOZYME PRECURSOR (FNR)
NCBI Description
                   >gi 442481_dbj_BAA04616_ (D17790) ferredoxin-NADP+
                   reductase [Oryza sativa] >gi_6069649_dbj_BAA85425.1
                   (AP000616) ESTs AU078647(E15\overline{5}7),C724\overline{0}0(E\overline{1}557) correspond to
                   a region of the predicted gene.; similar to
                   ferredoxin-NADP+ reductase (D17790) [Oryza sativa]
Seq. No.
                   415643
                   uC-osflcyp178a10b1
Seq. ID
Method
                   BLASTX
                   q4586449
NCBI GI
                   348
BLAST score
                   1.0e-32
E value
                   75
Match length
                   80
% identity
                   (AB025187) cytochrome c oxidase subunit 6b-1 [Oryza sativa]
NCBI Description
Seq. No.
                   415644
                   uC-osflcyp178a12b1
Seq. ID
                   BLASTX
Method
                   q4584525
NCBI GI
                   332
BLAST score
                   3.0e-31
E value
                   96
Match length
                   64
% identity
                   (AL049607) protein phosphatase 2C-like protein [Arabidopsis
NCBI Description
                   thaliana]
                   415645
Seq. No.
Seq. ID
                   uC-osflcyp178b01a1
                   BLASTX
Method
                   g4249382
NCBI GI
BLAST score
                   346
                   2.0e-32
E value
                   85
Match length
                   72
% identity
                   (AC005966) Strong similarity to gi 3337350 F13P17.3
NCBI Description
                   putative permease from Arabidopsis thaliana BAC
                   gb_AC004481. [Arabidopsis thaliana]
                    415646
Seq. No.
```

54275

uC-osflcyp178b02b1

BLASTX

```
q4467145
NCBI GI
                  192
BLAST score
                  1.0e-16
E value
                  89
Match length
                  53
% identity
                  (AL035540) farnesylated protein (ATFP6) [Arabidopsis
NCBI Description
                  thaliana]
                  415647
Seq. No.
                  uC-osflcyp178b03a1
Seq. ID
                  BLASTX
Method
                  g1345881
NCBI GI
                  289
BLAST score
                  7.0e-26
E value
                  64
Match length
                  89
% identity
                  CYTOCHROME B5 >gi_1076743 pir__S46307 cytochrome b5 - rice
NCBI Description
                  >gi 414705 emb_CAA53366_ (X75670) cytochrome b5 [Oryza
                  sativa]
                   415648
Seq. No.
                  uC-osflcyp178b03b1
Seq. ID
                  BLASTX
Method
                  g5921189
NCBI GI
                   154
BLAST score
                   2.0e-22
E value
                   130
Match length
                   45
% identity
                  CYTOCHROME P450 71C4 >gi_550542_emb_CAA57425_ (X81831)
NCBI Description
                   cytochrome P450 [Zea mays] >gi 1850903_emb_CAA72196_
                   (Y11368) cytochrome p450 [Zea mays]
                   415649
Seq. No.
                   uC-osflcyp178b04b1
Seq. ID
                   BLASTX
Method
                   g3935170
NCBI GI
                   480
BLAST score
                   3.0e-48
E value
                   157
Match length
                   57
% identity
                  (AC004557) F17L21.13 [Arabidopsis thaliana]
NCBI Description
                   415650
Seq. No.
                   uC-osflcyp178b05b1
Seq. ID
                   BLASTX
Method
                   q6091723
NCBI GI
                   492
BLAST score
                   1.0e-49
E value
                   160
Match length
                   59
 % identity
NCBI Description (AC010797) hypothetical protein [Arabidopsis thaliana]
                   415651
Seq. No.
                   uC-osflcyp178b08b1
Seq. ID
                   BLASTX
Method
                   q3738182
NCBI GI
BLAST score
                   217
```

```
2.0e-17
E value
                  145
Match length
                  34
% identity
NCBI Description (AL031854) probable t-complex protein 1, theta subunit
                  [Schizosaccharomyces pombe]
                  415652
Seq. No.
                  uC-osflcyp178b12a1
Seq. ID
                  BLASTN
Method
                  g1154858
NCBI GI
                  82
BLAST score
                  5.0e-38
E value
                  173
Match length
                  87
% identity
NCBI Description H.vulgare mRNA for L24 ribosomal protein
                   415653
Seq. No.
                  uC-osflcyp178c01a1
Seq. ID
                  BLASTX
Method
                   g1351014
NCBI GI
                   220
BLAST score
                   7.0e-18
E value
                   43
Match length
                   98
% identity
                  40S RIBOSOMAL PROTEIN S8 >gi 968902_dbj_BAA07207_ (D38010)
NCBI Description
                   ribosomal protein S8 [Oryza sativa]
                   415654
Seq. No.
                   uC-osflcyp178c01b1
Seq. ID
                   BLASTX
Method
                   q4582436
NCBI GI
BLAST score
                   147
                   3.0e-09
E value
                   66
Match length
                   53
% identity
NCBI Description (AC007196) unknown protein [Arabidopsis thaliana]
                   415655
Seq. No.
                   uC-osflcyp178c02a1
Seq. ID
                   BLASTX
Method
                   q729944
NCBI GI
BLAST score
                   276
                   2.0e-24
E value
Match length
                   71
                   68
 % identity
NCBI Description POLLEN ALLERGEN ZEA M 1 (ZEA M I) >gi_478272_pir__JC1524
                   major allergen mI protein - maize >gi_293902 (L14271) Zea
                   mI [Zea mays]
                   415656
 Seq. No.
                   uC-osflcyp178c03a1
 Seq. ID
                   BLASTX
 Method
                   g1363488
 NCBI GI
 BLAST score
                   167
                   1.0e-11
 E value
 Match length
                   42
 % identity
                   64
```

Seq. No.

415662

```
NCBI Description IAA8 protein - Arabidopsis thaliana >gi 972919 (U18410)
                  IAA8 [Arabidopsis thaliana] >gi 4314364 gb_AAD15575
                  (AC006340) auxin-induced IAA8 protein [Arabidopsis
                  thaliana]
                  415657
Seq. No.
                  uC-osflcyp178c03b1
Seq. ID
                  BLASTX
Method
NCBI GI
                  q4454452
                  405
BLAST score
E value
                  1.0e-39
                  94
Match length
                  80
% identity
NCBI Description (AC006234) unknown protein [Arabidopsis thaliana]
                  415658
Seq. No.
                  uC-osflcyp178c04a1
Seq. ID
Method
                  BLASTX
                  g2055262
NCBI GI
BLAST score
                  450
E value
                  6.0e-45
Match length
                  84
% identity
                  95
NCBI Description (AB003194) chitinase IIb [Oryza sativa]
                  415659
Seq. No.
                  uC-osflcyp178c04b1
Seq. ID
Method
                  BLASTX
                  g3377841
NCBI GI
                  304
BLAST score
                  1.0e-27
E value
Match length
                  75
                  80
% identity
                  (AF075598) contains similarity to phosphofructokinases
NCBI Description
                   (Pfam; PFK.hmm, score; 36.60) [Arabidopsis thaliana]
                   415660
Seq. No.
Seq. ID
                  uC-osflcyp178c05b1
                  BLASTX
Method
                  g4704640
NCBI GI
BLAST score
                   570
                   8.0e-59
E value
                  152
Match length
                   71
% identity
                  (AF110462) oleoyl-ACP thioesterase [Elaeis guineensis]
NCBI Description
                   415661
Seq. No.
                   uC-osflcyp178c06b1
Seq. ID
                   BLASTX
Method
                   g3242077
NCBI GI
BLAST score
                   478
E value
                   5.0e-48
                   143
Match length
% identity
                  (AJ003119) protein phosphatase 2C [Arabidopsis thaliana]
NCBI Description
```

```
uC-osflcyp178c07a1
Seq. ID
                  BLASTX
Method
                  g733454
NCBI GI
                  289
BLAST score
                  7.0e-26
E value
                  60
Match length
                  95
% identity
                  (U23188) chlorophyll a/b-binding apoprotein CP26 precursor
NCBI Description
                  [Zea mays]
                  415663
Seq. No.
                  uC-osflcyp178c08b1
Seq. ID
                  BLASTX
Method
                  q4098238
NCBI GI
                  350
BLAST score
                  5.0e-33
E value
                  128
Match length
                  56
% identity
NCBI Description (U76384) o-methyltransferase [Triticum aestivum]
                  415664
Seq. No.
                  uC-osflcyp178c09a1
Seq. ID
Method
                  BLASTX
                   g169661
NCBI GI
                   191
BLAST score
                   2.0e-14
E value
                   39
Match length
                   92
% identity
                  (M62756) S-adenosylhomocysteine hydrolase [Petroselinum
NCBI Description
                   crispum]
                   415665
Seq. No.
                   uC-osflcyp178c10b1
Seq. ID
                   BLASTX
Method
                   g1350625
NCBI GI
BLAST score
                   207
                   1.0e-16
E value
                   88
Match length
                   45
% identity
                   50S RIBOSOMAL PROTEIN L1, CHLOROPLAST PRECURSOR
NCBI Description
                   >gi_577089_emb_CAA58020_ (X82776) chloroplast ribosomal
                   protein L1 [Pist. sa
                   415666
 Seq. No.
                   uC-osflcyp178c12a1
 Seq. ID
Method
                   BLASTN
                   q1136121
 NCBI GI
                   123
 BLAST score
                   2.0e-62
 E value
                   296
 Match length
                   85
 % identity
 NCBI Description O.sativa mRNA for alpha-tub
                                                    Iclone OS'
                   415667
 Seq. No.
                   uC-osflcyp178c12b1
 Seq. ID
                   BLASTX
 Method
                   g3913427
 NCBI GI
```

```
202
BLAST score
                  3.0e-22
E value
Match length
                  119
                  52
% identity
                  S-ADENOSYLMETHIONINE DECARBOXYLASE PROENZYME (ADOMETDC)
NCBI Description
                   (SAMDC) >gi 1532073 emb CAA69075 (Y07767)
                  S-adenosylmethionine decarboxylase [Zea mays]
                  415668
Seq. No.
                  uC-osflcyp178d01a1
Seq. ID
                  BLASTN
Method
NCBI GI
                  g5922603
                  55
BLAST score
                   6.0e-22
E value
                  149
Match length
                   22
% identity
                  Oryza sativa genomic DNA, chromosome 1, clone:P0705D01
NCBI Description
                   415669
Seq. No.
                  uC-osflcyp178d01b1
Seq. ID
Method
                  BLASTX
                   q118104
NCBI GI
                   606
BLAST score
                   6.0e-63
E value
                   132
Match length
                   86
% identity
                   PEPTIDYL-PROLYL CIS-TRANS ISOMERASE (PPIASE) (ROTAMASE)
NCBI Description
                   (CYCLOPHILIN) (CYCLOSPORIN A-BINDING PROTEIN)
                   >gi 68408 pir CSZM peptidylprolyl isomerase (EC 5.2.1.8) -
                   maize >gi 168461 (M55021) cyclophilin [Zea mays]
                   >gi 829148 emb_CAA48638_ (X68678) cyclophilin [Zea mays]
                   415670
Seq. No.
Seq. ID
                   uC-osflcyp178d04a1
Method
                   BLASTX
                   q3367517
NCBI GI
                   212
BLAST score
                   7.0e-17
E value
                   78
Match length
                   49
% identity
                   (AC004392) Similar to F4I1.26 putative beta-glucosidase
NCBI Description
                   gi 3128187 from A. thaliana BAC gb_AC004521. ESTs
                   gb_N97083, gb_F19868 and gb_F15482 come from this gene.
                   [Arabidopsis thaliana]
                   415671
Seq. No.
                   uC-osflcyp178d05b1
Seq. ID
                   BLASTX
Method
                   g5689035
NCBI GI
                   208
BLAST score
                   9.0e-22
E value
                   127
Match length
 % identity
                   (AB022053) prolyl oligopeptidase [Mus musculus]
NCBI Description
                   415672
 Seq. No.
                   uC-osflcyp178d06b1
 Seq. ID
```

```
BLASTX
Method
                  g3757522
NCBI GI
BLAST score
                  381
                  1.0e-36
E value
                  118
Match length
% identity
                  71
NCBI Description (AC005167) putative splicing factor [Arabidopsis thaliana]
                  415673
Seq. No.
                  uC-osflcyp178d07a1
Seq. ID
Method
                  BLASTX
                  q829283
NCBI GI
                  315
BLAST score
                  6.0e-29
E value
                  75
Match length
                  87
% identity
NCBI Description (Z15018) heat shock protein hsp82 [Oryza sativa]
                  415674
Seq. No.
                  uC-osflcyp178d07b1
Seq. ID
                  BLASTX
Method
NCBI GI
                  g4539437
BLAST score
                  354
                  2.0e-33
E value
                  157
Match length
                  45
% identity
NCBI Description (AL049523) putative protein [Arabidopsis thaliana]
                  415675
Seq. No.
                  uC-osflcyp178d10b1
Seq. ID
                  BLASTX
Method
NCBI GI
                  q1169528
                  614
BLAST score
                  5.0e-64
E value
                  133
Match length
                   92
% identity
NCBI Description ENOLASE 2 (2-PHOSPHOGLYCERATE DEHYDRATASE 2)
                   (2-PHOSPHO-D-GLYCERATE HYDRO-LYASE 2) >gi_602253 (U17973)
                   enolase [Zea mays]
                   415676
Seq. No.
                   uC-osflcyp178d11b1
Seq. ID
                   BLASTX
Method
                   g1703380
NCBI GI
                   489
BLAST score
                   2.0e-49
E value
Match length
                   122
                   81
 % identity
NCBI Description ADP-RIBOSYLATION FACTOR >gi_1132483_dbj BAA04607_ (D17760)
                   ADP-ribosylation factor [Oryza sativa]
                   415677
 Seq. No.
 Seq. ID
                   uC-osflcyp178e01b1
                   BLASTX
Method
 NCBI GI
                   g2921304
                   631
 BLAST score
 E value
                   6.0e-69
```

```
153
Match length
% identity
NCBI Description (AF033496) herbicide safener binding protein [Zea mays]
                  415678
Seq. No.
                  uC-osflcyp178e04b1
Seq. ID
                  BLASTX
Method
                  g3915826
NCBI GI
BLAST score
                  444
                  2.0e-44
E value
                  112
Match length
                  84
% identity
NCBI Description 60S RIBOSOMAL PROTEIN L5
                  415679
Seq. No.
Seq. ID
                  uC-osflcyp178e06a1
                  BLASTX
Method
                  g3559805
NCBI GI
                  163
BLAST score
E value
                  4.0e-11
                  33
Match length
                  79
% identity
                  (AJ006787) putative phytochelatin synthetase [Arabidopsis
NCBI Description
                  thaliana]
                  415680
Seq. No.
                  uC-osflcyp178e07b1
Seq. ID
                  BLASTX
Method
                  q5911685
NCBI GI
BLAST score
                  210
                  1.0e-16
E value
                  63
Match length
                   57
% identity
NCBI Description (Y11996) PRT1 protein [Nicotiana tabacum]
                   415681
Seq. No.
                   uC-osflcyp178e08b1
Seq. ID
                   BLASTX
Method
                   g3024697
NCBI GI
BLAST score
                   311
                   8.0e-34
E value
                   94
Match length
                   79
% identity
NCBI Description T-COMPLEX PROTEIN 1, EPSILON SUBUNIT (TCP-1-EPSILON)
                   (CCT-EPSILON) >gi 2213618 (AC000103) F21J9.12 [Arabidopsis
                   thaliana]
                   415682
Seq. No.
Seq. ID
                   uC-osflcyp178e09a1
                   BLASTX
Method
NCBI GI
                   q5524155
                   392
BLAST score
                   5.0e-38
E value
Match length
                   116
                   56
% identity
NCBI Description (AF124815) cytochrome p450 [Mentha spicata]
```

```
415683
Seq. No.
Seq. ID
                  uC-osflcyp178e09b1
                  BLASTX
Method
NCBI GI
                  g5922624
                  554
BLAST score
                  4.0e-57
E value
                  128
Match length
                  88
% identity
                  (AP000492) ESTs C97742(C62458), AU078102(C62458) correspond
NCBI Description
                  to a region of the predicted gene.; similar to syntaxin
                  related protein AtVam3p (U88045) [Oryza sativa]
                  >qi 6016857 dbj BAA85200.1 (AP000570) ESTs
                  C97742(C62458), \overline{A}U078102(C62458) correspond to a region of
                  the predicted gene.; Similar to syntaxin related protein
                  AtVam3p (U88045) [Oryza sativa]
                   415684
Seq. No.
Seq. ID
                  uC-osflcyp178e10a1
                  BLASTX
Method
                  g1778147
NCBI GI
                  298
BLAST score
                  6.0e-27
E value
                   60
Match length
                   98
% identity
                  (U66403) phosphate/phosphoenolpyruvate translocator
NCBI Description
                   precursor [Zea mays]
                   415685
Seq. No.
                   uC-osflcyp178f01a1
Seq. ID
                   BLASTX
Method
NCBI GI
                   g4678321
                   185
BLAST score
                   1.0e-13
E value
                   63
Match length
                   60
% identity
NCBI Description (AL049658) putative protein [Arabidopsis thaliana]
                   415686
Seq. No.
Seq. ID
                   uC-osflcyp178f01b1
                   BLASTX
Method
                   q1345683
NCBI GI
BLAST score
                   272
                   7.0e-24
E value
                   68
Match length
                   78
% identity
NCBI Description CATALASE ISOZYME 3 >gi 487045 pir S37379 catalase (EC
                   1.11.1.6) 3 - maize >g\bar{i}_16843\bar{7} (L05934) catalase [Zea mays]
                   415687
Seq. No.
                   uC-osflcyp178f03b1
Seq. ID
Method
                   BLASTX
                   g4704613
NCBI GI
BLAST score
                   525
                   2.0e-53
E value
Match length
                   142
% identity
NCBI Description (AF109695) monodehydroascorbate reductase [Brassica juncea]
```

Seq. ID

```
415688
Seq. No.
Seq. ID
                  uC-osflcyp178f04a1
Method
                  BLASTX
NCBI GI
                  g4572671
BLAST score
                  170
                  6.0e-12
E value
                  92
Match length
% identity
                  49
                  (AC006954) putative cyclic nucleotide regulated ion channel
NCBI Description
                  [Arabidopsis thaliana]
                  415689
Seq. No.
Seq. ID
                  uC-osflcyp178f05b1
                  BLASTX
Method
                  g4455302
NCBI GI
                  591
BLAST score
                  3.0e-61
E value
                  147
Match length
                  72
% identity
NCBI Description (AL035528) putative protein [Arabidopsis thaliana]
                  415690
Seq. No.
Seq. ID
                  uC-osflcyp178f06b1
                  BLASTX
Method
NCBI GI
                  g1350986
BLAST score
                  619
                  1.0e-64
E value
Match length
                  148
% identity
                  85
NCBI Description
                 40S RIBOSOMAL PROTEIN S3A (CYC07 PROTEIN)
                  >gi_483431_dbj_BAA05059 (D26060) cyc07 [Oryza sativa]
                  415691
Seq. No.
Seq. ID
                  uC-osflcyp178f07a1
                  BLASTN
Method
NCBI GI
                  q2331130
BLAST score
                  208
                  1.0e-113
E value
                  208
Match length
                  100
% identity
NCBI Description Oryza sativa glycine-rich protein (OSGRP1) mRNA, complete
                  cds
Seq. No.
                  415692
Seq. ID
                  uC-osflcyp178f07b1
Method
                  BLASTX
NCBI GI
                  q5007084
BLAST score
                  486
                  2.0e-55
E value
Match length
                  121
% identity
                  (AF155333) NADP-specific isocitrate dehydrogenase [Oryza
NCBI Description
                  sativa]
Seq. No.
                  415693
```

uC-osflcyp178f08b1

```
BLASTX
Method
                                           g4096786
NCBI GI
BLAST score
                                           435
                                           3.0e-43
E value
                                           99
Match length
                                           86
% identity
NCBI Description (U39958) NADP-malic enzyme [Zea mays]
                                           415694
Seq. l >.
                                           uC-osflcyp178f09a1
Seq. IL
Method
                                           BLASTX
NCBI GI
                                           g1351014
                                           342
BLAST score
                                            4.0e-32
E value
                                            66
Match length
% identity
                                            100
                                          40S RIBOSOMAL PROTEIN S8 >gi 968902 dbj BAA07207 (D38010)
NCBI Description
                                            ribosomal protein S8 [Oryza sativa]
                                            415695
Seq. No.
Seq. ID
                                            uC-osflcyp178f12b1
Method
                                           BLASTX
                                            q1352200
NCBI GI
                                            297
BLAST score
                                            4.0e-27
E value
                                            79
Match length
% identity
                                            81
NCBI Description TRIOSE PHOSPHATE/PHOSPHATE TRANSLOCAT
                                                                                                                                                       JROPLAST
                                            PRECURSOR (CTPT) >gi_480909_pir__S374
                                                                                                                                                lose
                                            phosphate/3-phosphate/3-phosphate/3-phosphate/3-phosphate/3-phosphate/3-phosphate/3-phosphate/3-phosphate/3-phosphate/3-phosphate/3-phosphate/3-phosphate/3-phosphate/3-phosphate/3-phosphate/3-phosphate/3-phosphate/3-phosphate/3-phosphate/3-phosphate/3-phosphate/3-phosphate/3-phosphate/3-phosphate/3-phosphate/3-phosphate/3-phosphate/3-phosphate/3-phosphate/3-phosphate/3-phosphate/3-phosphate/3-phosphate/3-phosphate/3-phosphate/3-phosphate/3-phosphate/3-phosphate/3-phosphate/3-phosphate/3-phosphate/3-phosphate/3-phosphate/3-phosphate/3-phosphate/3-phosphate/3-phosphate/3-phosphate/3-phosphate/3-phosphate/3-phosphate/3-phosphate/3-phosphate/3-phosphate/3-phosphate/3-phosphate/3-phosphate/3-phosphate/3-phosphate/3-phosphate/3-phosphate/3-phosphate/3-phosphate/3-phosphate/3-phosphate/3-phosphate/3-phosphate/3-phosphate/3-phosphate/3-phosphate/3-phosphate/3-phosphate/3-phosphate/3-phosphate/3-phosphate/3-phosphate/3-phosphate/3-phosphate/3-phosphate/3-phosphate/3-phosphate/3-phosphate/3-phosphate/3-phosphate/3-phosphate/3-phosphate/3-phosphate/3-phosphate/3-phosphate/3-phosphate/3-phosphate/3-phosphate/3-phosphate/3-phosphate/3-phosphate/3-phosphate/3-phosphate/3-phosphate/3-phosphate/3-phosphate/3-phosphate/3-phosphate/3-phosphate/3-phosphate/3-phosphate/3-phosphate/3-phosphate/3-phosphate/3-phosphate/3-phosphate/3-phosphate/3-phosphate/3-phosphate/3-phosphate/3-phosphate/3-phosphate/3-phosphate/3-phosphate/3-phosphate/3-phosphate/3-phosphate/3-phosphate/3-phosphate/3-phosphate/3-phosphate/3-phosphate/3-phosphate/3-phosphate/3-phosphate/3-phosphate/3-phosphate/3-phosphate/3-phosphate/3-phosphate/3-phosphate/3-phosphate/3-phosphate/3-phosphate/3-phosphate/3-phosphate/3-phosphate/3-phosphate/3-phosphate/3-phosphate/3-phosphate/3-phosphate/3-phosphate/3-phosphate/3-phosphate/3-phosphate/3-phosphate/3-phosphate/3-phosphate/3-phosphate/3-phosphate/3-phosphate/3-phosphate/3-phosphate/3-phosphate/3-phosphate/3-phosphate/3-phosphate/3-phosphate/3-phosphate/3-phosphate/3-phosphate/3-phosphate/3-phosphate/3-phosphate/3-phosph
                                            phosphate/phosphate translocator [Zea mays]
                                            415696
Seq. No.
Seq. ID
                                            uC-osflcyp178g02a1
                                            BLASTX
Method
NCBI GI
                                            q586145
BLAST score
                                            176
                                            1.0e-12
E value
Match length
                                            33
                                            100
% identity
NCBI Description UBIQUINOL-CYTOCHROME C REDUCTASE IRON-SULFUR SUBUNIT
                                            PRECURSOR (RIESKE IRON-SULFUR PROTEIN) (RISP)
                                            >gi 488848 emb CAA55894 (X79332) Rieske iron sulphur
                                            protein [Solanum tuberosum]
Seq. No.
                                            415697
                                            uC-osflcyp178g02b1
Seq. ID
Method
                                            BLASTX
                                            q3142294
NCBI GI
BLAST score
                                            372
                                            1.0e-37
E value
                                            110
Match length
                                            75
 % identity
                                          (AC002411) Strong similarity to initiation factor @IF-2,
NCBI Description
                                            gb U37354 from S. pombe. ESTs gb T41979, gb N37284 and
                                             gb N37529 come from this gene. [Arabidopsis thaliana]
```

415698 Seq. No. Seq. ID uC-osflcyp178g03b1 BLASTX Method NCBI GI q1709619 BLAST score 431 E value 1.0e-42 105 Match length 44 % identity PROTEIN DISULFIDE ISOMERASE PRECURSOR (PDI) NCBI Description >gi 2146814 pir S69181 protein disulfide isomerase (EC 5.3.4.1) precursor - maize >gi 625148 (L39014) protein disulfide isomerase [Zea mays] 415699 Seq. No. Seq. ID uC-osflcyp178g04b1 BLASTX Method NCBI GI g3914006 BLAST score 699 E value 6.0e-74149 Match length 94 % identity MITOCHONDRIAL LON PROTEASE HOMOLOG 2 PRECURSOR >gi 1816588 NCBI Description (U85495) LON2 [Zea mays] 415700 Seq. No. Seq. ID uC-osflcyp178g05a1 Method BLASTX NCBI GI g1261917 BLAST score 145 5.0e-09 E value 39 Match length 64 % identity NCBI Description (X96979) lipid transfer protein 7a2b [Hordeum vulgare] Seq. No. 415701 Seq. ID uC-osflcyp178g05b1 Method BLASTX NCBI GI g3128228 BLAST score 690 E value 6.0e-75Match length 167 86 % identity NCBI Description (AC004077) putative ribosomal protein L18A [Arabidopsis thaliana] >gi 3337376 (AC004481) putative ribosomal protein L18A [Arabidopsis thaliana] Seq. No. 415702 uC-osflcyp178g06a1 Seq. ID Method BLASTX NCBI GI g5295980 BLAST score 146 E value 4.0e-09 27 Match length 96 % identity

NCBI Description (AB003323) MADS box-like protein [Oryza sativa]

```
415703
Seq. No.
Seq. ID
                  uC-osflcyp178g07b1
Method
                  BLASTX
NCBI GI
                  g4753651
BLAST score
                  451
                  4.0e-45
E value
                  111
Match length
                  77
% identity
                  (AL049751) ribosomal protein L13a like protein [Arabidopsis
NCBI Description
                  thaliana]
                  415704
Seq. No.
Seq. ID
                  uC-osflcyp178g08b1
                  BLASTX
Method
NCBI GI
                  g4160298
BLAST score
                  189
                  3.0e-14
E value
Match length
                  137
                  39
% identity
NCBI Description (AJ011892) cyclin D2.1 protein [Nicotiana tabacum]
                  415705
Seq. No.
Seq. ID
                  uC-osflcyp178g09b1
                  BLASTX
Method
                  g1350986
NCBI GI
                  640
BLAST score
                  4.0e-67
E value
                  139
Match length
                  91
% identity
NCBI Description 40S RIBOSOMAL PROTEIN S3A (CYC07 PROTEIN)
                  >gi 483431 dbj BAA05059_ (D26060) cyc07 [Oryza sativa]
                  415706
Seq. No.
Seq. ID
                  uC-osflcyp178g10b1
                  BLASTX
Method
                  g4895164
NCBI GI
                  364
BLAST score
                  5.0e-35
E value
                  94
Match length
% identity
                  77
                  (AC007231) putative disease resistance protein [Arabidopsis
NCBI Description
                  thaliana]
                  415707
Seq. No.
Seq. ID
                  uC-osflcyp178g11a1
Method
                  BLASTX
NCBI GI
                  g547712
BLAST score
                  292
                  3.0e-26
E value
Match length
                  57
% identity
                  98
                  EUKARYOTIC INITIATION FACTOR 4A (EIF-4A)
NCBI Description
                  >gi 542153 pir S38358 translation initiation factor eIF-4A
                  - rice >gi 303844 dbj BAA02152 (D12627) eukaryotic
                  initiation factor 4A [Oryza sativa]
```

415708

Seq. No.

Seq. ID

```
uC-osflcyp178g12b1
Seq. ID
                  BLASTX
Method
NCBI GI
                  g3935170
                  335
BLAST score
                  3.0e-31
E value
                  141
Match length
                  50
% identity
                  (AC004557) F17L21.13 [Arabidopsis thaliana]
NCBI Description
                  415709
Seq. No.
Seq. ID
                  uC-osflcyp178h01b1
                  BLASTX
Method
                  g82695
NCBI GI
BLAST score
                  376
                  1.0e-36
E value
                  85
Match length
                  92
% identity
                  glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1.12) 3 -
NCBI Description
                  maize (fragment) >gi_293887 (L13431)
                  glyceraldehyde-3-phosphate dehydrogenase [Zea mays]
Seq. No.
                  415710
Seq. ID
                  uC-osflcyp178h02b1
                  BLASTN
Method
                  g313026
NCBI GI
                  43
BLAST score
                   4.0e-15
E value
                  123
Match length
                  84
% identity
NCBI Description L.esculentum rpl38 mRNA for ribosomal protein L38
                   415711
Seq. No.
Seq. ID
                  uC-osflcyp178h03a1
                  BLASTX
Method
NCBI GI
                  q3169883
BLAST score
                   164
                   3.0e-11
E value
Match length
                   59
                   54
% identity
                  (AF033194) dehydroquinate dehydratase/shikimate:NADP
NCBI Description
                   oxidoreductase [Lycopersicon esculentum] >gi 3169888
                   (AF034411) dehydroquinate dehydratase/shikimate:NADP
                   oxidoreductase [Lycopersicon esculentum]
                   415712
Seq. No.
Seq. ID
                   uC-osflcyp178h03b1
                   BLASTX
Method
                   g3925265
NCBI GI
BLAST score
                   153
                   5.0e-10
E value
Match length
                   48
% identity
                  (Z93394) similar to Probable rabGAP domains [Caenorhabditis
NCBI Description
                   elegans]
Seq. No.
                   415713
```

54288

uC-osflcyp178h04b1

```
BLASTX
Method
                  g3294467
NCBI GI
                  318
BLAST score
                  2.0e-39
E value
                  110
Match length
                  85
% identity
NCBI Description (U89341) phosphoglucomutase 1 [Zea mays]
                  415714
Seq. No.
                  uC-osflcyp178h05b1
Seq. ID
                  BLASTX
Method
                  g4757796
NCBI GI
                  143
BLAST score
                  2.0e-09
E value
                  65
Match length
% identity
                  51
                  arsA (bacterial) arsenite transporter, ATP-binding, homolog
NCBI Description
                  1 >gi_1616741 (U60276) hASNA-I [Homo sapiens]
                  415715
Seq. No.
                  uC-osflcyp178h06a1
Seq. ID
                  BLASTX
Method
                  g1321661
NCBI GI
                  313
BLAST score
                  1.0e-28
E value
                  63
Match length
                   97
% identity
NCBI Description (D45423) ascorbate peroxidase [Oryza sativa]
                   415716
Seq. No.
Seq. ID
                   uC-osflcyp178h07a1
                  BLASTN
Method
                   q5360229
NCBI GI
BLAST score
                   316
                   1.0e-177
E value
                   372
Match length
                   96
% identity
NCBI Description Oryza sativa mRNA for Ran, complete cds
                   415717
Seq. No.
                   uC-osflcyp178h08a1
Seq. ID
                   BLASTN
Method
                   q5420609
NCBI GI
                   35
BLAST score
                   5.0e-10
E value
                   67
Match length
                   88
% identity
NCBI Description Genomic sequence for Arabidopsis thaliana BAC F28C11 from
                   chromosome I, complete sequence
Seq. No.
                   415718
                   uC-osflcyp178h09b1
Seq. ID
                   BLASTX
Method
NCBI GI
                   q417154
BLAST score
                   390
                   7.0e-38
E value
Match length
                   93
```

```
% identity
                  HEAT SHOCK PROTEIN 82 >gi 100685 pir__S25541 heat shock
NCBI Description
                  protein 82 - rice (strain Taichung Native One)
                  >gi 20256_emb_CAA77978_ (Z11920) heat shock protein 82
                  (HSP82) [Oryza sativa]
                  415719
Seq. No.
                  uC-osflcyp179a01a1
Seq. ID
Method
                  BLASTX
                  g3452497
NCBI GI
BLAST score
                  348
                  8.0e-33
E value
                  75
Match length
                  89
% identity
                  (Y17796) ketol-acid reductoisomerase [Pisum sativum]
NCBI Description
Seq. No.
                  415720
                  uC-osflcyp179a01b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3452497
                  668
BLAST score
E value
                  3.0e-70
Match length
                  163
                  80
% identity
                  (Y17796) ketol-acid reductoisomerase [Pisum sativum]
NCBI Description
                  415721
Seq. No.
Seq. ID
                  uC-osflcyp179a02a1
Method
                  BLASTX
                  g541951
NCBI GI
                  339
BLAST score
                  9.0e-32
E value
                  78
Match length
                  78
% identity
                  SPCP2 protein - soybean >gi_310578 (L12258) nodulin-26
NCBI Description
                  [Glycine max]
                   415722
Seq. No.
                  uC-osflcyp179a02b1
Seq. ID
                  BLASTX
Method
                  g1729971
NCBI GI
                   237
BLAST score
                   5.0e-20
E value
                  98
Match length
                   51
% identity
NCBI Description TONOPLAST INTRINSIC PROTEIN, GAMMA (GAMMA TIP)
                   (AQUAPORIN-TIP) >gi_1076745_pir__S52004 gamma-Tip protein -
                   rice >qi 473997 dbj BAA05017 (D25534) gamma-Tip [Oryza
                   sativa]
                   415723
Seq. No.
                   uC-osflcyp179a04a1
Seq. ID
                   BLASTX
Method
NCBI GI
                   g606817
BLAST score
                   165
                   2.0e-11
E value
                   31
Match length
```

% identity NCBI Description (U08404) carbonic anhydrase [Oryza sativa] >gi 5917783 gb AAD56038.1 AF182806 1 (AF182806) carbonic anhydrase 3 [Oryza sativa] 415724 Seq. No. uC-osflcyp179a04b1 Seq. ID BLASTX Method NCBI GI a606817 BLAST score 498 2.0e-57 E value 138 Match length 86 % identity (U08404) carbonic anhydrase [Oryza sativa] NCBI Description >gi 5917783 gb AAD56038.1 AF182806 1 (AF182806) carbonic anhydrase 3 [Oryza sativa] 415725 Seq. No. Seq. ID uC-osflcyp179a07a1 Method BLASTX NCBI GI q3913426 221 BLAST score 6.0e-18 E value 41 Match length 98 % identity S-ADENOSYLMETHIONINE DECARBOXYLASE PROENZYME (ADOMETDC) NCBI Description (SAMDC) >gi 1532048 emb CAA69074 (Y07766) S-adenosylmethionine decarboxylase [Oryza sativa] Seq. No. 415726 uC-osflcyp179a07b1 Seq. ID BLASTX Method q2129921 NCBI GI BLAST score 179 E value 5.0e-13 Match length 51 67 % identity NCBI Description hypothetical protein 1 - Madagascar periwinkle >gi 758694 (U12573) putative [Catharanthus roseus] Seq. No. 415727 uC-osflcyp179a08a1 Seq. ID Method BLASTX NCBI GI g1708191 BLAST score 275 3.0e-24E value Match length 73 % identity 63 HEXOSE CARRIER PROTEIN HEX6 >gi 467319 (L08188) hexose NCBI Description carrier protein [Ricinus communis] 415728 Seq. No. Seq. ID uC-osflcyp179a10b1 Method BLASTX NCBI GI q3776005 429 BLAST score

54291

2.0e-42

E value

```
105
Match length
                   79
% identity
                  (AJ010466) RNA helicase [Arabidopsis thaliana]
NCBI Description
                   415729
Seq. No.
Seq. ID
                  uC-osflcyp179a11a1
Method
                  BLASTX
NCBI GI
                  g124226
BLAST score
                   203
                   9.0e-16
E value
                   42
Match length
                   93
% identity
NCBI Description
                  INITIATION FACTOR 5A-2 (EIF-5A) (EIF-4D)
                   >gi 100278 pir S21059 translation initiation factor
                   eIF-5A.2 - curled-leaved tobacco >gi 19702 emb CAA45104
                   (X63542) eukaryotic initiation factor 5A (\overline{2}) [Nicotiana
                   plumbaginifolia]
Seq. No.
                   415730
Seq. ID
                   uC-osflcyp179a11b1
                   BLASTX
Method
                   g3789948
NCBI GI
BLAST score
                   611
                   1.0e-63
E value
Match length
                   122
                   93
% identity
                  (AF094773) translation initiation factor 5A [Oryza sativa]
NCBI Description
                   415731
Seq. No.
Seq. ID
                   uC-osflcyp179b01b1
Method
                   BLASTX
                   q2493646
NCBI GI
BLAST score
                   516
                   2.0e-52
E value
Match length
                   113
                   94
% identity
                 MITOCHONDRIAL CHAPERONIN HSP60-2 PRECURSOR >gi 309559
NCBI Description
                   (L21008) chaperonin 60 [Zea mays] >gi 309561 (\overline{L}21006)
                   mitochondrial chaperonin 60 [Zea mays]
Seq. No.
                   415732
Seq. ID
                   uC-osflcyp179b02a1
Method
                   BLASTX
NCBI GI
                   g4105782
BLAST score
                   163
                   4.0e-11
E value
                   34
Match length
                   79
% identity
NCBI Description (AF049922) PGP169-12 [Petunia x hybrida]
                   415733
Seq. No.
                   uC-osflcyp179b02b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   q4105782
                   536
BLAST score
                   7.0e-55
E value
                   129
Match length
```

```
79
% identity
                  (AF049922) PGP169-12 [Petunia x hybrida]
NCBI Description
                  415734
Seq. No.
                  uC-osflcyp179b04b1
Seq. ID
                  BLASTX
Method
                  q4160292
NCBI GI
                  231
BLAST score
                  5.0e-19
E value
                  111
Match length
                  42
% identity
NCBI Description (Y18209) alpha-N-acetylglucosaminidase [Nicotiana tabacum]
                  415735
Seq. No.
Seq. ID
                  uC-osflcyp179b05a1
                  BLASTN
Method
                  g5360229
NCBI GI
BLAST score
                  326
                  0.0e + 00
E value
Match length
                  394
                  96
% identity
NCBI Description Oryza sativa mRNA for Ran, complete cds
                  415736
Seq. No.
Seq. ID
                  uC-osflcyp179b05b1
                  BLASTX
Method
                  g5360230
NCBI GI
BLAST score
                  688
                  6.0e-81
E value
Match length
                  146
% identity
                  95
NCBI Description (AB015287) Ran [Oryza sativa]
                  415737
Seq. No.
Seq. ID
                  uC-osflcyp179b08a1
                  BLASTX
Method
                  g2696804
NCBI GI
BLAST score
                  290
                  5.0e-26
E value
Match length
                  57
% identity
                  95
NCBI Description (AB009665) water channel protein [Oryza sativa]
                   415738
Seq. No.
                  uC-osflcyp179b08b1
Seq. ID
Method
                  BLASTX
NCBI GI
                   g2894534
BLAST score
                   792
                  8.0e-85
E value
Match length
                  152
% identity
                  100
NCBI Description (AJ224327) aquaporin [Oryza sativa]
                   415739
Seq. No.
                   uC-osflcyp179b09a1
Seq. ID
Method
                  BLASTN
                   g218203
NCBI GI
```

BLAST score 233 E value 1.0e-128 Match length 244 % identity 99

NCBI Description Rice mRNA for GTP binding protein

Seq. No. 415740

Seq. ID uC-osflcyp179b09b1

Method BLASTX
NCBI GI g3024552
BLAST score 690
E value 9.0e-73
Match length 159
% identity 92

NCBI Description RAS-RELATED PROTEIN RGP2 (GTP-BINDING REGULATORY PROTEIN

RGP2) >gi_419797_pir__S30273 GTP-binding protein rgp2 - rice >gi_218204_dbj_BAA02437_ (D13152) GTP binding protein [Oryza sativa] >gi_446772_prf__1912297A rgp2 gene [Oryza

sativa]

Seq. No. 415741

Seq. ID uC-osflcyp179b10a1

Method BLASTX
NCBI GI g2764802
BLAST score 169
E value 8.0e-12
Match length 38
% identity 79

NCBI Description (X77795) ras-like gene [Zea mays]

Seq. No. 415742

Seq. ID uC-osflcyp179b11b1

Method BLASTX
NCBI GI g4185513
BLAST score 266
E value 2.0e-32
Match length 96
% identity 72

NCBI Description (AF102823) actin depolymerizing factor 5 [Arabidopsis

thaliana] >gi 4185517 (AF102825) actin depolymerizing

factor 5 [Arabidopsis thaliana]

Seq. No. 415743

Seq. ID uC-osflcyp179b12b1

Method BLASTX
NCBI GI g5668770
BLAST score 211
E value 8.0e-17
Match length 103
% identity 52

NCBI Description (AC005916) T17H3.9 [Arabidopsis thaliana]

Seq. No. 415744

Seq. ID uC-osflcyp179c01b1

Method BLASTX NCBI GI g2827150 BLAST score 445

E value

Match length

47

7.0e-56 E value Match length 155 80 % identity (AF029895) acetyl-coenzyme A carboxylase [Triticum NCBI Description aestivum] 415745 Seq. No. Seq. ID uC-osflcyp179c02b1 Method BLASTX q3075488 NCBI GI BLAST score 476 7.0e-48 E value Match length 111 % identity 84 (AF058796) chlorophyll a/b-binding protein [Oryza sativa] NCBI Description 415746 Seq. No. Seq. ID uC-osflcyp179c04a1 Method BLASTX NCBI GI q6103011 243 BLAST score 1.0e-20 E value 62 Match length 79 % identity (X84225) precursor of photosystem II subunit (22KDa) NCBI Description [Nicotiana tabacum] 415747 Seq. No. Seq. ID uC-osflcyp179c05b1 Method BLASTX q3914603 NCBI GI BLAST score 478 4.0e-48 E value Match length 95 % identity 98 RIBULOSE BISPHOSPHATE CARBOXYLASE/OXYGENASE ACTIVASE, NCBI Description CHLOROPLAST PRECURSOR (RUBISCO ACTIVASE) >gi 1778414 (U74321) ribulose-1,5-bisphosphate carboxylase/oxygenase activase [Oryza sativa] 415748 Seq. No. Seq. ID uC-osflcyp179c10b1 BLASTX Method NCBI GI q5668640 BLAST score 509 E value 1.0e-51 Match length 148 % identity NCBI Description (AL109619) putative protein [Arabidopsis thaliana] 415749 Seq. No. uC-osflcyp179c11a1 Seq. ID Method BLASTX q2108252 NCBI GI BLAST score 167 1.0e-11

Seq. ID

BLASTX

Method

```
% identity
                  (Y10228) P-glycoprotein-2 [Arabidopsis thaliana]
NCBI Description
                  >gi_2108254_emb_CAA71276_ (Y10227) P-glycoprotein-2
                  [Arabidopsis thaliana] >gi_4538925_emb_CAB39661.1
                  (AL049483) P-glycoprotein-2 (pgp2) [Arabidopsis thaliana]
                  415750
Seq. No.
Seq. ID
                  uC-osflcyp179c11b1
                  BLASTX
Method
NCBI GI
                  g2108252
                  533
BLAST score
                  2.0e-54
E value
                  136
Match length
                  39
% identity
                  (Y10228) P-glycoprotein-2 [Arabidopsis thaliana]
NCBI Description
                  >gi_2108254_emb_CAA71276_ (Y10227) P-glycoprotein-2
                  [Arabidopsis thaliana] >gi 4538925 emb_CAB39661.1
                  (AL049483) P-glycoprotein-2 (pgp2) [Arabidopsis thaliana]
                  415751
Seq. No.
Seq. ID
                  uC-osflcyp179c12a1
Method
                  BLASTN
                  q722327
NCBI GI
                  64
BLAST score
                  2.0e-27
E value
                  152
Match length
% identity
                  86
NCBI Description Zea mays clone Zm-Rab2-B GTP binding protein (rab2) mRNA,
                  complete cds
Seq. No.
                  415752
                  uC-osflcyp179c12b1
Seq. ID
Method
                  BLASTX
                  q1346957
NCBI GI
                  602
BLAST score
E value
                  2.0e-62
                  119
Match length
                  96
% identity
NCBI Description RAS-RELATED PROTEIN RAB-2-B >gi_722328 (U22433) GTP binding
                  protein [Zea mays]
                  415753
Seq. No.
Seq. ID
                  uC-osflcyp179d01a1
Method
                  BLASTX
NCBI GI
                  a1170937
BLAST score
                  266
                  3.0e-23
E value
                  48
Match length
                  100
% identity
                  S-ADENOSYLMETHIONINE SYNTHETASE 1 (METHIONINE
NCBI Description
                  ADENOSYLTRANSFERASE 1) (ADOMET SYNTHETASE 1)
                  >gi 450549 emb CAA81481_ (Z26867) S-adenosyl methionine
                  synthetase [Oryza sativa]
Seq. No.
                  415754
                  uC-osflcyp179d01b1
```

NCBI GI g1170937 BLAST score 695 2.0e-73 E value Match length 131 100 % identity NCBI Description S-ADENOSYLMETHIONINE SYNTHETASE 1 (METHIONINE ADENOSYLTRANSFERASE 1) (ADOMET SYNTHETASE 1) >qi 450549 emb CAA81481 (Z26867) S-adenosyl methionine synthetase [Oryza sativa] 415755 Seq. No. uC-osflcyp179d02a1 Seq. ID Method BLASTN g3885887 NCBI GI 438 BLAST score 0.0e + 00E value 438 Match length 100 % identity Oryza sativa high mobility group protein (HMG) mRNA, NCBI Description complete cds 415756 Seq. No. Seq. ID uC-osflcyp179d02b1 BLASTX Method NCBI GI g3885888 BLAST score 213 5.0e-17 E value 90 Match length 54 % identity NCBI Description (AF093632) high mobility group protein [Oryza sativa] 415757 Seq. No. uC-osflcyp179d03b1 Seq. ID BLASTX Method NCBI GI q4101707 BLAST score 263 6.0e-23 E value 108 Match length 47 % identity NCBI Description (AF006080) glucose acyltransferase [Solanum berthaultii] Seq. No. 415758 uC-osflcyp179d04a1 Seq. ID BLASTX Method NCBI GI q559005 BLAST score 197 4.0e-15 E value 58 Match length 71 % identity NCBI Description (U15933) ascorbate peroxidase [Nicotiana tabacum] 415759 Seq. No.

Seq. ID uC-osflcyp179d04b1

Method BLASTX
NCBI GI g5081779
BLAST score 731
E value 3.0e-77

```
166
Match length
                  83
% identity
                  (AF150630) cellulose synthase [Gossypium hirsutum]
NCBI Description
                  415760
Seq. No.
                  uC-osflcyp179d05a1
Seq. ID
                  BLASTN
Method
                  g4768991
NCBI GI
                  57
BLAST score
                  4.0e-23
E value
                  69
Match length
                  96
% identity
                  Oryza sativa cholinephosphate cytidylyltransferase mRNA,
NCBI Description
                  partial cds
                  415761
Seq. No.
                  uC-osflcyp179d08b1
Seq. ID
                  BLASTX
Method
                  q4309732
NCBI GI
                  155
BLAST score
E value
                  4.0e-10
Match length
                  53
                  53
% identity
NCBI Description (AC006439) hypothetical protein [Arabidopsis thaliana]
                  415762
Seq. No.
                  uC-osflcyp179d09a1
Seq. ID
                  BLASTX
Method
                  g2098709
NCBI GI
                  171
BLAST score
                  4.0e-12
E value
                  68
Match length
                   47
% identity
NCBI Description (U82975) pectinesterase [Citrus sinensis]
                   415763
Seq. No.
Seq. ID
                  uC-osflcyp179d10b1
                  BLASTX
Method
                  g4539333
NCBI GI
BLAST score
                   320
                   9.0e-30
E value
                  100
Match length
                   61
% identity
NCBI Description (AL035539) putative amino acid transport protein
                   [Arabidopsis thaliana]
                   415764
Seq. No.
Seq. ID
                   uC-osflcyp179d11a1
                   BLASTN
Method
                   g4768991
NCBI GI
BLAST score
                   138
                   2.0e-71
E value
Match length
                   138
% identity
                   100
NCBI Description Oryza sativa cholinephosphate cytidylyltransferase mRNA,
                   partial cds
```

```
415765
Seq. No.
Seq. ID
                  uC-osflcyp179d11b1
Method
                  BLASTX
NCBI GI
                  g5280991
                  555
BLAST score
                  5.0e-57
E value
                  111
Match length
                  88
% identity
                  (Z97338) putative phosphocholine cytidylyltransferase
NCBI Description
                  [Arabidopsis thaliana]
                  415766
Seq. No.
Seq. ID
                  uC-osflcyp179d12a1
                  BLASTX
Method
                  g6103011
NCBI GI
                  289
BLAST score
                  7.0e-26
E value
                  102
Match length
                  46
% identity
                  (X84225) precursor of photosystem II subunit (22KDa)
NCBI Description
                  [Nicotiana tabacum]
                  415767
Seq. No.
Seq. ID
                  uC-osflcyp179d12b1
                  BLASTX
Method
                  g6103011
NCBI GI
                  515
BLAST score
                  2.0e-52
E value
                  115
Match length
                   48
% identity
                  (X84225) precursor of photosystem II subunit (22KDa)
NCBI Description
                   [Nicotiana tabacum]
                  415768
Seq. No.
Seq. ID
                  uC-osflcyp179e02a1
Method
                  BLASTX
                  q2529668
NCBI GI
                   174
BLAST score
                   2.0e-12
E value
Match length
                   44
                   70
% identity
                  (AC002535) putative photolyase/blue-light receptor
NCBI Description
                   [Arabidopsis thaliana] >gi 3319288 (AF053366)
                   photolyase/blue light photoreceptor PHR2 [Arabidopsis
                   thalianal
                   415769
Seq. No.
                   uC-osflcyp179e06a1
Seq. ID
                   BLASTX
Method
                   q6015059
NCBI GI
BLAST score
                   261
                   1.0e-22
E value
                   58
Match length
% identity
                  ELONGATION FACTOR 1-ALPHA (EF-1-ALPHA) >gi 2996096
NCBI Description
                   (AF030517) translation elongation factor-1 alpha; EF-1
```

alpha [Oryza sativa]

```
415770
Seq. No.
                   uC-osflcyp179e06b1
Seq. ID
                   BLASTX
Method
                   g119143
NCBI GI
BLAST score
                   286
                   4.0e-26
E value
                   77
Match length
                   83
% identity
                   ELONGATION FACTOR 1-ALPHA (EF-1-ALPHA)
NCBI Description
                   >gi_81606_pir__S06724 translation elongation factor eEF-1
alpha chain - Arabidopsis thaliana >gi_295788_emb_CAA34453_
                   (X16430) elongation factor 1-alpha [Arabidopsis thaliana]
                   >gi_1369927_emb_CAA34454_ (X16431) elongation factor
                   1-alpha [Arabidopsis thaliana] >gi 1369928 emb CAA34455
                   (X16431) elongation factor 1-alpha [Arabidopsis thaliana]
                   >qi 1532172 (U63815) EF-1alpha-Al [Arabidopsis thaliana]
                   >qi 1532173 (U63815) EF-1alpha-A2 [Arabidopsis thaliana]
                   >gi 1532174 (U63815) EF-lalpha-A3 [Arabidopsis thaliana]
                   415771
Seq. No.
Seq. ID
                   uC-osflcyp179e09b1
                   BLASTX
Method
                   g586021
NCBI GI
                   200
BLAST score
                   2.0e-15
E value
                   84
Match length
                   48
% identity
                   PROBABLE PEPTIDYL-TRNA HYDROLASE (PTH) (STAGE V SPORULATION
NCBI Description
                   PROTEIN C) >gi 2127242 pir S66083 stage V sporulation
                   protein - Bacillus subtilis >gi 467442 dbj BAA05288
                   (D26185) stage V sporulation [Bacillus subtilis]
                   >qi 2632320 emb CAB11829 (Z99104) thermosensitive mutant
                   blocks spore coat formation (stage V sporulation) [Bacillus
                   subtilis]
                   415772
Seq. No.
                   uC-osflcyp179e12a1
Seq. ID
                   BLASTN
Method
NCBI GI
                   g433216
                   248
BLAST score
                   1.0e-137
E value
                   271
Match length
                   98
% identity
NCBI Description
                  Rice mRNA for ascorbate peroxidase (gene name SS622),
                   partial cds
                   415773
Seq. No.
                   uC-osflcyp179e12b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g1076800
                   759
BLAST score
                   7.0e-81
E value
Match length
                   165
% identity
                   85
NCBI Description L-ascorbate peroxidase (EC 1.11.1.11), cytosolic isozyme -
```

maize >gi 600116 emb CAA84406 (Z34934) cytosolic ascorbate

Method NCBI GI

Method

Method

Method

peroxidase [Zea mays] >gi 1096503 prf 2111423A ascorbate peroxidase [Zea mays] 415774 Seq. No. uC-osflcyp179f02a1 Seq. ID BLASTX g4415931 BLAST score 186 8.0e-14 E value Match length 64 55 % identity (AC006418) unknown protein [Arabidopsis thaliana] NCBI Description >qi 4559393 gb AAD23053.1 AC006526_18 (AC006526) unknown protein [Arabidopsis thaliana] 415775 Seq. No. uC-osflcyp179f03a1 Seq. ID BLASTN NCBI GI g2331132 BLAST score 371 0.0e + 00E value 407 Match length % identity 98 Oryza sativa glycine-rich protein (OSGRP2) mRNA, complete NCBI Description 415776 Seq. No. Seq. ID uC-osflcyp179f03b1 BLASTX NCBI GI g2624326 BLAST score 475 8.0e-48 E value 93 Match length % identity 99 (AJ002893) OsGRP1 [Oryza sativa] NCBI Description 415777 Seq. No. uC-osflcyp179f04a1 Seq. ID BLASTN g6041757 NCBI GI BLAST score 36 1.0e-10 E value 56 Match length 91 % identity Genomic Sequence For Oryza sativa Clone 10P20, Lemont NCBI Description Strain, Complete Sequence, complete sequence 415778 uC-osflcyp179f04b1

Seq. No.

Seq. ID

Method BLASTN NCBI GI g6041757 BLAST score 287 1.0e-160 E value 339 Match length 96 % identity

NCBI Description Genomic Sequence For Oryza sativa Clone 10P20, Lemont

Strain, Complete Sequence, complete sequence

```
415779
Seq. No.
Seq. ID
                  uC-osflcyp179f06b1
Method
                  BLASTX
                  q4558672
NCBI GI
                  182
BLAST score
E value
                  3.0e-13
Match length
                  41
                  88
% identity
                  (AC007063) putative 1,3-beta-D-glucan synthase [Arabidopsis
NCBI Description
                  thaliana]
                  415780
Seq. No.
                  uC-osflcyp179f07b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g5852181
BLAST score
                  240
E value
                  4.0e-20
Match length
                  128
% identity
                  54
                  (AL117265) zhb0011.1 [Oryza sativa]
NCBI Description
Seq. No.
                  415781
                  uC-osflcyp179f08a1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2281085
BLAST score
                  215
E value
                  3.0e-17
Match length
                  64
% identity
                  64
                  (AC002333) CTR1 protein kinase isolog [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  415782
                  uC-osflcyp179f08b1
Seq. ID
Method
                  BLASTX
                  g2281085
NCBI GI
BLAST score
                  281
E value
                  4.0e-25
Match length
                  111
% identity
                  51
                  (AC002333) CTR1 protein kinase isolog [Arabidopsis
NCBI Description
                  thaliana]
                   415783
Seq. No.
                  uC-osflcyp179f09a1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1352347
BLAST score
                  287
                  1.0e-25
E value
Match length
                  65
% identity
                  85
                  ELONGATION FACTOR 1-BETA A1 (EF-1-BETA)
NCBI Description
                  >gi 480620 pir S37103 translation elongation factor eEF-1
                  beta-A1 chain - Arabidopsis thaliana (cv. Colombia)
                  >gi_398608_emb_CAA52751_ (X74733) elongation factor-1 beta
```

Al [Arabidopsis thaliana]

```
415784
Seq. No.
Seq. ID
                  uC-osflcyp179f09b1
                  BLASTX
Method
                  q232031
NCBI GI
BLAST score
                  405
                  2.0e-39
E value
                  79
Match length
                  100
% identity
                  ELONGATION FACTOR 1-BETA' (EF-1-BETA')
NCBI Description
                  >gi_322851_pir__S29224 translation elongation factor eEF-1
                  beta' chain - rice >gi 218161 dbj BAA02253 (D12821)
                  elongation factor 1 beta' [Oryza sativa]
                  415785
Seq. No.
Seq. ID
                  uC-osflcyp179f10b1
                  BLASTX
Method
NCBI GI
                  g4678208
BLAST score
                  285
E value
                  2.0e-25
                  74
Match length
                  70
% identity
                  (AC007134) putative sugar transporter [Arabidopsis
NCBI Description
                  thaliana]
                  415786
Seq. No.
Seq. ID
                  uC-osflcyp179f11b1
                  BLASTX
Method
                  g5921647
NCBI GI
BLAST score
                  427
                  5.0e-42
E value
                  135
Match length
                  63
% identity
NCBI Description (AF155332) flavonoid 3'-hydroxylase [Petunia x hybrida]
                  415787
Seq. No.
                  uC-osflcyp179g01b1
Seq. ID
                  BLASTX
Method
NCBI GI
                  q1763308
BLAST score
                  148
                  2.0e-10
E value
Match length
                  46
                  79
% identity
NCBI Description (U75429) histone H3 [Euplotes crassus]
Seq. No.
                  415788
Seq. ID
                  uC-osflcyp179g02b1
                  BLASTX
Method
NCBI GI
                  g1076486
BLAST score
                  371
E value
                  2.0e-35
Match length
                  116
                  65
% identity
NCBI Description cim1 protein - soybean >gi_555616 (U03860) cytokinin
                  induced message [Glycine max]
```

415789

Seq. No.

```
uC-osflcyp179g03a1
Seq. ID
                  BLASTN
Method
                  g218188
NCBI GI
BLAST score
                  45
                  5.0e-16
E value
                  170
Match length
                  81
% identity
NCBI Description Rice mRNA for poly-ubiquitin, partial sequence
                  415790
Seq. No.
                  uC-osflcyp179g03b1
Seq. ID
                  BLASTX
Method
                  q70644
NCBI GI
                  696
BLAST score
                  1.0e-73
E value
                  143
Match length
                  19
% identity
NCBI Description ubiquitin precursor - common sunflower (fragment)
                   415791
Seq. No.
Seq. ID
                  uC-osflcyp179g05b1
Method
                  BLASTX
                  q2995378
NCBI GI
                   452
BLAST score
                   6.0e-45
E value
                  106
Match length
% identity
                   81
NCBI Description (X69915) unnamed protein product [Triticum aestivum]
                   415792
Seq. No.
Seq. ID
                   uC-osflcyp179g06a1
Method
                  BLASTX
                   g347451
NCBI GI
BLAST score
                   163
                   4.0e-11
E value
                   31
Match length
                   100
% identity
                  (L22155) ribulose 1,5-bisphosphate carboxylase [Oryza
NCBI Description
                   sativa]
                   415793
Seq. No.
Seq. ID
                   uC-osflcyp179g06b1
Method
                   BLASTX
NCBI GI
                   q2407281
                   477
BLAST score
                   3.0e-49
E value
                   105
Match length
% identity
                  (AF017363) ribulose 1,5-bisphosphate carboxylase small
NCBI Description
                   subunit [Oryza sativa]
                   415794
Seq. No.
Seq. ID
                   uC-osflcyp179g09a1
Method
                   BLASTX
NCBI GI
                   g4097522
BLAST score
                   248
E value
                   4.0e-21
```

```
Match length
                  72
% identity
                  (U63534) cinnamyl alcohol dehydrogenase [Fragaria x
NCBI Description
                  ananassa]
                  415795
Seq. No.
                  uC-osflcyp179g09b1
Seq. ID
                  BLASTX
Method
NCBI GI
                  q1168732
                  320
BLAST score
                  2.0e-29
E value
                  95
Match length
                  63
% identity
                  CINNAMYL-ALCOHOL DEHYDROGENASE (CAD) >gi 421914 pir_S28045
NCBI Description
                  ELI3 protein - parsley (fragment) >gi_836638_emb_CAA48028_
                  (X67817) Eli3 [Petroselinum crispum]
                  415796
Seq. No.
Seq. ID
                  uC-osflcyp179g10a1
                  BLASTN
Method
                  g450548
NCBI GI
BLAST score
                  124
                  4.0e-63
E value
                  284
Match length
                  86
% identity
NCBI Description O.sativa (pRSAM-1) gene for S-adenosyl methionine
                  synthetase
                  415797
Seq. No.
Seq. ID
                  uC-osflcyp179g11a1
Method
                  BLASTX
                  q2118130
NCBI GI
                  186
BLAST score
                  8.0e-14
E value
                   36
Match length
% identity
                  cysteine proteinase (EC 3.4.22.-), glucose
NCBI Description
                   starvation-induced - maize (fragment)
                   >gi 559532 emb CAA57675 (X82185) cysteine proteinase [Zea
                  mays]
Seq. No.
                   415798
                   uC-osflcyp179g11b1
Seq. ID
                   BLASTX
Method
NCBI GI
                   q1706260
BLAST score
                   725
                   2.0e-79
E value
Match length
                   164
                   90
% identity
NCBI Description CYSTEINE PROTEINASE 1 PRECURSOR >gi 2118131 pir S59597
                   cysteine proteinase 1 precursor - maize
                   >gi 643597 dbj BAA08244 (D45402) cysteine proteinase [Zea
                   mays]
                   415799
Seq. No.
                   uC-osflcyp179h02a1
Seq. ID
                   BLASTX
Method
```

```
NCBI GI
                  g2267597
BLAST score
                  216
E value
                  2.0e-17
                  43
Match length
                  100
% identity
NCBI Description (AF009413) 10 kDa chaperonin [Oryza sativa]
                  415800
Seq. No.
Seq. ID
                  uC-osflcyp179h02b1
Method
                  BLASTX
                  g2267597
NCBI GI
BLAST score
                  458
E value
                  1.0e-45
Match length
                  94
                  99
% identity
                 (AF009413) 10 kDa chaperonin [Oryza sativa]
NCBI Description
                  415801
Seq. No.
Seq. ID
                  uC-osflcyp179h05b1
Method
                  BLASTX
                  g2462748
NCBI GI
BLAST score
                  504
                  4.0e-51
E value
                  131
Match length
                  71
% identity
NCBI Description
                  (AC002292) putative Clathrin Coat Assembly protein
                   [Arabidopsis thaliana]
                   415802
Seq. No.
Seq. ID
                  uC-osflcyp179h08b1
Method
                  BLASTX
                  g6103585
NCBI GI
                  357
BLAST score
                  6.0e-34
E value
Match length
                  94
% identity
                   69
                  (AF149311) raucaffricine-O-beta-D-glucosidase [Rauvolfia
NCBI Description
                   serpentina]
Seq. No.
                   415803
Seq. ID
                  uC-osflcyp179h09b1
Method
                  BLASTX
NCBI GI
                  q4914427
BLAST score
                   161
E value
                   6.0e-11
Match length
                  127
                   35
% identity
NCBI Description (AL050351) dnaJ-like protein [Arabidopsis thaliana]
Seq. No.
                   415804
Seq. ID
                   uC-osflcyp179h11a1
Method
                   BLASTN
NCBI GI
                   g450548
BLAST score
                   58
                   6.0e-24
E value
Match length
                  94
                   90
% identity
```

```
NCBI Description O.sativa (pRSAM-1) gene for S-adenosyl methionine
                  synthetase
Seq. No.
                  415805
Seq. ID
                  uC-osflcyp179h11b1
                  BLASTX
Method
NCBI GI
                  q1173104
BLAST score
                  492
                  1.0e-49
E value
                  164
Match length
                  52
% identity
                  RIBONUCLEASE 2 PRECURSOR >gi 289210 (M98336) ribonuclease
NCBI Description
                   [Arabidopsis thaliana] >gi 2642160 (AC003000) ribonuclease,
                  RNS2 [Arabidopsis thaliana]
                  415806
Seq. No.
Seq. ID
                  uC-osflcyp179h12a1
                  BLASTX
Method
NCBI GI
                  q1170937
BLAST score
                  238
                  6.0e-20
E value
                  44
Match length
                  98
% identity
NCBI Description
                  S-ADENOSYLMETHIONINE SYNTHETASE 1 (METHIONINE
                  ADENOSYLTRANSFERASE 1) (ADOMET SYNTHETASE 1)
                  >qi 450549 emb CAA81481 (Z26867) S-adenosyl methionine
                  synthetase [Oryza sativa]
Seq. No.
                   415807
                  uC-osflcyp179h12b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1170937
BLAST score
                   623
E value
                  2.0e-73
                  139
Match length
                  100
% identity
                  S-ADENOSYLMETHIONINE SYNTHETASE 1 (METHIONINE
NCBI Description
                  ADENOSYLTRANSFERASE 1) (ADOMET SYNTHETASE 1)
                  >gi 450549 emb CAA81481 (Z26867) S-adenosyl methionine
                   synthetase [Oryza sativa]
                   415808
Seq. No.
                   uC-osflm202002a02b1
Seq. ID
Method
                  BLASTX
                  g4678935
NCBI GI
BLAST score
                   212
                   6.0e-17
E value
                   97
Match length
% identity
                   47
NCBI Description (AL049711) putative protein [Arabidopsis thaliana]
                   415809
Seq. No.
                   uC-osflm202002a03b1
Seq. ID
Method
                  BLASTX
```

g3858935

1.0e-14

191

NCBI GI BLAST score

E value

E value Match length

54

80 Match length 51 % identity (AL021636) synaptobrevin-like protein [Arabidopsis NCBI Description thaliana] >gi_4103357 (AF025332) vesicle-associated membrane protein 7C; synaptobrevin 7C [Arabidopsis thaliana] 415810 Seq. No. uC-osflm202002a04b1 Seq. ID BLASTX Method NCBI GI q5732069 568 BLAST score 2.0e-58 E value 159 Match length 74 % identity (AF147263) contains similarity to Pfam family PF00036 - EF NCBI Description hand; score=11.7, E=0.66, N=1 [Arabidopsis thaliana] 415811 Seq. No. ${\tt uC-osflm202002a07b1}$ Seq. ID Method BLASTX g1352830 NCBI GI 640 BLAST score 4.0e-67 E value 133 Match length 94 % identity VACUOLAR ATP SYNTHASE CATALYTIC SUBUNIT A (V-ATPASE 69 KD NCBI Description SUBUNIT) >gi_1049253 (U36436) vacuolar ATPase 69 kDa subunit [Zea mays] 415812 Seq. No. uC-osflm202002a09b1 Seq. ID BLASTX Method q3935183 NCBI GI 213 BLAST score 4.0e-17 E value 83 Match length 49 % identity NCBI Description (AC004557) F17L21.26 [Arabidopsis thaliana] 415813 Seq. No. Seq. ID uC-osflm202002a12b1 BLASTX Method q5042423 NCBI GI 243 BLAST score 2.0e-20 E value 108 Match length % identity (AC006193) Hypothetical Protein [Arabidopsis thaliana] NCBI Description 415814 Seq. No. Seq. ID uC-osflm202002b01b1 BLASTX Method NCBI GI q4836919 BLAST score 212 5.0e-17

```
% identity
                  (AC007153) 99202 [Arabidopsis thaliana]
NCBI Description
                  415815
Seq. No.
                  uC-osflm202002b03b1
Seq. ID
                  BLASTX
Method
NCBI GI
                  g282994
                  295
BLAST score
                  1.0e-26
E value
                  65
Match length
                  89
% identity
                  Sip1 protein - barley >gi 167100 (M77475) seed imbibition
NCBI Description
                  protein [Hordeum vulgare]
Seq. No.
                  415816
                  uC-osflm202002b04b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2695711
BLAST score
                  383
                  6.0e-37
E value
                  97
Match length
                  74
% identity
                  (AJ001370) cytochome b5 [Olea europaea]
NCBI Description
                  415817
Seq. No.
                  uC-osflm202002b05b1
Seq. ID
Method
                  BLASTX
                  g4588906
NCBI GI
BLAST score
                  559
                  2.0e-57
E value
                  120
Match length
                  90
% identity
                  (AF118149) ribosomal protein S7 [Secale cereale]
NCBI Description
                  415818
Seq. No.
Seq. ID
                  uC-osflm202002b06b1
Method
                  BLASTX
NCBI GI
                  g1345809
                  391
BLAST score
                   7.0e-38
E value
                  73
Match length
                  99
% identity
                  CHALCONE SYNTHASE (NAREGENIN-CHALCONE SYNTHASE)
NCBI Description
                  >gi_2117713_pir__S58190 naringenin-chalcone synthase (EC
                  2.3.1.74) - rice >gi_927491_emb_CAA61955_ (X89859)
                  naringenin-chalcone synthase [Oryza sativa]
Seq. No.
                  415819
Seq. ID
                  uC-osflm202002b10b1
                  BLASTX
Method
NCBI GI
                  q129916
BLAST score
                  598
E value
                   4.0e-62
Match length
                  131
% identity
                  89
NCBI Description PHOSPHOGLYCERATE KINASE, CYTOSOLIC >gi 66911 pir TVWTGY
                  phosphoglycerate kinase (EC 2.7.2.3), cytosolic - wheat
```

>gi_21835_emb_CAA33302_ (X15232) phosphoglycerate kinase (AA 1 - 401) [Triticum aestivum] 415820 Seq. No. Seq. ID uC-osflm202002b12b1 BLASTN Method g2662340 NCBI GI BLAST score 35 2.0e-10 E value 115 Match length 83 % identity NCBI Description Oryza sativa mRNA for EF-1 alpha, complete cds 415821 Seq. No. Seq. ID uC-osflm202002c02b1 BLASTX Method NCBI GI g2894288 200 BLAST score E value 9.0e-16 87 Match length 48 % identity (AL021837) putative proteome subunit [Schizosaccharomyces NCBI Description pombe] 415822 Seq. No. uC-osflm202002c05b1 Seq. ID BLASTX Method q3046693 NCBI GI BLAST score 631 E value 6.0e-66 157 Match length % identity 71 (AL022140) receptor like protein (fragment) [Arabidopsis NCBI Description thaliana] 415823 Seq. No. uC-osflm202002c06b1 Seq. ID BLASTX Method NCBI GI q5080792 BLAST score 199 2.0e-15 E value Match length 85 48 % identity (AC007576) Unknown protein [Arabidopsis thaliana] NCBI Description 415824 Seq. No. uC-osflm202002c08b1 Seq. ID BLASTX Method g2894288 NCBI GI 205 BLAST score 5.0e-16 E value 87 Match length 48 % identity NCBI Description (AL021837) putative proteome subunit [Schizosaccharomyces pombe]

54310

415825

Seq. No.

Seq. ID uC-osflm202002c11b1 Method BLASTX NCBI GI q4127350 BLAST score 235 E value 1.0e-19 129 Match length 38 % identity (AJ010450) glutathione transferase [Alopecurus myosuroides] NCBI Description 415826 Seq. No. uC-osflm202002c12b1 Seq. ID BLASTX Method NCBI GI q3882081 467 BLAST score 5.0e-47E value 104 Match length % identity 29 NCBI Description (AJ012552) polyubiquitin [Vicia faba] >qi 5732081 qb AAD48980.1 AF162444 12 (AF162444) contains similarity to Pfam family PF00240 - Ubiquitin family; score=526.5, E=1.9e-154, N=3 [Arabidopsis thaliana] 415827 Seq. No. Seq. ID uC-osflm202002d03b1 BLASTX Method NCBI GI q2494261 BLAST score 344 1.0e-32 E value Match length 105 % identity 68 NCBI Description ELONGATION FACTOR TU, CHLOROPLAST PRECURSOR (EF-TU) >qi 99903 pir S21567 translation elongation factor Tu precursor - soybean chloroplast >gi 18776 emb CAA46864 (X66062) EF-Tu [Glycine max] >gi 448921 prf 1918220A elongation factor Tu [Glycine max] 415828 Seq. No. uC-osflm202002d04b1 Seq. ID Method BLASTX NCBI GI g1737492 BLAST score 427 4.0e-42 E value 108 Match length 71 % identity (U81318) poly(A)-binding protein [Triticum aestivum] NCBI Description 415829 Seq. No. uC-osflm202002d05b1 Seq. ID Method BLASTX g320618 NCBI GI BLAST score 328 E value 1.0e-30

Match length 87 % identity 76

NCBI Description chlorophyll a/b-binding protein I precursor - rice

>gi_218172_dbj_BAA00536_ (D00641) type I light-harvesting

chlorophyll a/b-binding protein [Oryza sativa]

```
>gi 227611 prf 1707316A chlorophyll a/b binding protein 1
                  [Oryza sativa]
Seq. No.
                  415830
Seq. ID
                  uC-osflm202002d10b1
Method
                  BLASTX
NCBI GI
                  g730290
BLAST score
                  270
E value
                  1.0e-23
Match length
                  109
                  50
% identity
NCBI Description
                  PECTATE LYASE PRECURSOR >gi 322883 pir S29612 pectate
                  lyase - trumpet lily >gi 19451 emb CAA78976 (Z17328)
                  pectate lyase [Lilium longiflorum] >gi 308902 (L18911)
                  pectate lyase [Lilium longiflorum]
Seq. No.
                  415831
Seq. ID
                  uC-osflm202002e01b1
Method
                  BLASTX
NCBI GI
                  q1076511
BLAST score
                  499
E value
                  2.0e-50
Match length
                  126
% identity
                  79
                  H+-transporting ATPase (EC 3.6.1.35) - kidney bean
NCBI Description
                  >gi_758250_emb_CAA59799_ (X85804) H(+)-transporting ATPase
                  [Phaseolus vulgaris]
Seq. No.
                  415832
                  uC-osflm202002e02b1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g6006355
BLAST score
                  187
E value
                  1.0e-101
                  191
Match length
                  99
% identity
NCBI Description Oryza sativa genomic DNA, chromosome 6, clone:P0493C11
Seq. No.
                  415833
                  uC-osflm202002e04b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1491615
                  207
BLAST score
E value
                  3.0e-16
                  66
Match length
                  62
% identity
                  (X99923) male sterility 2-like protein [Arabidopsis
NCBI Description
                  thaliana]
                  415834
Seq. No.
                  uC-osflm202002e07b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2462837
BLAST score
                  362
E value
                  6.0e-35
Match length
                  78
```

87

% identity

```
NCBI Description (AF000657) hypothetical protein [Arabidopsis thaliana]
                  415835
Seq. No.
                  uC-osflm202002e08b1
Seq. ID
                  BLASTX
Method
                  g2293480
NCBI GI
BLAST score
                  364
                  4.0e-35
E value
                  75
Match length
                  93
% identity
NCBI Description
                  (AF011331) glycine-rich protein [Oryza sativa]
                  415836
Seq. No.
                  uC-osflm202002e09b1
Seq. ID
                  BLASTX
Method
NCBI GI
                  g113621
BLAST score
                  485
                  3.0e-49
E value
                  95
Match length
                  97
% identity
                  FRUCTOSE-BISPHOSPHATE ALDOLASE, CYTOPLASMIC ISOZYME
NCBI Description
                  >gi_68196_pir__ADZM fructose-bisphosphate aldolase (EC
                  4.1.2.13), cytosolic - maize >gi 168420 (M16220) aldolase
                  [Zea mays] >gi 295850 emb CAA31366 (X12872) fructose
                  bisphosphate aldolase [Zea mays] >gi 225624 prf 1307278A
                  cytoplasmic aldolase [Zea mays]
Seq. No.
                  415837
                  uC-osflm202002e10b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q22160
BLAST score
                  183
                  1.0e-13
E value
                  67
Match length
                  55
% identity
NCBI Description (X02842) put. ATP/ADP translocator [Zea mays]
Seq. No.
                  415838
                  uC-osflm202002e12b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2613143
BLAST score
                  146
                  5.0e-17
E value
Match length
                  94
                  45
% identity
NCBI Description (AF030548) tubulin [Oryza sativa]
Seq. No.
                  415839
Seq. ID
                  uC-osflm202002f02b1
Method
                  BLASTN
NCBI GI
                  q4091009
BLAST score
                  126
E value
                  2.0e-64
Match length
                  326
% identity
                  94
NCBI Description Oryza sativa anther-specific protein gene, complete cds
```

Seq. No. 415840 uC-osflm202002f03b1 Seq. ID BLASTX Method NCBI GI q2266662 BLAST score 496 3.0e-50E value 105 Match length 96 % identity (Y14200) 14-3-3 protein [Hordeum vulgare] NCBI Description 415841 Seq. No. uC-osflm202002f04b1 Seq. ID Method BLASTX q2662343 NCBI GI 241 BLAST score 7.0e-36 E value Match length 129 % identity 64 NCBI Description (D63581) EF-1 alpha [Oryza sativa] 415842 Seq. No. uC-osflm202002f05b1 Seq. ID BLASTX Method NCBI GI q3882355 BLAST score 351 4.0e-33 E value 76 Match length 84 % identity (U92460) 12-oxophytodienoate reductase OPR1 [Arabidopsis NCBI Description thaliana] 415843 Seq. No. uC-osflm202002f07b1 Seq. ID Method BLASTX g2160322 NCBI GI 635 BLAST score 1.0e-66 E value 123 Match length % identity 97 (D16139) cytokinin binding protein CBP57 [Nicotiana NCBI Description sylvestris] 415844 Seq. No. uC-osflm202002f10b1 Seq. ID Method BLASTX NCBI GI g3913018 643 BLAST score 2.0e-67 E value 130 Match length 100 % identity FRUCTOSE-BISPHOSPHATE ALDOLASE, CHLOROPLAST PRECURSOR NCBI Description (ALDP) >gi_218155_dbj_BAA02730_ (D13513) chloroplastic aldolase [Oryza sativa] Seq. No. 415845 uC-osflm202002g04b1 Seq. ID Method BLASTX

54314

```
NCBI GI
                  g2914706
BLAST score
                  488
                  1.0e-50
E value
Match length
                  124
                  80
% identity
                  (AC003974) putative homeobox protein [Arabidopsis thaliana]
NCBI Description
                  415846
Seq. No.
Seq. ID
                  uC-osflm202002g05b1
                  BLASTX
Method
                  g6045133
NCBI GI
                  167
BLAST score
E value
                  1.0e-11
                  52
Match length
                   60
% identity
                  (AB033334) cycloartenol synthase [Luffa cylindrica]
NCBI Description
                   415847
Seq. No.
Seq. ID
                  uC-osflm202002g08b1
                  BLASTX
Method
                  q2618689
NCBI GI
                   227
BLAST score
                   7.0e-19
E value
Match length
                   67
                   64
% identity
                  (AC002510) unknown protein [Arabidopsis thaliana]
NCBI Description
                   415848
Seq. No.
Seq. ID
                   uC-osflm202002g10b1
Method
                   BLASTX
                   q4887543
NCBI GI
                   179
BLAST score
                   5.0e-13
E value
                   49
Match length
                   73
% identity
                  (AJ012278) ATP-dependent Clp protease subunit ClpP
NCBI Description
                   [Arabidopsis thaliana] >gi_5360579_dbj_BAA82065.1_
                   (AB022326) nClpP1 [Arabidopsis thaliana]
                   415849
Seq. No.
                   uC-osflm202002g11b1
Seq. ID
                   BLASTX
Method
                   g2673913
NCBI GI
                   162
BLAST score
                   7.0e-11
E value
                   39
Match length
                   79
% identity
NCBI Description (AC002561) hypothetical protein [Arabidopsis thaliana]
                   415850
Seq. No.
                   uC-osflm202002h01b1
Seq. ID
                   BLASTX
Method
NCBI GI
                   q5302811
                   330
BLAST score
                   1.0e-30
E value
                   74
Match length
                   77
% identity
```

Seq. ID

```
(Z97342) putative serine protease-like protein [Arabidopsis
NCBI Description
                  thaliana]
                  415851
Seq. No.
                  uC-osflm202002h03b1
Seq. ID
                  BLASTX
Method
                  q2281705
NCBI GI
                  346
BLAST score
                  1.0e-32
E value
                  71
Match length
                  93
% identity
                  (AF013979) ethylene responsive factor [Oryza sativa]
NCBI Description
                  415852
Seq. No.
                  uC-osflm202002h07b1
Seq. ID
Method
                  BLASTX
                  q1848212
NCBI GI
BLAST score
                  361
                  2.0e-34
E value
Match length
                  71
                  45
% identity
                  (Y11209) protein disulfide-isomerase precursor [Nicotiana
NCBI Description
                  tabacum]
                  415853
Seq. No.
                  uC-osflm202002h10b1
Seq. ID
                  BLASTX
Method
NCBI GI
                  g3309066
BLAST score
                  658
                  4.0e-69
E value
                  147
Match length
                  83
% identity
                  (AF073488) bifunctional dihydrofolate reductase-thymidylate
NCBI Description
                  synthase [Zea mays]
                   415854
Seq. No.
                  uC-osflm202002h11b1
Seq. ID
Method
                  BLASTN
                   g303843
NCBI GI
                   62
BLAST score
                   5.0e-27
E value
Match length
                  70
                   97
% identity
NCBI Description Rice mRNA for eukaryotic initiation factor 4A, complete cds
                   415855
Seq. No.
                   uC-osflm202099a01b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   q5931694
                   727
BLAST score
                   4.0e-77
E value
                   175
Match length
% identity
NCBI Description (Y18470) Exportin1 (XPO1) protein [Arabidopsis thaliana]
                   415856
Seq. No.
                   uC-osflm202099a02b1
```

54316

Method BLASTX · NCBI GI g4894182 BLAST score 638 8.0e-67 E value Match length 147 80 % identity NCBI Description (AJ242551) 12-oxophytodienoate reductase [Lycopersicon esculentum] 415857 Seq. No. Seq. ID uC-osflm202099a03b1 BLASTX Method NCBI GI q5091498 BLAST score 420 E value 2.0e-41 Match length 103 80 % identity NCBI Description (AB023482) ESTs AU058067(E20733), AAU058070(E20873) correspond to a region of the predicted gene.; Similar to Populus tremuloides caffeoyl-CoA 3-O-methyltransferase mRNA, complete cds.(U27116) [Oryza sativa] Seq. No. 415858 uC-osflm202099a07b1 Seq. ID Method BLASTX NCBI GI g6041792 BLAST score 740 1.0e-78 E value Match length 188 77 % identity NCBI Description (AC009755) unknown protein [Arabidopsis thaliana] 415859 Seq. No. uC-osflm202099a08b1 Seq. ID Method BLASTX NCBI GI g6094555 BLAST score 177 E value 1.0e-12 Match length 56 59 % identity NCBI Description (AC010676) unknown protein [Arabidopsis thaliana] Seq. No. 415860 Seq. ID uC-osflm202099a10b1 Method BLASTX NCBI GI g115787 BLAST score 149 E value 6.0e-20

Match length 85 % identity

NCBI Description CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I

CAB-2) (LHCP) >gi_82461_pir__S03706 chlorophyll a/b-binding protein 2R precursor - rice >gi_20182_emb_CAA32109_

(X13909) chlorophyll a/b-binding preprotein (AA -28 to 235)

[Oryza sativa]

Seq. No. 415861

Seq. ID uC-osflm202099a11b1 Method BLASTX NCBI GI g115577 BLAST score 603 8.0e-63 E value Match length 127 90 % identity PHOSPHOENOLPYRUVATE CARBOXYLASE, HOUSEKEEPING ISOZYME NCBI Description (PEPCASE) >gi 348536 pir S28614 phosphoenolpyruvate carboxylase (EC 4.1.1.31) - sugarcane hybrid H32-8560 >gi_169844 (M86661) phosphoenolpyruvate carboxylase [Saccharum sp.] Seq. No. 415862 uC-osflm202099b01b1 Seq. ID Method BLASTX NCBI GI g2493147 BLAST score 466 1.0e-46 E value 93 Match length 99 % identity NCBI Description VACUOLAR ATP SYNTHASE 16 KD PROTEOLIPID SUBUNIT >gi 857574 (U27098) H+-ATPase [Oryza sativa] Seq. No. 415863 Seq. ID uC-osflm202099b03b1 Method BLASTX NCBI GI g2501189 BLAST score 323 5.0e-30 E value 105 Match length 69 % identity NCBI Description THIAMINE BIOSYNTHETIC ENZYME 1-1 PRECURSOR >gi 2130146 pir S61419 thiamine biosynthetic enzyme thi1-1 - maize >gi $^{-}$ 596 $^{-}$ 078 (U17350) thiamine biosynthetic enzyme [Zea mays] Seq. No. 415864 uC-osflm202099b05b1 Seq. ID Method BLASTX g586021 NCBI GI BLAST score 233 E value 3.0e-19 Match length 94 47 % identity NCBI Description PROBABLE PEPTIDYL-TRNA HYDROLASE (PTH) (STAGE V SPORULATION PROTEIN C) >gi_2127242_pir__S66083 stage V sporulation protein - Bacillus subtilis >gi 467442 dbj BAA05288 (D26185) stage V sporulation [Bacillus subtilis] >gi_2632320_emb_CAB11829_ (Z99104) thermosensitive mutant blocks spore coat formation (stage V sporulation) [Bacillus

Seq. No. 415865

Seq. ID uC-osflm202099b09b1

subtilis]

Method BLASTX NCBI GI 94769012

```
BLAST score
                  517
                  2.0e-52
E value
Match length
                  122
                  84
% identity
                  (AF143746) CER1 [Oryza sativa]
NCBI Description
                  415866
Seq. No.
                  uC-osflm202099b10b1
Seq. ID
                  BLASTX
Method
NCBI GI
                  g3169719
                  555
BLAST score
                  5.0e-57
E value
                  159
Match length
% identity
                  67
                  (AF007109) similar to yeast dcp1 [Arabidopsis thaliana]
NCBI Description
                  415867
Seq. No.
                  uC-osflm202099c04b1
Seq. ID
                  BLASTX
Method
                  q3913426
NCBI GI
                  469
BLAST score
                  7.0e-47
E value
Match length
                  150
% identity
                  62
                  S-ADENOSYLMETHIONINE DECARBOXYLASE PROENZYME (ADOMETDC)
NCBI Description
                   (SAMDC) >gi 1532048_emb_CAA69074_ (Y07766)
                  S-adenosylmethionine decarboxylase [Oryza sativa]
                  415868
Seq. No.
                  uC-osflm202099c06b1
Seq. ID
                  BLASTX
Method
NCBI GI
                  q1519251
BLAST score
                  725
                   6.0e-77
E value
                  145
Match length
                   100
% identity
                  (U65957) GF14-c protein [Oryza sativa]
NCBI Description
                   415869
Seq. No.
                  uC-osflm202099c07b1
Seq. ID
                  BLASTX
Method
                   q2275202
NCBI GI
BLAST score
                   496
                   4.0e-50
E value
                   140
Match length
                   59
% identity
                  (AC002337) acyl-CoA synthetase isolog [Arabidopsis
NCBI Description
                   thaliana]
                   415870
Seq. No.
                   uC-osflm202099c09b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   a4586259
                   430
BLAST score
                   2.0e-42
E value
Match length
                   115
                   69
% identity
```

```
(AL049640) hydrolase-like protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  415871
                  uC-osflm202099c11b1
Seq. ID
                  BLASTX
Method
                  q5059160
NCBI GI
BLAST score
                  236
                  1.0e-19
E value
                  54
Match length
                  81
% identity
                  (AF143812) 1-D-deoxyxylulose 5-phosphate synthase
NCBI Description
                  [Lycopersicon esculentum]
                  415872
Seq. No.
                  uC-osflm202099c12b1
Seq. ID
Method
                  BLASTX
                  q1076746
NCBI GI
                  735
BLAST score
                  4.0e-78
E value
                  143
Match length
                  100
% identity
                  heat shock protein 70 - rice (fragment)
NCBI Description
                  >gi 763160 emb CAA47948 (X67711) heat shock protein 70
                   [Oryza sativa]
                  415873
Seq. No.
                  uC-osflm202099d01b1
Seq. ID
Method
                  BLASTX
                  g1729971
NCBI GI
                  440
BLAST score
                  1.0e-43
E value
                  118
Match length
                  75
% identity
                  TONOPLAST INTRINSIC PROTEIN, GAMMA (GAMMA TIP)
NCBI Description
                   (AQUAPORIN-TIP) >gi_1076745_pir__S52004 gamma-Tip protein -
                  rice >gi_473997_dbj_BAA05017_ (D25534) gamma-Tip [Oryza
                  sativa]
                   415874
Seq. No.
                  uC-osflm202099d04b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3482974
                   337
BLAST score
                   2.0e-31
E value
Match length
                  140
                   49
% identity
NCBI Description
                  (AL031369) ATP-dependent Clp proteinase-like protein
                   [Arabidopsis thaliana]
                   415875
Seq. No.
                  uC-osflm202099d06b1
Seq. ID
                  BLASTX
Method
NCBI GI
                  q4760700
BLAST score
                   377
E value
                   5.0e - 36
Match length
                   126
% identity
                   60
```

```
(AB024437) peroxidase 1 [Scutellaria baicalensis]
NCBI Description
Seq. No.
                  415876
                  uC-osflm202099d10b1
Seq. ID
Method
                  BLASTX
                  q3695403
NCBI GI
BLAST score
                  552
                  1.0e-56
E value
Match length
                  131
% identity
                  81
                  (AF096373) contains similarity to the pfkB family of
NCBI Description
                  carbohydrate kinases (Pfam: PF00294, E=1.6e-75)
                   [Arabidopsis thaliana] >gi 4538955 emb CAB39779.1
                   (AL049488) fructokinase-like protein [Arabidopsis thaliana]
Seq. No.
                  415877
                  uC-osflm202099d11b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3928150
BLAST score
                  559
E value
                  2.0e-57
Match length
                  132
                  83
% identity
NCBI Description
                  (AJ131049) hypothetical protein [Cicer arietinum]
Seq. No.
                  415878
                  uC-osflm202099e01b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2598575
BLAST score
                  335
                  2.0e-31
E value
                  88
Match length
                  72
% identity
NCBI Description (Y15293) MtN21 [Medicago truncatula]
                  415879
Seq. No.
                  uC-osflm202099e02b1
Seq. ID
Method
                  BLASTX
                  g320622
NCBI GI
                  773
BLAST score
                  1.0e-82
E value
                  160
Match length
                  92
% identity
NCBI Description probable protein kinase - maize (fragment) >gi 168618
                   (M62985) protein kinase [Zea mays]
                  415880
Seq. No.
Seq. ID
                  uC-osflm202099e03b1
Method
                  BLASTX
NCBI GI
                  q218157
BLAST score
                  657
E value
                  4.0e-69
Match length
                  138
% identity
                  (D13512) cytoplasmic aldolase [Oryza sativa]
NCBI Description
```

415881

Seq. No.

BLAST score

517

uC-osflm202099e08b1 Seq. ID Method BLASTX NCBI GI g4206765 157 BLAST score 3.0e-10 E value Match length 73 % identity 45 (AF104329) putative type 1 membrane protein [Arabidopsis NCBI Description thaliana] Seq. No. 415882 uC-osflm202099e11b1 Seq. ID BLASTX Method g1753085 NCBI GI BLAST score 202 E value 8.0e-16 Match length 71 % identity 56 (U25283) leucine zipper protein [Oryza sativa] NCBI Description 415883 Seq. No. uC-osflm202099f01b1 Seq. ID Method BLASTX NCBI GI g2648777 BLAST score 146 4.0e-09 E value Match length 86 % identity 41 (AE000980) long-chain-fatty-acid--CoA ligase (fadD-7) NCBI Description [Archaeoglobus fulgidus] 415884 Seq. No. uC-osflm202099f05b1 Seq. ID Method BLASTX NCBI GI g5921663 BLAST score 728 3.0e-77 E value Match length 171 78 % identity NCBI Description (AF162279) 10-formyltetrahydrofolate synthetase [Arabidopsis thaliana] Seq. No. 415885 uC-osflm202099f07b1 Seq. ID BLASTX Method NCBI GI g4582449 BLAST score 265 E value 6.0e-23 Match length 131 % identity 48 NCBI Description (AC007071) putative APG protein [Arabidopsis thaliana] Seq. No. 415886 uC-osflm202099f08b1 Seq. ID BLASTX Method NCBI GI g3024122

54322

Match length

% identity

113 99

1.0e-52 E value Match length 99 100 % identity NCBI Description S-ADENOSYLMETHIONINE SYNTHETASE 2 (METHIONINE ADENOSYLTRANSFERASE 2) (ADOMET SYNTHETASE 2) >gi 1778821 (U82833) S-adenosyl-L-methionine synthetase [Oryza sativa] 415887 Seq. No. uC-osflm202099f09b1 Seq. ID BLASTX Method NCBI GI g3021357 BLAST score 252 1.0e-21 E value Match length 79 66 % identity (AJ005082) UDP-galactose 4-epimerase [Cyamopsis NCBI Description tetragonoloba] 415888 Seq. No. uC-osflm202099f10b1 Seq. ID Method BLASTX NCBI GI g4220477 BLAST score 154 5.0e-10 E value 117 Match length % identity 40 NCBI Description (AC006069) unknown protein [Arabidopsis thaliana] 415889 Seq. No. uC-osflm202099f11b1 Seq. ID Method BLASTN g607894 NCBI GI BLAST score 245 E value 1.0e-135 373 Match length 92 % identity NCBI Description Oryza sativa IR54 anther specific (RTS2) gene, complete cds Seq. No. 415890 uC-osflm202099g01b1 Seq. ID Method BLASTX NCBI GI q3126854 BLAST score 397 1.0e-38 E value Match length 115 79 % identity NCBI Description (AF061577) chlorophyll a/b binding protein [Oryza sativa] Seq. No. 415891 uC-osflm202099g05b1 Seq. ID Method BLASTN NCBI GI q5360658 BLAST score 70 E value 7.0e-31

54323

NCBI Description Oryza sativa OsASA2 mRNA for anthranilate synthase alpha 2

subunit, complete cds

Seq. No. 415892

Seq. ID uC-osflm202099g06b1

Method BLASTX
NCBI GI g5921722
BLAST score 182
E value 3.0e-13
Match length 136
% identity 35

NCBI Description CHALCONE--FLAVONONE ISOMERASE (CHALCONE ISOMERASE)

>gi 3126969 (AF061808) chalcone isomerase [Elaeagnus

umbellata]

Seq. No. 415893

Seq. ID uC-osflm202099g09b1

Method BLASTX
NCBI GI g2130073
BLAST score 696
E value 1.0e-73
Match length 136
% identity 99

NCBI Description fructose-bisphosphate aldolase (EC 4.1.2.13) isoenzyme C-1,

cytosolic - rice >gi_786178_dbj_BAA08845_ (D50307) aldolase

C-1 [Oryza sativa] >gi 790970 dbj BAA08830 (D50301)

aldolase C-1 [Oryza sativa]

Seq. No. 415894

Seq. ID uC-osflm202099g11b1

Method BLASTX
NCBI GI g3513727
BLAST score 537
E value 6.0e-55
Match length 158
% identity 62

NCBI Description (AF080118) contains similarity to TPR domains (Pfam:

TPR.hmm: score: 11.15) and kinesin motor domains (Pfam: kinesin2.hmm, score: 17.49, 20.52 and 10.94) [Arabidopsis thaliana] >gi_4539358_emb_CAB40052.1_ (AL049525) putative

protein [Arabidopsis Thaliana]

Seq. No. 415895

Seq. ID uC-osflm202099h01b1

Method BLASTX
NCBI GI g1709563
BLAST score 409
E value 3.0e-40
Match length 106
% identity 79

NCBI Description PHENYLALANINE AMMONIA-LYASE >gi_2130081_pir__\$66313

phenylalanine ammonia-lyase (EC 4.3.1.5) - rice >gi 871494 emb CAA61198 (X87946) phenylalanine

ammonia-lyase [Oryza sativa]

Seq. No. 415896

Seq. ID uC-osflm202099h03b1

Method BLASTX

Seq. ID

```
g129232
NCBI GI
                  472
BLAST score
                  2.0e-47
E value
Match length
                  97
                  92
% identity
                  ORYZAIN BETA CHAIN PRECURSOR >gi 67645 pir KHRZOB oryzain
NCBI Description
                  (EC 3.4.22.-) beta precursor - rice
                  >gi 218183_dbj_BAA14403_ (D90407) oryzain beta precursor
                  [Oryza sativa]
Seq. No.
                  415897
                  uC-osflm202099h05b1
Seq. ID
                  BLASTX
Method
NCBI GI
                  g129916
                  663
BLAST score
                  9.0e-70
E value
Match length
                  146
                  89
% identity
                  PHOSPHOGLYCERATE KINASE, CYTOSOLIC >gi_66911_pir__TVWTGY
NCBI Description
                  phosphoglycerate kinase (EC 2.7.2.3), cytosolic - wheat
                  >gi_21835_emb_CAA33302_ (X15232) phosphoglycerate kinase
                   (AA 1 - 401) [Triticum aestivum]
                  415898
Seq. No.
                  uC-osflm202099h06b1
Seq. ID
                  BLASTX
Method
NCBI GI
                  q2352795
                  587
BLAST score
                  9.0e-61
E value
                  156
Match length
                  73
% identity
NCBI Description
                  (AF007793) retinoblastoma-related protein 1 [Zea mays]
                  415899
Seq. No.
                  uC-osflm202099h08b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3236259
BLAST score
                   426
                   7.0e-42
E value
                  133
Match length
                   62
% identity
                   (AC004684) putative alcohol dehydrogenase [Arabidopsis
NCBI Description
                   thaliana] >gi 4895207_gb_AAD32794.1_AC007661_31 (AC007661)
                  putative alcohol dehydrogenase [Arabidopsis Thaliana]
                   415900
Seq. No.
Seq. ID
                   uC-osflm202099h09b1
Method
                   BLASTX
NCBI GI
                   g1054843
BLAST score
                   312
E value
                   9.0e-29
                   109
Match length
% identity
                   54
                  (X92847) D12 oleate desaturase [Solanum commersonii]
NCBI Description
                   415901
Seq. No.
```

uC-osflm202099h11b1

```
Method
                  BLASTX
                  g4508077
NCBI GI
                  320
BLAST score
                  2.0e-29
E value
Match length
                  74
                  80
% identity
                  (AC005882) 62114 [Arabidopsis thaliana]
NCBI Description
                  415902
Seq. No.
                  uC-osflm202099h12b1
Seq. ID
                  BLASTX
Method
                  g1710841
NCBI GI
                  562
BLAST score
                  6.0e-58
E value
Match length
                  123
                  86
% identity
                  ADENOSYLHOMOCYSTEINASE (S-ADENOSYL-L-HOMOCYSTEINE
NCBI Description
                  HYDROLASE) (ADOHCYASE) >gi_758247_emb_CAA56278_ (X79905)
                  S-adenosylhomocysteine hydrolase [Phalaenopsis sp.]
                  415903
Seq. No.
                  uC-osflm202100a01b1
Seq. ID
Method
                  BLASTX
                  g477280
NCBI GI
                   381
BLAST score
                  1.0e-36
E value
                  100
Match length
% identity
                  70
                  mitochondrial processing peptidase (EC 3.4.99.41) 55K
NCBI Description
                  protein precursor - potato >gi 410633 bbs_136740 cytochrome
                   c reductase-processing peptidase subunit I, MPP subunit I,
                   P55 [potatoes, var. Marfona, tuber, Peptide Mitochondrial,
                   534 aa]
                   415904
Seq. No.
                   uC-osflm202100a02b1
Seq. ID
Method
                  BLASTX
NCBI GI
                   q1771162
                   336
BLAST score
                   3.0e-31
E value
Match length
                   144
                   51
% identity
                  (X98930) SBT2 [Lycopersicon esculentum]
NCBI Description
                   >gi_3687307_emb_CAA07000.1 (AJ006379) subtilisin-like
                   protease [Lycopersicon esculentum]
Seq. No.
                   415905
Seq. ID
                   uC-osflm202100a04b1
Method
                   BLASTX
NCBI GI
                   q5689255
BLAST score
                   169
```

4.0e-12 E value 91 Match length 49 % identity

NCBI Description (AB024337) blue-light photoreceptor [Oryza sativa]

Seq. No. 415906

Seq. ID

Seq. ID uC-osflm202100a06b1 Method BLASTX NCBI GI q4586027 BLAST score 193 E value 7.0e-15 Match length 54 69 % identity (AC007109) putative ribosomal protein L14 [Arabidopsis NCBI Description thaliana] Seq. No. 415907 Seq. ID uC-osflm202100a09b1 Method BLASTX NCBI GI g3915635 BLAST score 247 4.0e-21 E value Match length 109 51 % identity CYCLIN DELTA-1 >gi 2995130 emb CAA58285 (X83369) cyclin NCBI Description delta-1 [Arabidopsis thaliana] 415908 Seq. No. Seq. ID uC-osflm202100a11b1 Method BLASTX q3859659 NCBI GI BLAST score 372 1.0e-35 E value Match length 95 % identity 73 (AL031394) putative potassium transporter AtKT5p (AtKT5) NCBI Description [Arabidopsis thaliana] 415909 Seq. No. uC-osflm202100a12b1 Seq. ID BLASTX Method g1170937 NCBI GI 608 BLAST score 1.0e-68 E value 140 Match length 95 % identity S-ADENOSYLMETHIONINE SYNTHETASE 1 (METHIONINE NCBI Description ADENOSYLTRANSFERASE 1) (ADOMET SYNTHETASE 1) >qi 450549 emb CAA81481 (Z26867) S-adenosyl methionine synthetase [Oryza sativa] 415910 Seq. No. uC-osflm202100b02b1 Seq. ID BLASTX Method q4538624 NCBI GI BLAST score 159 1.0e-10 E value Match length 128 34 % identity NCBI Description (AJ133502) hypothetical protein [Nicotiana tabacum] 415911 Seq. No.

54327

uC-osflm202100b05b1

```
Method
                  BLASTX
NCBI GI
                  g1199467
BLAST score
                  254
E value
                  3.0e-22
Match length
                  73
                  60
% identity
                  (D64155) possible aldehyde decarbonylase [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  415912
                  uC-osflm202100b06b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g6056372
BLAST score
                  251
                  1.0e-25
E value
Match length
                  146
% identity
                  46
                  (AC009894) Very similar to receptor-like serine/threonine
NCBI Description
                  kinase [Arabidopsis thaliana]
                  415913
Seq. No.
Seq. ID
                  uC-osflm202100b07b1
Method
                  BLASTX
NCBI GI
                  g1730560
BLAST score
                  612
E value
                  9.0e-64
Match length
                  146
% identity
                  76
                 ALPHA-GLUCAN PHOSPHORYLASE, H ISOZYME (STARCH PHOSPHORYLASE
NCBI Description
                  H) >gi_510932_emb_CAA84494_ (Z35117) alpha 1,4-glucan
                  phosphorylase type H [Vicia faba]
                  415914
Seq. No.
                  uC-osflm202100b09b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q266463
BLAST score
                  411
E value
                  3.0e-40
                  89
Match length
% identity
                  87
                  3-ISOPROPYLMALATE DEHYDROGENASE PRECURSOR (BETA-IPM
NCBI Description
                  DEHYDROGENASE) (IMDH) (3-IPM-DH) >gi 82259 pir S25670
                  3-isopropylmalate dehydrogenase (EC 1.1.1.85) precursor -
                  potato >gi_22643_emb_CAA47720_ (X67310) 3-isopropylmalate
                  dehydrogenase [Solanum tuberosum] >gi_445064_prf__1908380A
                  beta isopropylmalate dehydrogenase [Solanum tuberosum]
Seq. No.
                  415915
Seq. ID
                  uC-osflm202100b10b1
Method
                  BLASTX
NCBI GI
                  q3913018
BLAST score
                  633
E value
                  3.0e-66
Match length
                  128
                  100
% identity
NCBI Description FRUCTOSE-BISPHOSPHATE ALDOLASE, CHLOROPLAST PRECURSOR
```

(ALDP) >gi_218155_dbj_BAA02730_ (D13513) chloroplastic

aldolase [Oryza sativa]

Seq. No. 415916 Seq. ID uC-osflm202100c01b1 Method BLASTX NCBI GI g1170937 BLAST score 702 2.0e-74 E value 135 Match length 99 % identity NCBI Description S-ADENOSYLMETHIONINE SYNTHETASE 1 (METHIONINE ADENOSYLTRANSFERASE 1) (ADOMET SYNTHETASE 1) >gi 450549 emb CAA81481 (Z26867) S-adenosyl methionine synthetase [Oryza sativa] 415917 Seq. No. Seq. ID uC-osflm202100c02b1 Method BLASTX NCBI GI g6063542 BLAST score 755 E value 4.0e-80 158 Match length % identity 100 NCBI Description (AP000615) EST C74302(E30840) corresponds to a region of the predicted gene.; similar to glyceraldehyde-3-phosphate dehydrogenase. (M64118) [Oryza sativa] Seq. No. 415918 Seq. ID uC-osflm202100c05b1 Method BLASTX NCBI GI g3915131 BLAST score 574 E value 3.0e-59 Match length 114 % identity 98 NCBI Description THIOREDOXIN H-TYPE (TRX-H) (PHLOEM SAP 13 KD PROTEIN-1) >gi_426442_dbj_BAA04864_ (D21836) thioredoxin h [Oryza satīva] >gi_454882_dbj_BAA05546_ (D26547) rice thioredoxin h [Oryza sativa] >gi_1930072 (U92541) thioredoxin h [Oryza sativa] Seq. No. 415919 Seq. ID uC-osflm202100c06b1 Method BLASTX NCBI GI q3935181 BLAST score 419 E value 2.0e-41Match length 89 % identity NCBI Description (AC004557) F17L21.24 [Arabidopsis thaliana] Seq. No. 415920 Seq. ID uC-osflm202100c07b1 Method BLASTX NCBI GI

54329

g115787

5.0e-52

511

BLAST score

E value

Match length 118
% identity 86

NCBI Description CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I CAB-2) (LHCP) >gi_82461_pir__S03706 chlorophyll a/b-binding protein 2R precursor - rice >gi_20182_emb_CAA32109_
(X13909) chlorophyll a/b-binding preprotein (AA -28 to 235)
[Oryza sativa]

 Seq. No.
 415921

 Seq. ID
 uC-osflm202100c09b1

 Method
 BLASTX

 NCBI GI
 g2737973

 BLAST score
 634

 E value
 2.0e-66

E value 2.0e-Match length 128 % identity 94

NCBI Description (U83625) protein kinase ZmMEK1 [Zea mays]

Seq. No. 415922

Seq. ID uC-osflm202100c12b1

Method BLASTN
NCBI GI g5410347
BLAST score 83
E value 1.0e-38
Match length 258

Match length 258 % identity 84

NCBI Description Sorghum bicolor BAC clone 110K5, partial sequence

Seq. No. 415923

Seq. ID uC-osflm202100d01b1

Method BLASTX
NCBI GI g730510
BLAST score 397
E value 1.0e-38
Match length 77
% identity 100

NCBI Description RAS-RELATED PROTEIN RIC1 >gi 542150 pir S38740 GTP-binding

protein - rice >gi_432607_gb_AAB28535_ (\$\overline{S}66160\$) ras-related GTP binding protein possessing GTPase activity=ric1 [Oryza sativa=rice, var. Yamahoushi, callus, Peptide, 202 aa]

[Oryza sativa]

Seq. No. 415924

Seq. ID uC-osflm202100d03b1

Method BLASTX
NCBI GI g4101705
BLAST score 392
E value 6.0e-38
Match length 139
% identity 49

NCBI Description (AF006079) glucose acyltransferase [Solanum berthaultii]

Seq. No. 415925

Seq. ID uC-osflm202100d10b1

Method BLASTX NCBI GI g2506384 BLAST score 216

2.0e-17 E value 67 Match length 60 % identity ENDOGLUCANASE E-4 PRECURSOR (ENDO-1, 4-BETA-GLUCANASE E-4) NCBI Description (CELLULASE E-4) (CELLULASE E4) >gi 1817723 (L20093) beta-1,4-endoglucanase precursor [Thermomonospora fusca] 415926 Seq. No. uC-osflm202100d11b1 Seq. ID BLASTX Method g322854 NCBI GI 628 BLAST score 3.0e-66 E value 132 Match length 99 % identity pollen-specific protein - rice >gi_20310_emb_CAA78897_ NCBI Description (Z16402) pollen specific gene [Oryza sativa] 415927 Seq. No. uC-osflm202100e01b1 Seq. ID BLASTX Method g4585882 NCBI GI 509 BLAST score 1.0e-62 E value 139 Match length 81 % identity NCBI Description (AC005850) PSI type III chlorophyll a/b-binding protein [Arabidopsis thaliana] 415928 Seq. No. uC-osflm202100e02b1 Seq. ID Method BLASTN NCBI GI g5006854 BLAST score 88 E value 1.0e-41 Match length 195 % identity 95 Oryza sativa homeodomain leucine zipper protein (hox5) NCBI Description mRNA, complete cds 415929 Seq. No. Seq. ID uC-osflm202100e04b1 Method BLASTX NCBI GI q1136120 BLAST score 597 5.0e-62 E value Match length 113 % identity

NCBI Description (X91806) alpha-tubulin [Oryza sativa]

Seq. No. 415930

Seg. ID uC-osflm202100e10b1

Method BLASTX
NCBI GI g2997589
BLAST score 628
E value 1.0e-65
Match length 147

% identity 80 (AF020813) glucose-6-phosphate/phosphate-translocator NCBI Description precursor [Zea mays] Seq. No. 415931 Seq. ID uC-osflm202100e11b1 BLASTX Method NCBI GI q2493318 BLAST score 296 1.0e-26 E value Match length 94 53 % identity BLUE COPPER PROTEIN PRECURSOR >gi_562779 emb CAA80963 NCBI Description (Z25471) blue copper protein [Pisum sativum] >gi 1098264 prf 2115352A blue Cu protein [Pisum sativum] Seq. No. 415932 Seq. ID uC-osflm202100e12b1 Method BLASTX NCBI GI g3142301 BLAST score 269 1.0e-23 E value Match length 136 % identity 49 (AC002411) Contains similarity to neural cell adhesion NCBI Description molecule 2, large isoform precursor gb M76710 from Xenopus laevis, and beta transducin from S. cerevisiae gb Q05946. ESTs gb N65081 gb Z30910, gb Z34190, gb Z34611, gb R30101, gb_H3630 415933 Seq. No. uC-osflm202100f01b1 Seq. ID BLASTX Method g2911799 NCBI GI 510 BLAST score 8.0e-52 E value 147 Match length 66 % identity (AF008184) 4-coumarate:CoA ligase 1 [Populus balsamifera NCBI Description subsp. trichocarpa X Populus deltoides] 415934 Seq. No. uC-osflm202100f03b1 Seq. ID Method BLASTN g3819495 NCBI GI 78 BLAST score 1.0e-35 E value 168 Match length 87 % identity NCBI Description Hordeum vulgare genomic DNA fragment; clone MWG2025.rev

415935 Seq. No.

uC-osflm202100f04b1 Seq. ID

Method BLASTX NCBI GI q3413716 413 BLAST score 2.0e-40 E value

```
128
Match length
% identity
                  69
                  (AC004747) unknown protein [Arabidopsis thaliana]
NCBI Description
                  >qi 3643589 (AC005395) unknown protein [Arabidopsis
                  thaliana]
                  415936
Seq. No.
                  uC-osflm202100f06b1
Seq. ID
                  BLASTX
Method
                  g2506139
NCBI GI
BLAST score
                  614
                  7.0e-64
E value
                  160
Match length
                  75
% identity
                  COATOMER DELTA SUBUNIT (DELTA-COAT PROTEIN) (DELTA-COP)
NCBI Description
                  (ARCHAIN) >gi 1314049 emb CAA91901 (Z67962)
                  archain/delta-COP [Oryza sativa]
                  415937
Seq. No.
                  uC-osflm202100f08b1
Seq. ID
                  BLASTX
Method
NCBI GI
                  g124226
                  558
BLAST score
                  2.0e-57
E value
                  121
Match length
                  87
% identity
NCBI Description
                  INITIATION FACTOR 5A-2 (EIF-5A) (EIF-4D)
                  >gi_100278_pir__S21059 translation initiation factor
                  eIF-5A.2 - curled-leaved tobacco >gi_19702_emb_CAA45104_
                   (X63542) eukaryotic initiation factor 5A (2) [Nicotiana
                  plumbaginifolia]
                  415938
Seq. No.
                  uC-osflm202100f09b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3757529
BLAST score
                  268
E value
                  2.0e-23
                  95
Match length
                  56
% identity
                  (AC005167) tetracycline transporter-like protein
NCBI Description
                   [Arabidopsis thaliana]
                  415939
Seq. No.
                  uC-osflm202100f10b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1323748
BLAST score
                  234
E value
                  2.0e-19
                  105
Match length
% identity
                   50
NCBI Description (U32430) thiol protease [Triticum aestivum]
                  415940
Seq. No.
                  uC-osflm202100f12b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g5123712
```

```
BLAST score
                  575
                  2.0e-59
E value
Match length
                  144
% identity
                  74
NCBI Description (AL079347) putative protein [Arabidopsis thaliana]
Seq. No.
                  415941
Seq. ID
                  uC-osflm202100g01b1
Method
                  BLASTX
NCBI GI
                  q2662343
BLAST score
                  663
E value
                  1.0e-69
Match length
                  127
                  100
% identity
NCBI Description (D63581) EF-1 alpha [Oryza sativa]
                  415942
Seq. No.
                  uC-osflm202100g02b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4158221
BLAST score
                  358
                  7.0e-34
E value
Match length
                  69
% identity
                  99
NCBI Description (Y18624) reversibly glycosylated polypeptide [Oryza sativa]
                  415943
Seq. No.
                  uC-osflm202100g04b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3184283
BLAST score
                  606
E value
                  5.0e-63
Match length
                  160
                  76
% identity
NCBI Description (AC004136) putative TBP-binding protein [Arabidopsis
                  thaliana]
Seq. No.
                  415944
                  uC-osflm202100q05b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2598575
BLAST score
                  479
E value
                  4.0e-48
Match length
                  116
                  78
% identity
NCBI Description (Y15293) MtN21 [Medicago truncatula]
Seq. No.
                  415945
Seq. ID
                  uC-osflm202100g08b1
Method
                  BLASTX
NCBI GI
                  q4680661
BLAST score
                  234
E value
                  2.0e-19
Match length
                  132
                  34
% identity
```

NCBI Description (AF132945) CGI-11 protein [Homo sapiens]

Seq. No. Seq. ID uC-osflm202100g09b1 Method BLASTX NCBI GI q4758294 BLAST score 338 1.0e-31 E value Match length 132 49 % identity glutamyl-prolyl-tRNA synthetase NCBI Description >gi_135104_sp_P07814_SYEP_HUMAN MULTIFUNCTIONAL AMINOACYL-TRNA SYNTHETASE [INCLUDES: GLUTAMYL-TRNA SYNTHETASE (GLUTAMATE--TRNA LIGASE); PROLYL-TRNA SYNTHETASE (PROLINE--TRNA LIGASE)] >gi_68554_pir__SYHUQT glutamyl-prolyl-tRNA synthetase - human >gi_31958_emb_CAA38224_ (X54326) glutaminyl-tRNA synthetase [Homo sapiens] 415947 Seq. No. uC-osflm202100g10b1 Seq. ID Method BLASTX g100490 NCBI GI BLAST score 680 E value 1.0e-71 Match length 136 % identity 29 NCBI Description polyubiquitin - garden snapdragon (fragment) >gi_16071_emb_CAA48140_ (X67957) ubiquitin [Antirrhinum majus] 415948 Seq. No. Seq. ID uC-osflm202100g12b1 Method BLASTX NCBI GI q3643602 BLAST score 200 E value 1.0e-15 Match length 112 % identity 40 NCBI Description (AC005395) putative tonoplast intrinsic protein [Arabidopsis thaliana] Seq. No. 415949 Seq. ID uC-osflm202100h03b1 Method BLASTX NCBI GI g2281705 BLAST score 549 E value 4.0e-61 Match length 125 % identity 96 NCBI Description (AF013979) ethylene responsive factor [Oryza sativa] Seq. No. 415950 Seq. ID uC-osflm202100h05b1 Method BLASTX NCBI GI g417488 BLAST score 594 E value 1.0e-61 Match length 151

415946

```
% identity
                  ALPHA-GLUCAN PHOSPHORYLASE, H ISOZYME (STARCH PHOSPHORYLASE
NCBI Description
                  H) >gi_100452_pir_A40995 starch phosphorylase (EC 2.4.1.1)
                  H - potato >gi 169473 (M69038) alpha-glucan phosphorylase
                  type H isozyme [Solanum tuberosum]
                  415951
Seq. No.
                  uC-osflm202100h06b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4567207
                  205
BLAST score
                  4.0e-16
E value
Match length
                  66
                  56
% identity
                  (AC007168) unknown protein [Arabidopsis thaliana]
NCBI Description
                  415952
Seq. No.
Seq. ID
                  uC-osflm202100h08b1
                  BLASTX
Method
                  g1524370
NCBI GI
BLAST score
                  277
                  1.0e-24
E value
                  85
Match length
                  64
% identity
                  (X92491) TOM20 [Solanum tuberosum]
NCBI Description
Seq. No.
                  415953
Seq. ID
                  uC-osflm202100h11b1
Method
                  BLASTX
                  g1835731
NCBI GI
BLAST score
                  559
E value
                  1.0e-57
Match length
                  106
                  100
% identity
NCBI Description (U86018) photosystem II 10 kDa polypeptide [Oryza sativa]
Seq. No.
                  415954
                  uC-osflm202100h12b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  a733456
                  697
BLAST score
E value
                  1.0e-73
Match length
                  155
% identity
                  (U23189) chlorophyll a/b-binding apoprotein CP26 precursor
NCBI Description
                   [Zea mays]
Seq. No.
                   415955
Seq. ID
                  uC-osflm202101a03b1
                  BLASTX
Method
NCBI GI
                  q2662343
BLAST score
                  458
E value
                   1.0e-45
Match length
                  133
% identity
                   71
```

NCBI Description (D63581) EF-1 alpha [Oryza sativa]

NCBI GI

415956 Seq. No. Seq. ID uC-osflm202101a04b1 BLASTX Method g1360090 NCBI GI BLAST score 541 2.0e-55 E value 159 Match length 65 % identity (X95576) C1C-Nt1 [Nicotiana tabacum] NCBI Description 415957 Seq. No. uC-osflm202101a06b1 Seq. ID BLASTX Method NCBI GI g2662343 610 BLAST score 2.0e-64 E value Match length 136 99 % identity (D63581) EF-1 alpha [Oryza sativa] NCBI Description 415958 Seq. No. uC-osflm202101a08b1 Seq. ID Method BLASTX g3915023 NCBI GI 582 BLAST score 4.0e-60 E value Match length 165 % identity 67 SUCROSE-PHOSPHATE SYNTHASE 1 NCBI Description (UDP-GLUCOSE-FRUCTOSE-PHOSPHATE GLUCOSYLTRANSFERASE 1) >gi_2588888_dbj_BAA23213_ (AB005023) sucrose-phosphate synthase [Citrus unshiu] 415959 Seq. No. uC-osflm202101a09b1Seq. ID BLASTX Method NCBI GI q967125 BLAST score 247 7.0e-21E value 60 Match length 75 % identity (U08140) calcium dependent protein kinase [Vigna radiata] NCBI Description 415960 Seq. No. uC-osflm202101a10b1 Seq. ID BLASTN Method NCBI GI g5257255 BLAST score 41 1.0e-13 E value Match length 61 92 % identity NCBI Description Oryza sativa genomic DNA, chromosome 8, clone:P0026F07 415961 Seq. No. Seq. ID uC-osflm202101b03b1 BLASTX Method

54337

g1362152

BLAST score 581 5.0e-60 E value Match length 166 % identity 75 ribosomal protein S6 kinase homolog (clone Aspk11) - oat NCBI Description >gi_871986_emb_CAA56313_ (X79992) putative pp70 ribosomal protein S6 kinase [Avena sativa] 415962 Seq. No. uC-osflm202101b04b1 Seq. ID BLASTX Method NCBI GI g3258575 BLAST score 194 8.0e-15 E value Match length 50 72 % identity (U89959) Hypothetical protein [Arabidopsis thaliana] NCBI Description 415963 Seq. No. uC-osflm202101b05b1 Seq. ID BLASTX Method NCBI GI g3914422 BLAST score 581 4.0e-60 E value Match length 114 92 % identity PROFILIN >gi_2154728_emb_CAA69669_ (Y08389) profilin 2 NCBI Description [Cynodon dactylon] >gi 2154730_emb_CAA69670_ (Y08390) profilin 1 [Cynodon dactylon] 415964 Seq. No. uC-osflm202101b08b1 Seq. ID BLASTX Method g4741844 NCBI GI 518 BLAST score 1.0e-52 E value 116 Match length 93 % identity NCBI Description (AF112964) small GTP-binding protein [Triticum aestivum] 415965 Seq. No. uC-osflm202101b09b1 Seq. ID BLASTX Method g6009521 NCBI GI 318 BLAST score 3.0e-29 E value 143 Match length 47 % identity NCBI Description (AB021491) p100 co-activator [Mus musculus] 415966 Seq. No. uC-osflm202101b10b1 Seq. ID BLASTX Method g129591 NCBI GI 425 BLAST score E value 8.0e-42

54338

109

Match length

77 % identity PHENYLALANINE AMMONIA-LYASE >gi 295824 emb CAA34226 NCBI Description (X16099) phenylalanine ammonia-lyase [Oryza sativa] 415967 Seq. No. uC-osflm202101b12b1 Seq. ID BLASTX Method NCBI GI g1174613 BLAST score 537 7.0e-55 E value Match length 127 87 % identity 26S PROTEASE REGULATORY SUBUNIT 6A HOMOLOG (TAT-BINDING NCBI Description PROTEIN HOMOLOG 1) (TBP-1) >gi_556560_dbj_BAA04614_ (D17788) rice homologue of Tat binding protein [Oryza sativa] 415968 Seq. No. uC-osflm202101c01b1 Seq. ID BLASTX Method NCBI GI g3046815 BLAST score 180 5.0e-13 E value 41 Match length % identity 78 NCBI Description (AL021687) cytochrome P450 [Arabidopsis thaliana] 415969 Seq. No. uC-osflm202101c02b1 Seq. ID BLASTX Method NCBI GI q6091756 BLAST score 422 2.0e-41 E value Match length 131 56 % identity NCBI Description (AC009327) putative peroxidase [Arabidopsis thaliana] Seq. No. 415970 uC-osflm202101c03b1 Seq. ID BLASTN Method NCBI GI q5912298 BLAST score 69 2.0e-30 E value Match length 266 82 % identity NCBI Description Oryza sativa mRNA for gigantea homologue, partial Seq. No. 415971 uC-osflm202101c04b1 Seq. ID Method BLASTX NCBI GI g1657950 BLAST score 530 E value 5.0e-54 Match length 147 % identity 71

NCBI Description (U73467) MipE [Mesembryanthemum crystallinum]

BLAST score

495

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Seq. No.
                   415972
                  uC-osflm202101c06b1
Seq. ID
Method
                  BLASTX
                  q4028549
NCBI GI
BLAST score
                  286
                  2.0e-25
E value
Match length
                  156
% identity
                   40
                  (AF093690) ubiquitin hydrolase B [Dictyostelium discoideum]
NCBI Description
                   415973
Seq. No.
Seq. ID
                  uC-osflm202101c07b1
Method
                  BLASTX
NCBI GI
                  g2944187
BLAST score
                  214
                   9.0e-28
E value
Match length
                  136
                   49
% identity
                  (AF011336) putative E1-E2 ATPase [Mus musculus]
NCBI Description
                   415974
Seq. No.
                  uC-osflm202101c08b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1710521
BLAST score
                   575
                   2.0e-59
E value
Match length
                   115
                   97
% identity
NCBI Description 60S RIBOSOMAL PROTEIN L24 >gi 1154859 emb CAA63960
                   (X94296) L24 ribosomal protein [Hordeum vulgare]
                   415975
Seq. No.
                   uC-osflm202101c09b1
Seq. ID
Method
                   BLASTX
                   g4559380
NCBI GI
BLAST score
                   614
                   6.0e-64
E value
Match length
                   162
% identity
                   65
NCBI Description (AC006526) putative auxin-responsive GH3 protein
                   [Arabidopsis thaliana]
                   415976
Seq. No.
                   uC-osflm202101c10b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g5912299
BLAST score
                   368
E value
                   4.0e-35
                   125
Match length
% identity
NCBI Description (AJ133787) gigantea homologue [Oryza sativa]
                   415977
Seq. No.
                   uC-osflm202101c11b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   q136636
```

6.0e-50 E value 94 Match length 96 % identity UBIQUITIN-CONJUGATING ENZYME E2-17 KD 1 (UBIQUITIN-PROTEIN NCBI Description LIGASE 1) (UBIQUITIN CARRIER PROTEIN 1) >gi_1076424_pir__S43781 ubiquitin-conjugating enzyme UBC1 -Arabidopsis thaliana >gi 442594 pdb_1AAK_ Ubiquitin Conjugating Enzyme (E.C. $\overline{6}$.3.2.1 $\overline{9}$) > \overline{gi} 29 $\overline{8}$ 1894_pdb_2AAK_ Ubiquitin Conjugating Enzyme From Arabidopsis Thaliana >gi 166924 (M62721) ubiquitin carrier protein [Arabidopsis thaliana] >gi 431260 (L19351) ubiquitin conjugating enzyme [Arabidopsis thaliana]

Seq. No. 415978

Seq. ID uC-osflm202101d01b1

Method BLASTX
NCBI GI g20322
BLAST score 710
E value 3.0e-75
Match length 153
% identity 93

NCBI Description (X16280) Actin (AA 1-377) [Oryza sativa]

Seq. No. 415979

Seq. ID uC-osflm202101d02b1

Method BLASTX
NCBI GI g3256770
BLAST score 147
E value 4.0e-09
Match length 124
% identity 35

NCBI Description (AP000002) 318aa long hypothetical UDP-glucose 4-epimerase

[Pyrococcus horikoshii]

Seq. No. 415980

Seq. ID uC-osflm202101d04b1

Method BLASTX
NCBI GI g3335365
BLAST score 193
E value 1.0e-20
Match length 89
% identity 65

NCBI Description (AC003028) high affinity calcium antiporter [Arabidopsis

thaliana]

Seq. No. 415981

Seq. ID uC-osflm202101d06b1

Method BLASTX
NCBI GI g3367520
BLAST score 354
E value 2.0e-33
Match length 139
% identity 49

NCBI Description (AC004392) Similar to protein kinase APK1A,

tyrosine-serine-threonine kinase gb_D12522 from A.

thaliana. [Arabidopsis thaliana]

```
Seq. No.
                  415982
Seq. ID
                  uC-osflm202101d08b1
                  BLASTX
Method
                  g115583
NCBI GI
BLAST score
                  703
                  2.0e-74
E value
                  146
Match length
% identity
                  93
                  PHOSPHOENOLPYRUVATE CARBOXYLASE 2 (PEPCASE) (CP28)
NCBI Description
                  >gi_100758_pir__S18240 phosphoenolpyruvate carboxylase (EC
                  4.1.1.31) - sorghum >gi_22593_emb_CAA42549_ (X59925)
                  phosphoenolpyruvate carboxylase [Sorghum bicolor]
                   415983
Seq. No.
                  uC-osflm202101d09b1
Seq. ID
                  BLASTX
Method
NCBI GI
                   q20322
BLAST score
                   829
E value
                   4.0e-89
                   167
Match length
                   98
% identity
NCBI Description (X16280) Actin (AA 1-377) [Oryza sativa]
                   415984
Seq. No.
                   uC-osflm202101e02b1
Seq. ID
                   BLASTX
Method
                   g1362162
NCBI GI
BLAST score
                   197
E value
                   1.0e-17
Match length
                   65
                   70
% identity
NCBI Description beta-glucosidase BGQ60 precursor - barley >gi_804656
                   (L41869) beta-glucosidase [Hordeum vulgare]
                   415985
Seq. No.
                   uC-osflm202101e03b1
Seq. ID
                   BLASTX
Method
                   g1244566
NCBI GI
BLAST score
                   628
                   1.0e-65
E value
                   167
Match length
                   72
% identity
                  (U39321) acetyl-CoA carboxylase [Triticum aestivum]
NCBI Description
                   >gi_1588584_prf__2208491A Ac-CoA carboxylase [Triticum
                   aestivum]
                   415986
Seq. No.
                   uC-osflm202101e04b1
Seq. ID
                   BLASTX
Method
NCBI GI
                   g2832628
                   367
BLAST score
                   6.0e-35
E value
                   118
Match length
% identity
                  (AL021711) putative protein [Arabidopsis thaliana]
NCBI Description
                   415987
Seq. No.
```

 $uC\hbox{-}osflm202101e05b1$ Seq. ID Method BLASTX NCBI GI g417154 BLAST score 861 7.0e-93 E value 168 Match length 99 % identity HEAT SHOCK PROTEIN 82 >gi 100685 pir S25541 heat shock NCBI Description protein 82 - rice (strain Taichung Native One) >gi_20256_emb_CAA77978_ (Z11920) heat shock protein 82 (HSP82) [Oryza sativa] Seq. No. 415988 uC-osflm202101e06b1 Seq. ID BLASTX Method q3292814 NCBI GI BLAST score 223 5.0e-18 E value Match length 47 89 % identity (AL031018) putative protein [Arabidopsis thaliana] NCBI Description Seq. No. 415989 uC-osflm202101e08b1 Seq. ID BLASTX Method q3582335 NCBI GI BLAST score 368 5.0e - 35E value Match length 127 % identity 53 NCBI Description (AC005496) unknown protein [Arabidopsis thaliana] 415990 Seq. No. uC-osflm202101e09b1 Seq. ID BLASTX Method g4099408 NCBI GI 656 BLAST score 8.0e-69 E value Match length 139 88 % identity (U86763) delta-type tonoplast intrinsic protein [Triticum NCBI Description aestivum] 415991 Seq. No. uC-osflm202101e10b1 Seq. ID BLASTX Method g4454472 NCBI GI 174 BLAST score 3.0e-12 E value Match length 90 49 % identity NCBI Description (AC006234) unknown protein [Arabidopsis thaliana] 415992 Seq. No. uC-osflm202101e11b1 Seq. ID Method BLASTX

54343

g1706331

NCBI GI

NCBI Description

```
764
BLAST score
                  2.0e-81
E value
                  169
Match length
                  87
% identity
                 PYRUVATE DECARBOXYLASE ISOZYME 3 (PDC) >gi 476284 (U07338)
NCBI Description
                  pyruvate decarboxylase [Oryza sativa]
                  415993
Seq. No.
                  uC-osflm202101e12b1
Seq. ID
                  BLASTX
Method
                  g126201
NCBI GI
                  230
BLAST score
                  5.0e-19
E value
                  92
Match length
                  51
% identity
NCBI Description 3-ISOPROPYLMALATE DEHYDROGENASE PRECURSOR (BETA-IPM
                  DEHYDROGENASE) (IMDH) (3-IPM-DH) >gi 81676_pir___S20510
                  3-isopropylmalate dehydrogenase (EC 1.1.1.85) precursor -
                  rape >gi 17827 emb CAA42596 (X59970) 3-isopropylmalate
                  dehydrogenase [Brassica napus]
                   415994
Seq. No.
                  uC-osflm202101f02b1
Seq. ID
                  BLASTX
Method
                  g3482908
NCBI GI
                  162
BLAST score
                  7.0e-11
E value
Match length
                  82
                   41
% identity
NCBI Description (AC005551) R26529 2, partial CDS [Homo sapiens]
Seq. No.
                   415995
                  uC-osflm202101f03b1
Seq. ID
                   BLASTX
Method
                   q133872
NCBI GI
                   409
BLAST score
                   6.0e-40
E value
Match length
                   147
                   54
% identity
                  30S RIBOSOMAL PROTEIN S1, CHLOROPLAST PRECURSOR (CS1)
NCBI Description
                   >gi_282838_pir__S26494 ribosomal protein S1, chloroplast -
                   spinach >gi_322404_pir__A44121 small subunit ribosomal
                   protein CS1, CS-S2 - spinach >gi_18060_emb_CAA46927_
                   (X66135) ribosomal protein S1 [Spinacia oleracea]
                   >gi_170143 (M82923) chloroplast ribosomal protein S1
                   [Spinacia oleracea]
Seq. No.
                   415996
Seq. ID
                   uC-osflm202101f04b1
                   BLASTX
Method
                   q475048
NCBI GI
                   464
BLAST score
E value
                   5.0e-52
Match length
                   161
% identity
```

[Arabidopsis thaliana]

(X72581) tonoplast intrinsic protein gamma (gamma-TIP)

E value

```
415997
Seq. No.
                  uC-osflm202101f06b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4680201
                  311
BLAST score
                  2.0e-28
E value
Match length
                  99
                  69
% identity
                  (AF114171) hypothetical protein [Sorghum bicolor]
NCBI Description
                  415998
Seq. No.
                  uC-osflm202101f07b1
Seq. ID
                  BLASTX
Method
                  q1323748
NCBI GI
                  204
BLAST score
                   6.0e-16
E value
                   69
Match length
% identity
                  54
NCBI Description (U32430) thiol protease [Triticum aestivum]
                   415999
Seq. No.
                   uC-osflm202101f08b1
Seq. ID
Method
                   BLASTX
                   q4938492
NCBI GI
BLAST score
                   422
                   2.0e-41
E value
                   95
Match length
% identity
                   82
NCBI Description (AL078464) putative villin, fragment [Arabidopsis thaliana]
                   416000
Seq. No.
                   uC-osflm202101f09b1
Seq. ID
Method
                   BLASTX
                   q3915826
NCBI GI
                   560
BLAST score
                   1.0e-57
E value
                   130
Match length
% identity
                   85
NCBI Description 60S RIBOSOMAL PROTEIN L5
                   416001
Seq. No.
                   uC-osflm202101f10b1
Seq. ID
                   BLASTN
Method
                   q218146
NCBI GI
                   234
BLAST score
                   1.0e-129
E value
                   293
Match length
                   95
% identity
NCBI Description Rice mRNA for mitochondrial F1-ATPase
                   416002
Seq. No.
                   uC-osflm202101f11b1
Seq. ID
                   BLASTX
Method
                   g3935148
NCBI GI
                   227
BLAST score
                   2.0e-18
```

```
70
Match length
% identity
                  63
                  (AC005106) T25N20.12 [Arabidopsis thaliana]
NCBI Description
                  416003
Seq. No.
                  uC-osflm202101f12b1
Seq. ID
                  BLASTX
Method
                  g4585977
NCBI GI
                  304
BLAST score
                  1.0e-27
E value
                  84
Match length
                  63
% identity
                 (AC005287) Unknown protein [Arabidopsis thaliana]
NCBI Description
                  416004
Seq. No.
                  uC-osflm202101g02b1
Seq. ID
Method
                  BLASTX
                  g231924
NCBI GI
                  343
BLAST score
                  4.0e-32
E value
                  73
Match length
                  88
% identity
NCBI Description CYTOCHROME C1, HEME PROTEIN PRECURSOR (CLONE PC18I)
                  416005
Seq. No.
                  uC-osflm202101g04b1
Seq. ID
                  BLASTX
Method
                  g2117937
NCBI GI
                  788
BLAST score
                   3.0e-84
E value
                  167
Match length
                   87
% identity
                  UTP--glucose-1-phosphate uridylyltransferase (EC 2.7.7.9) -
NCBI Description
                   barley >gi_1212996_emb_CAA62689_ (X91347) UDP-glucose
                  pyrophosphorylase [Hordeum vulgare]
Seq. No.
                   416006
Seq. ID
                   uC-osflm202101g05b1
Method
                   BLASTX
NCBI GI
                   q4586049
                   543
BLAST score
E value
                   1.0e-55
                   163
Match length
% identity
NCBI Description (AC007020) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   416007
Seq. ID
                   uC-osflm202101g06b1
Method
                   BLASTX
NCBI GI
                   g113460
BLAST score
                   239
E value
                   3.0e-30
Match length
                   84
% identity
                   88
                  ADP, ATP CARRIER PROTEIN 2 PRECURSOR (ADP/ATP TRANSLOCASE 2)
NCBI Description
                   (ADENINE NUCLEOTIDE TRANSLOCATOR 2) (ANT 2)
                   >gi 100851 pir S16568 ADP, ATP carrier protein precursor -
```

maize >gi_22164_emb_CAA41812_ (X59086) adenine nucleotide
translocator [Zea mays]

Seq. No. 416008

Seq. ID uC-osflm202101h04b1

Method BLASTX
NCBI GI 94158221
BLAST score 926
E value 1.0e-100
Match length 169
% identity 98

NCBI Description (Y18624) reversibly glycosylated polypeptide [Oryza sativa]

Seq. No. 416009

Seq. ID uC-osflm202101h06b1

Method BLASTX
NCBI GI g1321661
BLAST score 786
E value 4.0e-84
Match length 148
% identity 100

NCBI Description (D45423) ascorbate peroxidase [Oryza sativa]

Seq. No. 416010

Seq. ID uC-osflm202101h07b1

Method BLASTX
NCBI GI g3249066
BLAST score 457
E value 1.0e-45
Match length 145
% identity 65

NCBI Description (AC004473) Similar to S. cerevisiae SIK1P protein

gb_984964. ESTs gb_F15433 and gb_AA395158 come from this

gene. [Arabidopsis thaliana]

Seq. No. 416011

Seq. ID uC-osflm202101h09b1

Method BLASTX
NCBI GI g126386
BLAST score 183
E value 2.0e-13
Match length 67
% identity 48

NCBI Description POLLEN ALLERGEN LOL P 2-A (LOL P II-A)

>gi_82449_pir__A34291 pollen allergen Lol p IIA - perennial

ryegrass

Seq. No. 416012

Seq. ID uC-osflm202101h10b1

Method BLASTX
NCBI GI g2293480
BLAST score 426
E value 5.0e-42
Match length 84
% identity 98

NCBI Description (AF011331) glycine-rich protein [Oryza sativa]

Seq. ID

```
Seq. No.
                   416013
                   uC-osflm202101h12b1
Seq. ID
Method
                   BLASTX
                   q4006978
NCBI GI
BLAST score
                   188
                   6.0e-14
E value
Match length
                   87
% identity
                   43
                  (AJ131335) pollen allergen (group II) [Cynodon dactylon]
NCBI Description
                   416014
Seq. No.
                   uC-osflm202102a02b1
Seq. ID
Method
                   BLASTX
                   q400803
NCBI GI
BLAST score
                   351
                   2.0e-33
E value
                   69
Match length
                   90
% identity
                   2,3-BISPHOSPHOGLYCERATE-INDEPENDENT PHOSPHOGLYCERATE MUTASE
NCBI Description
                   (PHOSPHOGLYCEROMUTASE) (BPG-INDEPENDENT PGAM) (PGAM-I)
                   >qi 283033 pir A42807 phosphoglycerate mutase (EC
                   5.4.2.1), \overline{2}, 3-\overline{b} isphosphoglycerate-independent - maize
                   >gi_168588 (M80912) 2,3-bisphosphoglycerate-independent
                   phosphoglycerate mutase [Zea mays]
                   416015
Seq. No.
                   uC-osflm202102a06b1
Seq. ID
                   BLASTX
Method
NCBI GI
                   q2244807
BLAST score
                   431
                   1.0e-42
E value
                   132
Match length
                   71
% identity
NCBI Description (Z97336) hypothetical protein [Arabidopsis thaliana]
                   416016
Seq. No.
                   uC-osflm202102a07b1
Seq. ID
                   BLASTX
Method
                   g3738319
NCBI GI
                   217
BLAST score
                   4.0e-29
E value
                   95
Match length
                   67
% identity
NCBI Description (AC005170) hypothetical protein [Arabidopsis thaliana]
                   416017
Seq. No.
                   uC-osflm202102a09b1
Seq. ID
                   BLASTN
Method
                   g5042437
NCBI GI
BLAST score
                   34
                   2.0e-09
E value
Match length
                   42
                   95
% identity
NCBI Description Oryza sativa BAC T49B20 genomic sequence, complete sequence
                   416018
Seq. No.
                   uC-osflm202102a10b1
```

Match length

% identity

157 75

```
BLASTX
Method
NCBI GI
                  g2342719
                  227
BLAST score
                  7.0e-19
E value
Match length
                  78
                  60
% identity
                  (AC002341) SF16 protein isolog [Arabidopsis thaliana]
NCBI Description
                  416019
Seq. No.
                  uC-osflm202102a11b1
Seq. ID
                  BLASTX
Method
                  g5733874
NCBI GI
BLAST score
                  310
                  2.0e-28
E value
                  116
Match length
                   53
% identity
                  (AC007932) F11A17.8 [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   416020
Seq. ID
                  uC-osflm202102b04b1
                   BLASTX
Method
                   q417360
NCBI GI
                   192
BLAST score
                   1.0e-14
E value
                   65
Match length
                   58
% identity
                   HIGH MOBILITY GROUP-LIKE NUCLEAR PROTEIN 2
NCBI Description
                   >gi_2131280_pir__S67767 high mobility group-like protein
                   NHP2 - yeast (Saccharomyces cerevisiae)
                   >gi_666101_emb_CAA40885_ (X57714) high mobility group-like
                   nuclear protein 2 [Saccharomyces cerevisiae]
                   >gi 1429348 emb_CAA67483_ (X99000) high-mobility-group-like
                   protein [Saccharomyces cerevisiae]
                   >qi 1431346 emb CAA98786 (Z74256) ORF YDL208w
                   [Saccharomyces cerevisiae]
                   416021
Seq. No.
                   uC-osflm202102b07b1
Seq. ID
                   BLASTX
Method
NCBI GI
                   q1777375
BLAST score
                   411
                   3.0e-46
E value
                   110
Match length
% identity
NCBI Description (D78573) aspartate kinase-homoserine dehydrogenase [Oryza
                   sativa]
                   416022
Seq. No.
                   uC-osflm202102b12b1
Seq. ID
Method
                   BLASTX
                   g2708741
NCBI GI
                   497
BLAST score
                   3.0e-50
E value
```

NCBI Description (AC003952) hypothetical protein [Arabidopsis thaliana]

416023 Seq. No. Seq. ID uC-osflm202102c01b1 BLASTX Method NCBI GI g1170937 BLAST score 261 4.0e-26 E value 64 Match length % identity 98 S-ADENOSYLMETHIONINE SYNTHETASE 1 (METHIONINE NCBI Description ADENOSYLTRANSFERASE 1) (ADOMET SYNTHETASE 1) >gi_450549_emb_CAA81481 (Z26867) S-adenosyl methionine synthetase [Oryza sativa] Seq. No. 416024 Seq. ID uC-osflm202102c04b1 BLASTX Method NCBI GI q5734703 BLAST score 220 E value 1.0e-17 97 Match length 54 % identity (AC008075) Similar to gb_X90982 phosphoenolpyruvate NCBI Description carboxylase (ppc1) from Solanum tuberosum. [Arabidopsis thaliana] 416025 Seq. No. uC-osflm202102c08b1 Seq. ID BLASTX Method g4589726 NCBI GI BLAST score 251 5.0e-22 E value 47 Match length 96 % identity (AB003137) DnaJ homolog protein [Salix gilgiana] NCBI Description >gi 4589739 dbj_BAA76888.1_ (AB003138) DnaJ homolog protein [Salix gilgiana] 416026 Seq. No. uC-osflm202102d01b1 Seq. ID BLASTX Method g6091730 NCBI GI 274 BLAST score 5.0e-24E value 101 Match length 50 % identity NCBI Description (AC010797) putative cytochrome P450 [Arabidopsis thaliana] 416027 Seq. No. uC-osflm202102d03b1 Seq. ID BLASTX Method g4006818 NCBI GI 331 BLAST score 1.0e-30 E value Match length 130 49 % identity (AC005970) putative translation initiation factor eIF-2B, NCBI Description

54350

alpha subunit [Arabidopsis thaliana]

```
416028
Seq. No.
                  uC-osflm202102d04b1
Seq. ID
Method
                  BLASTX
                  q1170937
NCBI GI
                  714
BLAST score
                  1.0e-75
E value
                  135
Match length
                  99
% identity
                  S-ADENOSYLMETHIONINE SYNTHETASE 1 (METHIONINE
NCBI Description
                  ADENOSYLTRANSFERASE 1) (ADOMET SYNTHETASE 1)
                  >gi_450549_emb_CAA81481_ (Z26867) S-adenosyl methionine
                  synthetase [Oryza sativa]
                  416029
Seq. No.
                  uC-osflm202102d05b1
Seq. ID
                  BLASTX
Method
NCBI GI
                  q531829
BLAST score
                  182
                   2.0e-13
E value
Match length
                  77
                   51
% identity
                  (U12390) beta-galactosidase alpha peptide [cloning vector
NCBI Description
                  pSport1]
                   416030
Seq. No.
                   uC-osflm202102d08b1
Seq. ID
Method
                   BLASTX
                   g4337196
NCBI GI
                   427
BLAST score
                   5.0e-42
E value
Match length
                   162
                   52
% identity
                  (AC006403) putative serine/threonine receptor kinase
NCBI Description
                   [Arabidopsis thaliana]
                   416031
Seq. No.
                   uC-osflm202102d09b1
Seq. ID
                   BLASTX
Method
                   g417154
NCBI GI
                   772
BLAST score
                   2.0e-82
E value
Match length
                   154
                   98
% identity
                   HEAT SHOCK PROTEIN 82 >gi_100685_pir__S25541 heat shock
NCBI Description
                   protein 82 - rice (strain Taichung Native One)
                   >gi_20256_emb_CAA77978_ (Z11920) heat shock protein 82
                   (HSP82) [Oryza sativa]
                   416032
Seq. No.
                   uC-osflm202102d10b1
Seq. ID
                   BLASTX
Method
NCBI GI
                   q4115337
BLAST score
                   671
                   1.0e-70
E value
Match length
                   135
                   18
% identity
```

```
NCBI Description (L81141) ubiquitin [Pisum sativum]
                   416033
Seq. No.
                   uC-osflm202102e01b1
Seq. ID
                   BLASTX
Method
                   g2664198
NCBI GI
                   213
BLAST score
                   6.0e-17
E value
                   51
Match length
                   75
% identity
NCBI Description
                  (AJ003215) GTL1 [Arabidopsis thaliana]
                   416034
Seq. No.
                   uC-osflm202102e02b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2662343
                   621
BLAST score
                   3.0e-70
E value
                   145
Match length
                   99
% identity
NCBI Description (D63581) EF-1 alpha [Oryza sativa]
Seq. No.
                   416035
                   uC-osflm202102e03b1
Seq. ID
                   BLASTX
Method
                   g4530591
NCBI GI
BLAST score
                   299
                   6.0e-27
E value
                   82
Match length
                   73
% identity
                   (AF132475) heme oxygenase 1 [Arabidopsis thaliana]
NCBI Description
                   >gi_4530593_gb_AAD22108.1_ (AF132476) heme oxygenase 1
[Arabidopsis thaliana] >gi_4877362_dbj_BAA77758.1_
                   (AB021857) plastid heme oxygenase [Arabidopsis thaliana]
                   >gi_4877397_dbj_BAA77759.1_ (AB021858) plastid heme
                   oxygenase [Arabidopsis thaliana] >gi_4883666_gb_AAB95301.2_
                   (AC003105) heme oxygenase 1 (HO1) [Arabidopsis thaliana]
                   416036
Seq. No.
                   uC-osflm202102e05b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2129921
BLAST score
                   175
                   2.0e-12
E value
                   50
Match length
% identity
NCBI Description hypothetical protein 1 - Madagascar periwinkle >gi_758694
                   (U12573) putative [Catharanthus roseus]
                   416037
Seq. No.
Seq. ID
                   uC-osflm202102e06b1
                   BLASTN
Method
NCBI GI
                   q4091009
BLAST score
                   260
                   1.0e-144
E value
Match length
                   320
% identity
                   99
```

```
NCBI Description Oryza sativa anther-specific protein gene, complete cds
                    416038
Seq. No.
                    uC-osflm202102e10b1
Seq. ID
                    BLASTX
Method
                    g118306
NCBI GI
                    282
BLAST score
                    5.0e-25
E value
                    134
Match length
                    40
% identity
                    AROMATIC-L-AMINO-ACID DECARBOXYLASE (DOPA DECARBOXYLASE)
NCBI Description
                    (TRYPTOPHAN DECARBOXYLASE) >gi_68027_pir__DCJAAP
                    aromatic-L-amino-acid decarbox\overline{y}lase \overline{(EC 4.1.1.28)}
                    Madagascar periwinkle >gi_18226_emb_CAA47898_ (X67662) tryptophan decarboxylase [Catharanthus roseus] >gi_167490
                     (M25151) tryptophan decarboxylase (EC 4.1.1.28)
                    [Catharanthus roseus]
                    416039
Seq. No.
                    uC-osflm202102e11b1
Seq. ID
                    BLASTX
Method
NCBI GI
                    g543711
                    553
BLAST score
                    9.0e-57
E value
                    118
Match length
                    97
% identity
NCBI Description 14-3-3-LIKE PROTEIN S94 >gi_419796_pir__S30927 14-3-3 protein homolog - rice >gi_303859_dbj_BAA03711_ (D16140)
                    brain specific protein [Oryza sativa]
                    416040
Seq. No.
                    uC-osflm202102e12b1
Seq. ID
                    BLASTX
Method
                    q4582468
NCBI GI
                    650
BLAST score
E value
                     4.0e-68
Match length
                    137
% identity
NCBI Description (AC007071) putative 40S ribosomal protein; contains
                    C-terminal domain [Arabidopsis thaliana]
                     416041
Seq. No.
                    uC-osflm202102f02b1
Seq. ID
                    BLASTX
Method
NCBI GI
                     q2286153
BLAST score
                     518
E value
                     9.0e-53
Match length
                     113
% identity
NCBI Description (AF007581) cytoplasmic malate dehydrogenase [Zea mays]
                     416042
Seq. No.
Seq. ID
                     uC-osflm202102f03b1
                     BLASTX
Method
NCBI GI
                     g3915847
                     363
BLAST score
                     9.0e-44
E value
```

Match length 114 84 % identity 40S RIBOSOMAL PROTEIN S2 >gi 2335095 (AC002339) putative NCBI Description 40S ribosomal protein S2 [Arabidopsis thaliana] Seq. No. 416043 uC-osflm202102f05b1 Seq. ID Method BLASTX NCBI GI g140474 BLAST score 147 4.0e-09 E value Match length 142 30 % identity NCBI Description HYPOTHETICAL 69.2 KD PROTEIN IN HSP30-PMP1 INTERGENIC REGION >gi_83212_pir__S19434 probable transport protein YCR023c - yeast (Saccharomyces cerevisiae) >gi 1907167 emb CAA42315 (X59720) YCR023c, len:611 [Saccharomyces cerevisiae] Seq. No. 416044 Seq. ID uC-osflm202102f10b1 Method BLASTX g2055230 NCBI GI BLAST score 192 E value 2.0e-14 Match length 119 % identity 40 NCBI Description (AB000130) SRC2 [Glycine max] Seq. No. 416045 Seq. ID uC-osflm202102f11b1 Method BLASTX NCBI GI q5478530 BLAST score 555 E value 5.0e-57 Match length 149 % identity (AF130441) UVB-resistance protein UVR8 [Arabidopsis NCBI Description thaliana] Seq. No. 416046 Seq. ID uC-osflm202102f12b1 Method BLASTX NCBI GI g3540201 BLAST score 327 E value 3.0e-30 Match length 137 % identity NCBI Description (AC004260) Putative nuclear protein [Arabidopsis thaliana] Seq. No. 416047 Seq. ID uC-osflm202102q04b1 Method BLASTN NCBI GI g5441876 BLAST score 43 E value 1.0e-14 Match length 66

```
% identity
                  93
                  Oryza sativa genomic DNA, chromosome 2, clone:P0437H03
NCBI Description
                  (contig b)
                  416048
Seq. No.
                  uC-osflm202102g05b1
Seq. ID
                  BLASTX
Method
                  g4105798
NCBI GI
                  642
BLAST score
                  3.0e-67
E value
                  153
Match length
                  62
% identity
                  (AF049930) PGP237-11 [Petunia x hybrida]
NCBI Description
                  416049
Seq. No.
                  uC-osflm202102g06b1
Seq. ID
Method
                  BLASTX
                  q4049341
NCBI GI
                   382
BLAST score
                   1.0e-36
E value
                   115
Match length
                   65
% identity
                  (AL034567) putative protein [Arabidopsis thaliana]
NCBI Description
                   416050
Seq. No.
                   uC-osflm202102g07b1
Seq. ID
                   BLASTX
Method
                   q4558666
NCBI GI
BLAST score
                   312
                   1.0e-28
E value
                   89
Match length
                   62
% identity
NCBI Description (AC007063) putative Na/H antiporter isolog [Arabidopsis
                   thaliana]
                   416051
Seq. No.
                   uC-osflm202102g08b1
Seq. ID
                   BLASTX
Method
                   g1814403
NCBI GI
                   734
BLAST score
                   2.0e-78
 E value
                   157
 Match length
                   91
 % identity
 NCBI Description (U84889) methionine synthase [Mesembryanthemum
                   crystallinum]
                   416052
 Seq. No.
                   uC-osflm202102h02b1
 Seq. ID
                   BLASTX
 Method
                   g136632
 NCBI GI
                   308
 BLAST score
                   7.0e-45
 E value
                   124
 Match length
 % identity
                   UBIQUITIN-ACTIVATING ENZYME E1 1 >gi_100841_pir__A38373
 NCBI Description
                   ubiquitin--protein ligase (EC 6.3.2.19) E1 - wheat
                   >gi_285451_pir__A42873 ubiquitin-activating enzyme E1, UBA1
```



- Wheat >gi_170780 (M55604) ubiquitin-activating enzyme E1 [Triticum aestivum]

Seq. No. 416053

Seq. ID uC-osflm202102h03b1

Method BLASTX
NCBI GI 94262154
BLAST score 242
E value 2.0e-20
Match length 95
% identity 51

% identity 51 NCBI Description (AC005275) putative protein phosphatase regulatory subunit

[Arabidopsis thaliana]

Seq. No. 416054

Seq. ID uC-osflm202102h04b1

Method BLASTX
NCBI GI g3337356
BLAST score 598
E value 5.0e-62
Match length 122
% identity 96

NCBI Description (AC004481) putative protein transport protein SEC61 alpha

subunit [Arabidopsis thaliana]

Seq. No. 416055

Seq. ID uC-osflm202102h05b1

Method BLASTX
NCBI GI g4836892
BLAST score 492
E value 1.0e-57
Match length 157
% identity 47

NCBI Description (AC007369) Putative RNA helicase [Arabidopsis thaliana]

Seq. No. 416056

Seq. ID uC-osflm202102h06b1

Method BLASTX
NCBI GI g1041704
BLAST score 235
E value 2.0e-19
Match length 88
% identity 62

NCBI Description (U30478) expansin At-EXP5 [Arabidopsis thaliana]

Seq. No. 416057

Seq. ID uC-osflm202102h07b1

Method BLASTX
NCBI GI g2129559
BLAST score 149
E value 2.0e-09
Match length 67
% identity 52

NCBI Description cellulase homolog OR16pep - Arabidopsis thaliana

>gi_1022807_gb_AAB60304.1_ (U37702) cellulase [Arabidopsis thaliana] >gi_3493633 (AF074092) cellulase [Arabidopsis thaliana] >gi_3598956 (AF074375) cellulase [Arabidopsis

```
thaliana] >gi_3978258 (AF073875) endo-1,4-beta-D-glucanase
                  KORRIGAN [Arabidopsis thaliana]
                  416058
Seq. No.
                  uC-osflm202102h08b1
Seq. ID
                  BLASTX
Method
NCBI GI
                  q4883617
BLAST score
                  424
                  1.0e-41
E value
Match length
                  132
                  59
% identity
                 (AC006922) unknown protein [Arabidopsis thaliana]
NCBI Description
                  416059
Seq. No.
                  uC-osflm202102h10b1
Seq. ID
                  BLASTX
Method
NCBI GI
                  q3309269
BLAST score
                   433
E value
                   1.0e-42
                   104
Match length
                   80
% identity
                  (AF074940) ferric leghemoglobin reductase-2 precursor
NCBI Description
                   [Glycine max]
                   416060
Seq. No.
                   uC-osflm202102h12b1
Seq. ID
                   BLASTX
Method
NCBI GI
                   g4886756
BLAST score
                   693
                   3.0e-73
E value
Match length
                   163
                   77
% identity
                  (AF088917) cellulose synthase catalytic subunit
NCBI Description
                   [Arabidopsis thaliana]
                   416061
Seq. No.
                   uC-osflm202103d06b1
Seq. ID
                   BLASTX
Method
                   g4105561
NCBI GI
BLAST score
                   251
                   2.0e-21
E value
Match length
                   87
                   63
% identity
NCBI Description (AF047444) ribulose-5-phosphate-3-epimerase [Oryza sativa]
                   416062
Seq. No.
                   uC-osflm202103e04b1
Seq. ID
                   BLASTX
Method
                   g4582436
NCBI GI
                   152
BLAST score
                   5.0e-10
E value
                   52
Match length
                   62
% identity
                  (AC007196) unknown protein [Arabidopsis thaliana]
NCBI Description
```

416063

uC-osflm202103e10b1

Seq. No.

Seq. ID

```
Method
                  BLASTX
                  g2911042
NCBI GI
BLAST score
                  315
                  4.0e-29
E value
                  104
Match length
                  64
% identity
                  (AL021961) Phosphoglycerate dehydrogenase - like protein
NCBI Description
                   [Arabidopsis thaliana]
                  416064
Seq. No.
Seq. ID
                  uC-osflm202103f05b1
                  BLASTX
Method
NCBI GI
                  g5295980
BLAST score
                   362
                  2.0e-34
E value
Match length
                  112
% identity
                  70
NCBI Description (AB003323) MADS box-like protein [Oryza sativa]
                   416065
Seq. No.
                  uC-osflm202103f07b1
Seq. ID
Method
                  BLASTN
NCBI GI
                   g2773153
BLAST score
                   318
                   1.0e-179
E value
Match length
                   362
                   97
% identity
NCBI Description Oryza sativa abscisic acid- and stress-inducible protein
                   (Asr1) mRNA, complete cds
                   416066
Seq. No.
                   uC-osflm202103f08b1
Seq. ID
                   BLASTX
Method
                   g3264767
NCBI GI
                   231
BLAST score
                   4.0e-19
E value
                   72
Match length
                   62
% identity
NCBI Description (AF071893) AP2 domain containing protein [Prunus armeniaca]
                   416067
Seq. No.
                   uC-osflm202103f10b1
Seq. ID
                   BLASTX
Method
                   g1129134
NCBI GI
                   235
BLAST score
                   8.0e-20
E value
                   63
Match length
                   65
% identity
                  (X94105) old yellow enzyme NADPH dehydrogenase [Chenopodium
NCBI Description
                   rubrum]
                   416068
Seq. No.
                   uC-osflm202103g05b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3395431
                   277
BLAST score
```

2.0e-24

E value

BLAST score

421

```
Match length
                  88
                  61
% identity
                  (AC004683) unknown protein [Arabidopsis thaliana]
NCBI Description
                  416069
Seq. No.
                  uC-osflm202103g10b1 .
Seq. ID
Method
                  BLASTX
                  g320618
NCBI GI
                  375
BLAST score
                  4.0e-36
E value
                  91
Match length
                  79
% identity
                  chlorophyll a/b-binding protein I precursor - rice
NCBI Description
                  >gi_218172_dbj_BAA00536_ (D00641) type I light-harvesting
                  chlorophyll a/b-binding protein [Oryza sativa]
                  >gi_227611_prf__1707316A chlorophyll a/b binding protein 1
                   [Oryza sativa]
                  416070
Seq. No.
                  uC-osflm202103g12b1
Seq. ID
                  BLASTX
Method
                  g2213629
NCBI GI
BLAST score
                  261
                  6.0e-23
E value
                  72
Match length
                  72
% identity
NCBI Description (AC000103) F21J9.21 [Arabidopsis thaliana]
                   416071
Seq. No.
                  uC-osflm202103h04b1
Seq. ID
                   BLASTX
Method
                   g4455258
NCBI GI
                   174
BLAST score
                   2.0e-12
E value
                   67
Match length
                   46
% identity
                  (AL035523) acid phosphatase-like protein [Arabidopsis
NCBI Description
                   thaliana]
                   416072
Seq. No.
                   uC-osflm202103h05b1
Seq. ID
                   BLASTX
Method
                   g3193303
NCBI GI
                   337
BLAST score
                   2.0e-31
E value
                   102
Match length
                   65
% identity
                   (AF069298) similar to several proteins containing a tandem
NCBI Description
                   repeat region such as Plasmodium falciparum GGM tandem
                   repeat protein (GB:U27807); partial CDS [Arabidopsis
                   thaliana]
                   416073
Seq. No.
                   uC-osflm202103h10b1
Seq. ID
                   BLASTX
Method
NCBI GI
                   g3786009
```

Seq. No.

416079

E value 2.0e-41 Match length 121 69 % identity (AC005499) unknown protein [Arabidopsis thaliana] NCBI Description 416074 Seq. No. uC-osflm202103h11b1 Seq. ID BLASTX Method g5016095 NCBI GI 468 BLAST score 6.0e-47E value Match length 115 83 % identity (AF003551) lysine-ketoglutarate reductase/saccharopine NCBI Description dehydrogenase bifunctional enzyme [Zea mays] 416075 Seq. No. uC-osflm202104a04b1 Seq. ID BLASTN Method q1296954 NCBI GI 97 BLAST score 3.0e-47E value Match length 171 % identity 98 NCBI Description O.sativa mRNA for novel protein, osr40cl 416076 Seq. No. Seq. ID uC-osflm202104a07b1 Method BLASTX q4531442 NCBI GI 165 BLAST score 2.0e-11 E value Match length 109 % identity 40 NCBI Description (AC006224) hypothetical protein [Arabidopsis thaliana] 416077 Seq. No. uC-osflm202104b02b1 Seq. ID BLASTX Method g4914407 NCBI GI 254 BLAST score 2.0e-22 E value Match length 66 74 % identity NCBI Description (AL050352) putative protein [Arabidopsis thaliana] 416078 Seq. No. Seq. ID uC-osflm202104b04b1 BLASTN Method g3721941 NCBI GI 80 BLAST score 4.0e-37 E value Match length 96 % identity NCBI Description Oryza sativa mRNA for chitinase, complete cds

```
uC-osflm202104b08b1
Seq. ID
                  BLASTX
Method
                  q5106764
NCBI GI
BLAST score
                  561
                  1.0e-57
E value
                  155
Match length
                  74
% identity
                  (AF073329) eukaryotic translation initiation factor 3 large
NCBI Description
                  subunit [Zea mays]
                   416080
Seq. No.
Seq. ID
                  uC-osflm202104c07b1
                  BLASTN
Method
                  g218207
NCBI GI
                   52
BLAST score
                   3.0e-21
E value
                   52
Match length
                   100
% identity
                  Oryza sativa mRNA for the small subunit of
NCBI Description
                   ribulose-1,5-bisphosphate carboxylase, complete cds, clone
                   posss1139
                   416081
Seq. No.
Seq. ID
                   uC-osflm202104c11b1
                   BLASTN
Method
                   q4666286
NCBI GI
                   61
BLAST score
                   3.0e-26
E value
                   77
Match length
                   95
% identity
                   Oryza sativa mRNA for cytosolic monodehydroascorbate
NCBI Description
                   reductase, complete cds
                   416082
Seq. No.
                   uC-osflm202104d01b1
Seq. ID
                   BLASTX
Method
                   g3122671
NCBI GI
                   441
BLAST score
                   1.0e-43
E value
Match length
                   111
                   76
% identity
NCBI Description HYPOTHETICAL RAE1-LIKE PROTEIN >gi_2129676_pir__S71241
                   probable export protein - Arabidopsis thaliana >gi_1297188
                   (U53501) Theoretical protein with similarity to Swiss-Prot
                   Accession Number P41838 poly A+ RNA export protein
                   [Arabidopsis thaliana]
                   416083
Seq. No.
                   uC-osflm202104d02b1
Seq. ID
Method
                   BLASTX
                   g4467157
NCBI GI
                   321
BLAST score
                   1.0e-29
E value
Match length
                   133
                   52
 % identity
                   (AL035540) disease resistance response like protein
 NCBI Description
                   [Arabidopsis thaliana]
```

```
416084
Seq. No.
                  uC-osflm202104d03b1
Seq. ID
                  BLASTX
Method
                  q1652745
NCBI GI
                  147
BLAST score
                  4.0e-09
E value
Match length
                  150
                  29
% identity
                  (D90908) hypothetical protein [Synechocystis sp.]
NCBI Description
                  416085
Seq. No.
                  uC-osflm202104d04b1
Seq. ID
                  BLASTX
Method
                  q3287695
NCBI GI
BLAST score
                   565
                   4.0e-58
E value
                   136
Match length
% identity
                   77
                  (AC003979) Similar to hypothetical protein C34B7.2
NCBI Description
                  gb 1729503 from C. elegans cosmid gb_Z83220. [Arabidopsis
                   thaliana]
                   416086
Seq. No.
                   uC-osflm202104d05b1
Seq. ID
                   BLASTX
Method
                   g1632822
NCBI GI
BLAST score
                   704
E value
                   2.0e-82
                   157
Match length
                   99
% identity
NCBI Description (Y08962) transmembrane protein [Oryza sativa] >gi_1667594
                   (U77297) transmembrane protein [Oryza sativa]
                   416087
Seq. No.
                   uC-osflm202104d07b1
Seq. ID
                   BLASTX
Method
                   g2370312
NCBI GI
                   471
BLAST score
                   4.0e-47
E value
Match length
                   132
                   69
% identity
                   (AJ000995) DnaJ-like protein [Medicago sativa]
NCBI Description
                   >gi_3202020_gb_AAC19391.1_ (AF069507) DnaJ-like protein
                   MsJ1 [Medicago sativa]
                   416088
Seq. No.
Seq. ID
                   uC-osflm202104d08b1
                   BLASTX
Method
NCBI GI
                   q557474
                   189
BLAST score
                   4.0e-14
E value
Match length
                   149
% identity
                  (U15179) ORF1 [Bacteroides ovatus]
NCBI Description
Seq. No.
                   416089
```

```
uC-osflm202104d09b1
Seq. ID
                  BLASTX
Method
                  q4033735
NCBI GI
BLAST score
                  162
                  7.0e-11
E value
                  158
Match length
% identity
                  31
                  (AF054284) spliceosomal protein SAP 155 [Homo sapiens]
NCBI Description
Seq. No.
                  416090
                  uC-osflm202104d11b1
Seq. ID
                  BLASTX
Method
                  q3021508
NCBI GI
BLAST score
                   571
                  7.0e-59
E value
                  170
Match length
% identity
                   69
                  (AJ001769) glucose-6-phosphate dehydrogenase [Nicotiana
NCBI Description
                   tabacum]
                   416091
Seq. No.
                   uC-osflm202104e03b1
Seq. ID
                   BLASTX
Method
                   g3914603
NCBI GI
BLAST score
                   741
                   2.0e-89
E value
Match length
                   168
                   97
% identity
                  RIBULOSE BISPHOSPHATE CARBOXYLASE/OXYGENASE ACTIVASE,
NCBI Description
                   CHLOROPLAST PRECURSOR (RUBISCO ACTIVASE) >gi_1778414
                   (U74321) ribulose-1,5-bisphosphate carboxylase/oxygenase
                   activase [Oryza sativa]
                   416092
Seq. No.
                   uC-osflm202104e05b1
Seq. ID
                   BLASTX
Method
                   g3426039
NCBI GI
                   409
BLAST score
                   7.0e-40
E value
Match length
                   133
                   59
% identity
NCBI Description (AC005168) unknown protein [Arabidopsis thaliana]
                   416093
Seq. No.
                   uC-osflm202104e06b1
Seq. ID
                   BLASTX
Method
                   g4938492
NCBI GI
                   565
BLAST score
                   4.0e-58
E value
Match length
                   172
                   61
% identity
NCBI Description (AL078464) putative villin, fragment [Arabidopsis thaliana]
                   416094
Seq. No.
                   uC-osflm202104e07b1
Seq. ID
                   BLASTX
Method
                   g231587
NCBI GI
```

BLAST score 412 3.0e-40E value Match length 139 % identity 65 ATP SYNTHASE BETA CHAIN, MITOCHONDRIAL PRECURSOR NCBI Description >gi_283001_pir__S25304 H+-transporting ATP synthase (EC 3.6.1.34) beta chain precursor, mitochondrial - rice >gi 218147_dbj_BAA01372_ (D10491) mitochondrial F1-ATPase [Oryza sativa] 416095 Seq. No. uC-osflm202104e08b1 Seq. ID Method BLASTX q5123547 NCBI GI BLAST score 397 2.0e-38 E value Match length 137 55 % identity NCBI Description (AL079344) putative protein [Arabidopsis thaliana] 416096 Seq. No. uC-osflm202104e09b1 Seq. ID BLASTN Method NCBI GI g471330 276 BLAST score 1.0e-154 E value 399 Match length 94 % identity NCBI Description O.sativa Adhl gene, 5' flanking region Seq. No. 416097 uC-osflm202104e11b1 Seq. ID BLASTN Method g5803242 NCBI GI 311 BLAST score 1.0e-174 E value 493 Match length 100 % identity NCBI Description Oryza sativa genomic DNA, chromosome 6, clone:P0535G04 416098 Seq. No. uC-osflm202104e12b1 Seq. ID BLASTX Method g4539359 NCBI GI 256 BLAST score 6.0e-22 E value 72 Match length 62 % identity NCBI Description (AL049525) putative protein [Arabidopsis thaliana] 416099 Seq. No. uC-osflm202104f02b1 Seq. ID BLASTX Method

Method BLASTX
NCBI GI g3080389
BLAST score 170
E value 7.0e-12
Match length 36

```
89
% identity
                  (AL022603) putative membrane associated protein
NCBI Description
                   [Arabidopsis thaliana]
                  416100
Seq. No.
                  uC-osflm202104f03b1
Seq. ID
Method
                  BLASTN
                  g5803242
NCBI GI
                  223
BLAST score
                  1.0e-122
E value
                  401
Match length
                  99
% identity
NCBI Description Oryza sativa genomic DNA, chromosome 6, clone:P0535G04
                   416101
Seq. No.
                   uC-osflm202104f04b1
Seq. ID
Method
                   BLASTX
                   g2463584
NCBI GI
BLAST score
                   302
                   3.0e-27
E value
                   113
Match length
                   49
% identity
NCBI Description (D38532) FBSB precursor [Ananas comosus]
                   416102
Seq. No.
                   uC-osflm202104f06b1
Seq. ID
                   BLASTX
Method
                   g2129826
NCBI GI
BLAST score
                   221
                   6.0e-18
E value
                   87
Match length
                   51
% identity
NCBI Description dynamin-like protein phragmoplastin 5 - soybean >gi_1218004
                   (U36430) SDL5A [Glycine max]
                   416103
Seq. No.
                   uC-osflm202104f08b1
Seq. ID
                   BLASTX
Method
                   g4558665
NCBI GI
                   414
 BLAST score
                   2.0e-40
 E value
                   166
 Match length
                   48
 % identity
NCBI Description (AC007063) putative white protein [Arabidopsis thaliana]
                   416104
 Seq. No.
                   uC-osflm202104f09b1
 Seq. ID
                   BLASTX
 Method
                   g3834302
 NCBI GI
                   677
 BLAST score
                   2.0e-71
 E value
 Match length
                   159
                   81
 % identity
                   (AC005679) Similar to gb_D45384 vacuolar H+-pyrophosphatase
 NCBI Description
                    from Oryza sativa. ESTs gb_F14272 and gb_F14273 come from
```

this gene. [Arabidopsis thaliana]

```
416105
Seq. No.
                   uC-osflm202104f12b1
Seq. ID
                   BLASTX
Method
NCBI GI
                   q5738367
BLAST score
                   285
                   2.0e-25
E value
                   151
Match length
                   46
% identity
                   (AL078620) putative protein [Arabidopsis thaliana]
NCBI Description
                   416106
Seq. No.
                   uC-osflm202104g01b1
Seq. ID
                   BLASTX
Method
                   g417154
NCBI GI
                   745
BLAST score
                   3.0e-79
E value
                   151
Match length
                   99
% identity
                   HEAT SHOCK PROTEIN 82 >gi_100685_pir__S25541 heat shock
NCBI Description
                   protein 82 - rice (strain Taichung Native One)
                   >gi_20256_emb_CAA77978_ (Z11920) heat shock protein 82
                    (HSP82) [Oryza sativa]
                    416107
Seq. No.
Seq. ID
                   uC-osflm202104g02b1
                   BLASTX
Method
                    q401237
NCBI GI
                    769
BLAST score
E value
                    4.0e-82
Match length
                    170
                    85
% identity
                   UBIQUITIN-ACTIVATING ENZYME E1 2 >gi_170684 (M90663)
NCBI Description
                    ubiquitin activating enyme [Triticum aestivum]
                    416108
Seq. No.
                    uC-osflm202104g03b1
Seq. ID
                    BLASTX
Method
                    q131211
NCBI GI
BLAST score
                    154
                    6.0e-10
E value
Match length
                    31
                    100
 % identity
NCBI Description PHOTOSYSTEM I REACTION CENTRE SUBUNIT IX (PSI-J)
                    >gi_1363533_pir__S58571 photosystem I protein psaJ - maize
chloroplast >gi_552734 (J04502) ORF42 [Zea mays]
                    >gi_902241_emb_CAA60305_ (X86563) psaJ [Zea mays]
                    416109
 Seq. No.
                    uC\hbox{-}osflm202104g06b1
 Seq. ID
                    BLASTX
Method
                    g4102600
 NCBI GI
                    252
 BLAST score
                    6.0e-27
 E value
 Match length
                    158
                    52
 % identity
```

NCBI Description (AF013467) ARF6 [Arabidopsis thaliana]

```
416110
Seq. No.
                  uC-osflm202104g09b1
Seq. ID
                  BLASTX
Method
NCBI GI
                  q6056399
BLAST score
                  187
                  8.0e-14
E value
                  52
Match length
                  67
% identity
                  (AC009324) AP2 domain containing protein RAP2.12
NCBI Description
                   [Arabidopsis thaliana]
                  416111
Seq. No.
Seq. ID
                  uC-osflm202104g10b1
                  BLASTX
Method
                  q1703200
NCBI GI
                  164
BLAST score
                   3.0e-11
E value
                  83
Match length
                   48
% identity
NCBI Description PROTEIN KINASE AFC2 >gi_601789 (U16177) protein kinase
                   [Arabidopsis thaliana] >gi_642130_dbj_BAA08214_ (D45353)
                   protein kinase [Arabidopsis thaliana]
                   >gi_4220516_emb_CAA22989_ (AL035356) protein kinase (AFC2)
                   [Arabidopsis thaliana]
                   416112
Seq. No.
Seq. ID
                   uC-osflm202104g11b1
                   BLASTX
Method
NCBI GI
                   q5830788
BLAST score
                   474
                   2.0e-47
E value
Match length
                   136
                   68
% identity
NCBI Description (AL117188) thioredoxin reductase (NADPH) 2 [Arabidopsis
                   thaliana]
                   416113
Seq. No.
                   uC-osflm202104g12b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   q3023713
BLAST score
                   538
                   2.0e-67
E value
                   149
Match length
                   83
 % identity
 NCBI Description ENOLASE (2-PHOSPHOGLYCERATE DEHYDRATASE)
                   (2-PHOSPHO-D-GLYCERATE HYDRO-LYASE) (OSE1) >gi_780372
                   (U09450) enolase [Oryza sativa]
                   416114
 Seq. No.
                   uC-osflm202104h03b1
 Seq. ID
                   BLASTX
 Method
```

Method BLASTX
NCBI GI g2665890
BLAST score 390
E value 1.0e-37
Match length 139
% identity 57

NCBI Description (AF035944) calcium-dependent protein kinase [Fragaria x

% identity

ananassa]

416115 Seq. No. uC-osflm202104h06b1 Seq. ID BLASTX Method q3879192 NCBI GI 368 BLAST score 5.0e-35 E value 164 Match length 48 % identity (Z50795) weak similarity with yeast cat8 regulatory protein NCBI Description (Swiss Prot accession number P39113); cDNA EST EMBL: Z14554 comes from this gene; cDNA EST EMBL: T02057 comes from this gene; cDNA EST EMBL: D75504 comes from this gene 416116 Seq. No. Seq. ID uC-osflm202104h07b1 BLASTX Method NCBI GI q730125 697 BLAST score 1.0e-73 E value 155 Match length 83 % identity NADPH-CYTOCHROME P450 REDUCTASE >gi_322739_pir__S31502 NCBI Description NADPH--ferrihemoprotein reductase $(\overline{EC}\ 1.6.\overline{2}.4)$ - Madagascar periwinkle >gi_18139_emb_CAA49446_ (X69791) NADPH--ferrihemoprotein reductase [Catharanthus roseus] Seq. No. 416117 uC-osflm202104h12b1 Seq. ID BLASTX Method q1944573 NCBI GI 544 BLAST score 4.0e-56 E value 149 Match length 82 % identity NCBI Description (Z49146) phenylalanine ammonia-lyase [Hordeum vulgare] Seq. No. 416118 uC-osflm202106a02b1 Seq. ID Method BLASTX q4544449 NCBI GI 463 BLAST score 7.0e-47E value 142 Match length 65 % identity NCBI Description (AC006592) putative peroxidase [Arabidopsis thaliana] 416119 Seq. No. uC-osflm202106a04b1 Seq. ID BLASTX Method g1698670 NCBI GI 294 BLAST score 2.0e-26 E value 98 Match length 52

NCBI Description (U66241) S-like RNase [Zea mays]

```
416120
Seq. No.
                  uC-osflm202106a07b1
Seq. ID
                  BLASTX
Method
                  q1296955
NCBI GI
                  715
BLAST score
                  1.0e-75
E value
                  134
Match length
                  49
% identity
                  (X95402) duplicated domain structure protein [Oryza sativa]
NCBI Description
                   416121
Seq. No.
                  uC-osflm202106a08b1
Seq. ID
                  BLASTX
Method
NCBI GI
                  q5441874
BLAST score
                  162
                   7.0e-11
E value
                  77
Match length
                   43
% identity
                  (AP000366) Similar to maize transposon MuDR mudrA-like
NCBI Description
                   protein. (AC002340) [Oryza sativa]
                   416122
Seq. No.
                   uC-osflm202106a09b1
Seq. ID
                   BLASTX
Method
                   q1705678
NCBI GI
                   698
BLAST score
                   8.0e-74
E value
Match length
                   151
                   49
% identity
                  CELL DIVISION CYCLE PROTEIN 48 HOMOLOG (VALOSIN CONTAINING
NCBI Description
                   PROTEIN HOMOLOG) (VCP) >gi_862480 (U20213)
                   valosin-containing protein [Glycine max]
                   416123
Seq. No.
                   uC-osflm202106a10b1
Seq. ID
                   BLASTX
Method
                   q4103324
NCBI GI
                   585
BLAST score
                   1.0e-60
E value
                   136
Match length
                   82
% identity
                  (AF022716) GDP-mannose pyrophosphorylase [Solanum
NCBI Description
                   tuberosum]
                   416124
Seq. No.
                   uC-osflm202106a11b1
Seq. ID
                   BLASTX
Method
                   g3126854
NCBI GI
                   547
BLAST score
                   3.0e-56
E value
                   110
Match length
                   94
% identity
NCBI Description (AF061577) chlorophyll a/b binding protein [Oryza sativa]
Seq. No.
                   uC-osflm202106b01b1
Seq. ID
```

```
BLASTX
Method
                    q4467128
NCBI GI
                    150
BLAST score
                    1.0e-09
E value
Match length
                    95
                    34
% identity
                    (AL035538) putative protein [Arabidopsis thaliana]
NCBI Description
                    416126
Seq. No.
                    uC-osflm202106b02b1
Seq. ID
                    BLASTX
Method
                    q1173194
NCBI GI
BLAST score
                    490
                    2.0e-49
E value
                    159
Match length
                     60
% identity
                    30S RIBOSOMAL PROTEIN S13, CHLOROPLAST PRECURSOR (CS13)
NCBI Description
                     >gi 2119093_pir__S59594 ribosomal protein S13 precursor,
                    chloroplast - Arabidopsis thaliana >gi_16767_emb_CAA79013
                     (Z17611) chloroplast 30S ribosomal protein S13 [Arabidopsis
                     thaliana] >gi_662869_emb_CAA88028_ (Z47986) chloroplast ribosomal protein S13 [Arabidopsis thaliana]
                     >gi_1107483_emb_CAA63021_ (X91955) 30S ribosomal protein
S13 [Arabidopsis thaliana] >gi_1515107_emb_CAA60413_
(X86734) plastid ribosomal protein S13 [Arabidopsis
                     thaliana]
                     416127
Seq. No.
                     uC-osflm202106b03b1
Seq. ID
                     BLASTX
Method
                     g1170937
NCBI GI
                     286
BLAST score
                     1.0e-25
E value
                     86
Match length
                     71
 % identity
NCBI Description S-ADENOSYLMETHIONINE SYNTHETASE 1 (METHIONINE
                     ADENOSYLTRANSFERASE 1) (ADOMET SYNTHETASE 1)
                     >gi_450549_emb_CAA81481_ (Z26867) S-adenosyl methionine
                     synthetase [Oryza sativa]
                     416128
 Seq. No.
                     uC-osflm202106b05b1
 Seq. ID
                     BLASTX
 Method
                     g2443887
 NCBI GI
                     498
 BLAST score
                     3.0e-50
 E value
                     189
 Match length
                     58
 % identity
 NCBI Description (AC002294) Similar to transcription factor
                     gb Z46606 1658307 and others [Arabidopsis thaliana]
                     416129
 Seq. No.
                     uC-osflm202106b07b1
 Seq. ID
                     BLASTX
 Method
                     q3913018
 NCBI GI
                     771
 BLAST score
```

3.0e-82

E value

```
157
Match length
                  98
% identity
                  FRUCTOSE-BISPHOSPHATE ALDOLASE, CHLOROPLAST PRECURSOR
NCBI Description
                   (ALDP) >gi 218155 dbj_BAA02730_ (D13513) chloroplastic
                  aldolase [Oryza sativa]
                  416130
Seq. No.
                  uC-osflm202106b08b1
Seq. ID
                  BLASTX
Method
NCBI GI
                  g4836875
                  748
BLAST score
                  2.0e-79
E value
                  172
Match length
                  91
% identity
                   (AC007260) 1cl prt seq No definition line found
NCBI Description
                   [Arabidopsis thaliana]
                  416131
Seq. No.
                  uC-osflm202106b10b1
Seq. ID
                  BLASTX
Method
                  g1684857
NCBI GI
BLAST score
                  624
                  3.0e-65
E value
                  127
Match length
                   39
% identity
                  (U77940) polyubiquitin [Phaseolus vulgaris]
NCBI Description
Seq. No.
                   416132
                  uC-osflm202106b12b1
Seq. ID
                  BLASTX
Method
                   g4678209
NCBI GI
BLAST score
                   317
                   3.0e-29
E value
                   128
Match length
                   52
% identity
                  (AC007134) putative sugar transporter [Arabidopsis
NCBI Description
                   thaliana]
                   416133
Seq. No.
                   uC-osflm202106c01b1
Seq. ID
                   BLASTX
Method
                   g3882355
NCBI GI
                   351
BLAST score
                   1.0e-42
E value
Match length
                   96
% identity
NCBI Description
                   (U92460) 12-oxophytodienoate reductase OPR1 [Arabidopsis
                   thaliana]
                   416134
Seq. No.
                   uC-osflm202106c02b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   q6056413
BLAST score
                   249
E value
                   3.0e-21
                   73
Match length
% identity
                   66
```

```
NCBI Description (AC009525) Unknown protein [Arabidopsis thaliana]
Seq. No.
                  416135
                  uC-osflm202106c04b1
Seq. ID
                  BLASTX
Method
NCBI GI
                  q231924
BLAST score
                  494
                  9.0e-50
E value
                  103
Match length
                  89
% identity
                  CYTOCHROME C1, HEME PROTEIN PRECURSOR (CLONE PC18I)
NCBI Description
                  416136
Seq. No.
                  uC-osflm202106c06b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2244908
BLAST score
                  162
E value
                  5.0e-11
Match length
                  58
                  59
% identity
                  (Z97339) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  416137
                  uC-osflm202106c07b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4585882
BLAST score
                  466
E value
                  9.0e-48
Match length
                  141
% identity
                  71
                  (AC005850) PSI type III chlorophyll a/b-binding protein
NCBI Description
                  [Arabidopsis thaliana]
                  416138
Seq. No.
                  uC-osflm202106c08b1
Seq. ID
                  BLASTX
Method
                  g134102
NCBI GI
BLAST score
                  771
                  3.0e-82
E value
                  178
Match length
                  88
% identity
                  RUBISCO SUBUNIT BINDING-PROTEIN ALPHA SUBUNIT PRECURSOR (60
NCBI Description
                  KD CHAPERONIN ALPHA SUBUNIT) (CPN-60 ALPHA)
                  >gi_72959_pir__HHWTBA ribulose-bisphosphate carboxylase
                  subunit-binding protein alpha chain - wheat (fragment)
                  >gi 1345582_emb_CAA30699_ (X07851) rubisco subunit
                  binding-protein alpha subunit (543 AA) [Triticum
                  aestivum]
Seq. No.
                  416139
                  uC-osflm202106c11b1
Seq. ID
                  BLASTX
Method
NCBI GI
                  g283008
BLAST score
                  762
E value
                  3.0e-81
                  175
Match length
% identity
                  86
```

```
sucrose synthase (EC 2.4.1.13) - rice
NCBI Description
                   >gi 20366_emb_CAA46017_ (X64770) sucrose synthase [Oryza
                   satival
                   416140
Seq. No.
                   uC-osf1m202106c12b1
Seq. ID
                   BLASTX
Method
                   q1076791
NCBI GI
                   620
BLAST score
                   1.0e-64
E value
                   114
Match length
                   98
% identity
                   calcium-binding protein - maize >gi_2119370_pir__S58170
Calreticulin precursor - maize >gi_577612_emb_CAA86728_
NCBI Description
                   (Z46772) calcium-binding protein [Zea mays]
                   >gi_927572_emb_CAA61939_ (X89813) Calreticulin precursor
                   [Zea mays] >gi_1587033_prf__2205314A calreticulin [Zea
                   mays]
                   416141
Seq. No.
                   uC-osflm202106d01b1
Seq. ID
                   BLASTX
Method
                   g113742
NCBI GI
                   244
BLAST score
                   2.0e-20
E value
                   164
Match length
                    33
% identity
                   AMINOPEPTIDASE N (ALPHA-AMINOACYLPEPTIDE HYDROLASE)
NCBI Description
                   >gi_147142 (M15273) peptidase N [Escherichia coli]
                   >gi_147144 (M15676) aminopeptidase N [Escherichia coli]
                    >gi_1787163 (AE000195) aminopeptidase N [Escherichia coli]
                    >gi_4062498_dbj_BAA35684_ (D90731) Aminopeptidase n (EC
                    3.4.11.2) (alpha-aminoacylpeptide hydrolase). [Escherichia
                    coli]
                    416142
Seq. No.
Seq. ID
                    uC-osflm202106d03b1
                    BLASTN
Method
                    q3859567
NCBI GI
                    225
BLAST score
                    1.0e-123
E value
Match length
                    477
                    87
% identity
NCBI Description Oryza sativa clone FIL1 unknown mRNA
                    416143
Seq. No.
                    uC-osflm202106d05b1
Seq. ID
Method
                    BLASTX
NCBI GI
                    q2196878
                    768
BLAST score
                    7.0e-82
E value
                    185
Match length
 % identity
                    76
                   (Y08292) NADH glutamate dehydrogenase [Nicotiana
NCBI Description
                    plumbaginifolia]
```

416144

Seq. No.

```
uC-osflm202106d06b1
Seq. ID
Method
                  BLASTX
                  g3386618
NCBI GI
                  153
BLAST score
                  6.0e-10
E value
                  134
Match length
                  37
% identity
                  (AC004665) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                  416145
Seq. No.
                  uC-osflm202106d08b1
Seq. ID
Method
                  BLASTX
                  g3335347
NCBI GI
BLAST score
                  717
                  5.0e-79
E value
Match length
                  172
                  77
% identity
                   (AC004512) Contains similarity to ARI, RING finger protein
NCBI Description
                   qb X98309 from Drosophila melanogaster. ESTs gb T44383,
                   gb W43120, gb N65868, gb H36013, gb AA042241, gb T76869 and
                   gb AA042359 come from this gene. [Arabidopsis thaliana]
                   416146
Seq. No.
                  uC-osflm202106d10b1
Seq. ID
                  BLASTX
Method
NCBI GI
                   g2570503
                   156
BLAST score
E value
                   2.0e-21
                   86
Match length
                   69
% identity
                  (AF022734) zinc inducible protein [Oryza sativa]
NCBI Description
Seq. No.
                   416147
                   uC-osflm202106d11b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g1654144
BLAST score
                   717
E value
                   5.0e-76
                   166
Match length
                   86
% identity
                  (U38471) small GTP-binding protein rab [Brassica rapa]
NCBI Description
                   416148
Seq. No.
                   uC-osflm202106d12b1
Seq. ID
                   BLASTX
Method
                   g6016720
NCBI GI
BLAST score
                   272
E value
                   9.0e-24
                   69
Match length
                   71
% identity
                   (AC009325) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   416149
Seq. No.
Seq. ID
                   uC-osflm202106e01b1
                   BLASTX
Method
                   q4874301
NCBI GI
BLAST score
                   369
```

% identity

82

```
E value
                   3.0e-35
Match length
                   103
% identity
                   74
NCBI Description
                   (AC006053) proton-ATPase-like protein [Arabidopsis
                   thaliana]
Seq. No.
                   416150
                   uC-osflm202106e03b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g4589726
BLAST score
                   464
E value
                   3.0e-49
Match length
                   141
% identity
                   68
                   (AB003137) DnaJ homolog protein [Salix gilgiana]
NCBI Description
                   >gi_4589739_dbj_BAA76888.1_ (AB003138) DnaJ homolog protein
                   [Salix gilgiana]
Seq. No.
                   416151
Seq. ID
                   uC-osflm202106e04b1
Method
                   BLASTX
NCBI GI
                   g5734747
BLAST score
                   353
E value
                   3.0e-33
Match length
                   134
% identity
                   51
NCBI Description
                  (AC007651) Hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   416152
Seq. ID
                   uC-osflm202106e05b1
Method
                   BLASTX
NCBI GI
                   g5731259
BLAST score
                   431
E value
                   2.0e-42
Match length
                   114
                   68
% identity
NCBI Description
                  (AF166351) alanine:glyoxylate aminotransferase 2 homolog
                   [Arabidopsis thaliana]
Seq. No.
                   416153
Seq. ID
                   uC-osflm202106e09b1
Method
                   BLASTX
NCBI GI
                   g4204300
BLAST score
                   262
E value
                   1.0e-22
Match length
                   94
% identity
                   53
NCBI Description
                  (AC003027) Unknown protein [Arabidopsis thaliana]
Seq. No.
                   416154
Seq. ID
                   uC-osflm202106e11b1
Method
                  BLASTN
NCBI GI
                   a4138731
BLAST score
                   43
E value
                   9.0e-15
Match length
                  155
```

```
NCBI Description Zea mays mRNA for proline-rich protein
Seq. No.
                   416155
Seq. ID
                  uC-osflm202106e12b1
Method
                  BLASTX
NCBI GI
                  q2582381
BLAST score
                  885
                  1.0e-95
E value
                  174
Match length
% identity
                   90
NCBI Description
                  (AF021220) cation-chloride co-transporter [Nicotiana
                  tabacum]
Seq. No.
                  416156
Seq. ID
                  uC-osflm202106f01b1
Method
                  BLASTX
NCBI GI
                  g4995051
BLAST score
                  247
                  6.0e-21
E value
Match length
                  69
% identity
                   68
NCBI Description
                  (Y12695) Isovaleryl-CoA Dehydrogenase [Arabidopsis
                  thaliana]
Seq. No.
                  416157
                  uC-osflm202106f02b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4679028
BLAST score
                  294
                  2.0e-26
E value
                  120
Match length
                  47
% identity
                  (AF077207) HSPC021 [Homo sapiens]
NCBI Description
                  >gi 5106781 gb AAD39841.1 (AF083243) HSPC025 [Homo
                  sapiens]
                  416158
Seq. No.
Seq. ID
                  uC-osflm202106f03b1
Method
                  BLASTX
NCBI GI
                  g5734634
BLAST score
                  383
E value
                  7.0e-37
Match length
                  111
% identity
                  65
                  (AP000391) Similar to putative lipase (AC006232) [Oryza
NCBI Description
                  sativa]
Seq. No.
                  416159
Seq. ID
                  uC-osflm202106f04b1
Method
                  BLASTN
NCBI GI
                  g444046
BLAST score
                  98
E value
                  2.0e-47
Match length
                  102
% identity
                  99
```

NCBI Description Z.mays OBF1 mRNA for ocs-element binding factor

BLAST score

353

```
416160
Seq. No.
Seq. ID
                  uC-osflm202106f05b1
Method
                  BLASTX
NCBI GI
                  g231924
BLAST score
                  524
E value
                  3.0e-53
Match length
                  107
                  91
% identity
NCBI Description CYTOCHROME C1, HEME PROTEIN PRECURSOR (CLONE PC18I)
                  416161
Seq. No.
                  uC-osflm202106f06b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g626029
BLAST score
                  422
E value
                  2.0e-41
Match length
                  103
                  75
% identity
                  pollen allergen Lol p XI - perennial ryegrass
NCBI Description
                  >gi 1582249 prf 2118270A allergen Lol p XI [Lolium
                  perenne]
                  416162
Seq. No.
                  uC-osflm202106f07b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4249402
BLAST score
                  155
E value
                  4.0e-10
Match length
                  96
% identity
                  41
NCBI Description
                 (AC006072) unknown protein [Arabidopsis thaliana]
Seq. No.
                  416163
Seq. ID
                  uC-osflm202106f09b1
Method
                  BLASTN
NCBI GI
                  g4809270
BLAST score
                  34
E value
                  2.0e-09
Match length
                  62
% identity
                  89
NCBI Description Arabidopsis thaliana BAC T1N24
Seq. No.
                   416164
Seq. ID
                  uC-osflm202106f10b1
Method
                  BLASTX
NCBI GI
                   q4803951
BLAST score
                  702
E value
                   3.0e-74
Match length
                  169
% identity
NCBI Description
                  (AC006202) unknown protein [Arabidopsis thaliana]
Seq. No.
                   416165
Seq. ID
                  uC-osflm202106g01b1
Method
                  BLASTX
NCBI GI
                  g1730560
```

E value 2.0e-33 Match length 84 % identity 75 ALPHA-GLUCAN PHOSPHORYLASE, H ISOZYME (STARCH PHOSPHORYLASE NCBI Description H) $>gi_510932$ _emb_CAA84494_ (Z35117) alpha 1,4-glucan phosphorylase type H [Vicia faba] 416166 Seq. No. Seq. ID uC-osflm202106g02b1 Method BLASTX NCBI GI g3540207 BLAST score 336 E value 2.0e-31 Match length 145 % identity 50 NCBI Description (AC004260) Putative protein kinase [Arabidopsis thaliana] Seq. No. 416167 Seq. ID uC-osflm202106g03b1 Method BLASTX g5882728 NCBI GI BLAST score 168 E value 1.0e-11 Match length 120 % identity 37 NCBI Description (AC008263) ESTs gb_T75898, gb_R65457, gb AA597517 and gb_AA597420 come from this gene. [Arabidopsis thaliana] Seq. No. 416168 Seq. ID uC-osflm202106g04b1 Method BLASTX NCBI GI g3941412 BLAST score 389 E value 1.0e-37 Match length 73 % identity 92 NCBI Description (AF062860) putative transcription factor [Arabidopsis thaliana] Seq. No. 416169 Seq. ID uC-osflm202106q05b1 Method BLASTX NCBI GI g6041789 BLAST score 338 E value 1.0e-31 Match length 162 % identity 49 (AC009755) putative N2, N2-dimethylguanosine tRNA NCBI Description methyltransferase [Arabidopsis thaliana] Seq. No. 416170 Seq. ID uC-osflm202106g06b1 Method BLASTX NCBI GI g1304215 BLAST score 518 E value 1.0e-52 Match length 122

Match length

94

```
% identity
                  65
                  (D84392) precursor of rice 22 kDa protein of photosystem II
NCBI Description
                   (PSII-S) [Oryza sativa]
Seq. No.
                  416171
                  uC-osflm202106g07b1
Seq. ID
Method
                  BLASTX
                  g4760370
NCBI GI
BLAST score
                  377
E value
                  4.0e-36
                  119
Match length
                  63
% identity
                  (AF082565) ATP dependent copper transporter [Arabidopsis
NCBI Description
                  thaliana] >gi 4760380 gb AAD29115.1 (AF091112) ATP
                  dependent copper transporter [Arabidopsis thaliana]
                  416172
Seq. No.
                  uC-osflm202106q08b1
Seq. ID
                  BLASTX
Method
NCBI GI
                  g3253095
BLAST score
                  176
                  1.0e-12
E value
                  86
Match length
                  44
% identity
                  (AB015643) Polygalacturonase-inhibiting protein [Citrus sp.
NCBI Description
                  cv. sannumphung]
                  416173
Seq. No.
                  uC-osflm202106g09b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2792238
                  370
BLAST score
E value
                  3.0e-35
Match length
                  178
                   45
% identity
NCBI Description (AF032697) NBS-LRR type resistance protein [Oryza sativa]
Seq. No.
                  416174
                  uC-osflm202106g10b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1170937
BLAST score
                  214
E value
                   2.0e-17
Match length
                   60
                   77
% identity
NCBI Description
                  S-ADENOSYLMETHIONINE SYNTHETASE 1 (METHIONINE
                  ADENOSYLTRANSFERASE 1) (ADOMET SYNTHETASE 1)
                   >gi_450549_emb_CAA81481_ (Z26867) S-adenosyl methionine
                   synthetase [Oryza sativa]
Seq. No.
                   416175
Seq. ID
                  uC-osflm202106q11b1
Method
                  BLASTX
NCBI GI
                   g4835793
BLAST score
                   348
E value
                   1.0e-32
```

Method

BLASTX

% identity 69 (AC007296) Similar to gb_U90212 DNA binding protein ACBF NCBI Description from Nicotiana tabacum and contains 3 PF_00076 RNA recognition motif domains. ESTs gb_T44278, gb_R65195, gb N65904, gb H37499, gb_R90487, gb_N95952, gb_T4427 416176 Seq. No. uC-osflm202106h04b1 Seq. ID Method BLASTX NCBI GI q5803272 BLAST score 459 E value 4.0e-49 Match length 151 72 % identity (AP000399) ESTs AU055950(S20175), C73125(E2952), NCBI Description AU055951(S20175) correspond to a region of the predicted gene; similar to acyl-ACP thioesterase (U92878) [Oryza sativa] 416177 Seq. No. uC-osflm202106h05b1 Seq. ID Method BLASTX NCBI GI g1854378 BLAST score 746 2.0e-79 E value Match length 186 % identity 77 (AB001338) Sucrose-Phosphate Synthase [Saccharum NCBI Description officinarum] Seq. No. 416178 uC-osflm202106h06b1 Seq. ID Method BLASTX NCBI GI q21693 BLAST score 345 E value 1.0e-62 Match length 154 % identity NCBI Description (X66012) cathepsin B [Triticum aestivum] 416179 Seq. No. uC-osflm202106h08b1 Seq. ID Method BLASTX NCBI GI g131283 BLAST score 834 E value 1.0e-89 Match length 173 % identity PHOTOSYSTEM II 44 KD REACTION CENTER PROTEIN (P6 PROTEIN) NCBI Description (CP43) >gi_72710_pir__F2RZ44 photosystem II chlorophyll a-binding protein psbC - rice chloroplast >gi_11965_emb_CAA34014_ (X15901) PSII 43kDa protein [Oryza sativa] 416180 Seq. No. Seq. ID uC-osflm202106h10b1

```
NCBI GI
                  q2245378
BLAST score
                   424
E value
                  1.0e-41
Match length
                  147
% identity
                  53
NCBI Description
                  (U83245) auxin response factor 1 [Arabidopsis thaliana]
                  >gi 5080809 gb AAD39318.1 AC007258 7 (AC007258) auxin
                  response factor 1 [Arabidopsis thaliana]
Seq. No.
                  416380
Seq. ID
                  uC-osflm202110b12b1
Method
                  BLASTX
NCBI GI
                  q1706551
BLAST score
                  454
E value
                  4.0e-45
Match length
                  118
                  79
% identity
NCBI Description GLUCAN ENDO-1, 3-BETA-GLUCOSIDASE PRECURSOR
                   ((1->3)-BETA-GLUCAN ENDOHYDROLASE) ((1->3)-BETA-GLUCANASE)
                   (BETA-1,3-ENDOGLUCANASE) >gi 924953 (U30323) beta
                  1,3-glucanase [Triticum aestivum]
Seq. No.
                  416381
Seq. ID
                  uC-osflm202110c01b1
Method
                  BLASTN
NCBI GI
                  g2429617
BLAST score
                  257
E value
                  1.0e-142
Match length
                  261
% identity
                  100
NCBI Description Oryza sativa mRNA for ferrochelatase, partial cds
Seq. No.
                  416382
Seq. ID
                  uC-osflm202110c04b1
Method
                  BLASTX
NCBI GI
                  g5802627
BLAST score
                  227
E value
                  1.0e-18
Match length
                  79
% identity
                  63
NCBI Description (AF176089) COP8 [Arabidopsis thaliana]
Seq. No.
                  416383
Seq. ID
                  uC-osflm202110c05b1
Method
                  BLASTX
NCBI GI
                  g4539004
BLAST score
                  197
E value
                  3.0e-15
Match length
                  94
% identity
NCBI Description (AL049481) putative protein kinase [Arabidopsis thaliana]
Seq. No.
                  416384
Seq. ID
                  uC-osflm202110c10b1
Method
                  BLASTX
NCBI GI
```

q4586117

190

BLAST score

E value 3.0e-14 Match length 87 % identity 53 NCBI Description (AL049638) putative protein [Arabidopsis thaliana] 416385 Seq. No. Seq. ID uC-osflm202110c11b1 Method BLASTX NCBI GI g1617274 BLAST score 253 E value 3.0e-28 Match length 108 62 % identity NCBI Description (Z72152) AMP-binding protein [Brassica napus] Seq. No. 416386 Seq. ID $uC\hbox{-}osflm202110d01b1$ Method BLASTX NCBI GI g2492487 BLAST score 648 E value 6.0e-68 Match length 144 % identity 92 NCBI Description 14-3-3-LIKE PROTEIN B (14-3-3B) >gi 1070354 emb CAA63658 (X93170) Hv14-3-3b [Hordeum vulgare] Seq. No. 416387 Seq. ID uC-osflm202110d02b1 Method BLASTX NCBI GI g320618 BLAST score 537 E value 5.0e-55 Match length 120 % identity 86 NCBI Description chlorophyll a/b-binding protein I precursor - rice >gi_218172_dbj_BAA00536 (D00641) type I light-harvesting chlorophyll a/b-binding protein [Oryza sativa] >gi 227611 prf 1707316A chlorophyll a/b binding protein 1 [Oryza sativa] 416388 Seq. No. Seq. ID uC-osflm202110d03b1 Method BLASTX NCBI GI g2384760 BLAST score 650 E value 4.0e-68 Match length 128 % identity NCBI Description (AF016897) GDP dissociation inhibitor protein OsGDI2 [Oryza

sativa]

416389 Seq. No.

Seq. ID uC-osflm202110d08b1

Method BLASTN NCBI GI q5052006 BLAST score 52 E value 2.0e-20

BLAST score

```
104
Match length
                  88
% identity
NCBI Description Oryza sativa subsp. indica apoplastic invertase (INV1)
                  gene, complete cds
                  416390
Seq. No.
Seq. ID
                  uC-osflm202110d12b1
Method
                  BLASTN
                  g5822826
NCBI GI
BLAST score
                  144
E value
                  4.0e-75
Match length
                  261
% identity
                  89
NCBI Description Oryza sativa D1 gene for alpha-subunit of GTP-binding
                  protein, wild type, partial sequence
Seq. No.
                  416391
Seq. ID
                  uC-osflm202110e01b1
Method
                  BLASTX
NCBI GI
                  g2244850
BLAST score
                  361
E value
                  3.0e - 34
Match length
                  129
% identity
                  63
NCBI Description (297337) hypothetical protein [Arabidopsis thaliana]
                  416392
Seq. No.
Seq. ID
                  uC-osflm202110e08b1
Method
                  BLASTX
NCBI GI
                  g547712
BLAST score
                  299
E value
                  4.0e-27
                  92
Match length
% identity
                  64
NCBI Description EUKARYOTIC INITIATION FACTOR 4A (EIF-4A)
                  >gi 542153 pir S38358 translation initiation factor eIF-4A
                  - rice >gi 303844 dbj BAA02152 (D12627) eukaryotic
                  initiation factor 4A [Oryza sativa]
                  416393
Seq. No.
Seq. ID
                  uC-osflm202110e12b1
Method
                  BLASTX
NCBI GI
                  g3858935
BLAST score
                  432
E value
                  1.0e-42
Match length
                  139
% identity
                  57
                  (AL021636) synaptobrevin-like protein [Arabidopsis
NCBI Description
                  thaliana] >gi 4103357 (AF025332) vesicle-associated
                  membrane protein 7C; synaptobrevin 7C [Arabidopsis
                  thaliana]
Seq. No.
                  416394
Seq. ID
                  uC-osflm202110f01b1
Method
                  BLASTX
NCBI GI
                  q3702803
```

```
E value
                  2.0e-13
Match length
                  99
                  40
% identity
NCBI Description
                  (AF055480) antifreeze protein [Daucus carota]
                  >gi_4455920_emb_CAB37347.1_ (AJ131340) antifreeze
                  polypeptide [Daucus carota]
                  416395
Seq. No.
Seq. ID
                  uC-osflm202110f02b1
Method
                  BLASTX
NCBI GI
                  q3880625
BLAST score
                  190
E value
                  3.0e-14
Match length
                  78
% identity
                  47
NCBI Description
                  (Z93785) predicted using Genefinder; similar to RNA
                  recognition motif. (aka RRM, RBD, or RNP domain); cDNA EST
                  EMBL:T01682 comes from this gene; cDNA EST EMBL:M75823
                  comes from this gene; cDNA EST EMBL: D27559 comes from this
Seq. No.
                  416396
Seq. ID
                  uC-osflm202110f10b1
Method
                  BLASTX
NCBI GI
                  q2191136
BLAST score
                  181
E value
                  4.0e-13
Match length
                  102
% identity
                  (AF007269) Similar to UTP-Glucose Glucosyltransferase;
NCBI Description
                  coded for by A. thaliana cDNA T46230; coded for by A.
                  thaliana cDNA H76538; coded for by A. thaliana cDNA H76290
                   [Arabidopsis thaliana]
Seq. No.
                  416397
Seq. ID
                  uC-osflm202110g01b1
Method
                  BLASTX
NCBI GI
                  g3319357
BLAST score
                  403
                  3.0e-39
E value
Match length
                  150
% identity
                  55
NCBI Description
                 (AF077407) contains similarity to phosphoenolpyruvate
                  synthase (ppsA) (GB:AE001056) [Arabidopsis thaliana]
Seq. No.
                  416398
Seq. ID
                  uC-osflm202110q04b1
Method
                  BLASTX
NCBI GI
                  g4185141
BLAST score
                  439
                  2.0e-43
E value
Match length
                  145
% identity
                  (AC005724) putative calmodulin-binding protein [Arabidopsis
NCBI Description
                  thaliana]
```

Seq. No. 416399

Seq. ID uC-osflm202110g05b1

Method BLASTX NCBI GI g2832627 BLAST score 251 2.0e-21 E value Match length 89 % identity 57 (AL021711) xyloglucan endo-transglycosylase-like protein NCBI Description [Arabidopsis thaliana] Seq. No. 416400 uC-osflm202110g09b1 Seq. ID Method BLASTX g3063694 NCBI GI BLAST score 344 E value 3.0e - 32Match length 153 53 % identity NCBI Description (AL022537) putative protein [Arabidopsis thaliana] 416401 Seq. No. Seq. ID uC-osflm202110g11b1 Method BLASTX NCBI GI g320618 BLAST score 727 E value 3.0e-77 Match length 142 % identity 98 NCBI Description chlorophyll a/b-binding protein I precursor - rice >gi_218172_dbj_BAA00536_ (D00641) type I light-harvesting chlorophyll a/b-binding protein [Oryza sativa] >gi_227611_prf__1707316A chlorophyll a/b binding protein 1 [Oryza sativa] Seq. No. 416402 Seq. ID uC-osflm202110q12b1 Method BLASTX NCBI GI g2129929 BLAST score 867 E value 1.0e-93 Match length 167 96 % identity NCBI Description DNA-directed RNA polymerase (EC 2.7.7.6) II chain RPB2 tomato >gi_1049068 (U28403) RNA polymerase II subunit 2 [Solanum lycopersicum] Seq. No. 416403 Seq. ID uC-osflm202110h01b1

Method BLASTX NCBI GI q547712 BLAST score 328 E value 1.0e-30 Match length 66 % identity 94

NCBI Description EUKARYOTIC INITIATION FACTOR 4A (EIF-4A)

>gi_542153_pir__S38358 translation initiation factor eIF-4A

- rice >gi_303844_dbj_BAA02152 (D12627) eukaryotic

initiation factor 4A [Oryza sativa]

BLAST score

```
Seq. No.
                   416404
Seq. ID
                   uC-osflm202110h02b1
Method
                   BLASTX
NCBI GI
                   q4263722
BLAST score
                   625
E value
                   2.0e-65
Match length
                   135
% identity
                   87
NCBI Description (AC006223) putative glucan synthase [Arabidopsis thaliana]
                   416405
Seq. No.
Seq. ID
                   uC-osflm202110h03b1
Method
                   BLASTN
NCBI GI
                   a5821066
BLAST score
                   35
E value
                   5.0e-10
Match length
                   51
                   92
% identity
NCBI Description Oryza sativa gene for WHO4, complete cds
                   416406
Seq. No.
Seq. ID
                   uC-osflm202110h04b1
Method
                   BLASTN
NCBI GI
                   q5803242
BLAST score
                   194
E value
                   1.0e-105
Match length
                   473
% identity
                   100
NCBI Description Oryza sativa genomic DNA, chromosome 6, clone:P0535G04
Seq. No.
                   416407
Seq. ID
                   uC-osflm202110h05b1
Method
                   BLASTN
NCBI GI
                   q1311478
BLAST score
                   158
E value
                   2.0e-83
Match length
                   201
% identity
                   95
NCBI Description Oryza sativa DNA for sucrose phosphate synthase, complete
                   cds
Seq. No.
                   416408
Seq. ID
                   uC-osflm202110h08b1
Method
                  BLASTX
NCBI GI
                   g3044214
BLAST score
                  278
E value
                  1.0e-24
Match length
                  78
% identity
                   68
NCBI Description (AF057044) acyl-CoA oxidase [Arabidopsis thaliana]
Seq. No.
                   416409
Seq. ID
                  uC-osflm202110h09b1
Method
                  BLASTX
NCBI GI
                   q549063
```

Match length

```
E value
                    9.0e-64
Match length
                    130
% identity
                    98
                   TRANSLATIONALLY CONTROLLED TUMOR PROTEIN HOMOLOG (TCTP)
NCBI Description
                   >gi_1072464_pir__A38958 IgE-dependent histamine-releasing
factor homolog - rice >gi_303835_dbj_BAA02151_ (D12626)
                   21kd polypeptide [Oryza sativa]
Seq. No.
                   416410
Seq. ID
                   uC-osflm202110h11b1
Method
                   BLASTX
NCBI GI
                   q5714762
BLAST score
                   515
E value
                   3.0e-52
Match length
                   106
% identity
NCBI Description (AF173881) serine/threonine protein phosphatase PP2A-4
                   catalytic subunit [Oryza sativa subsp. indica]
Seq. No.
                   416411
Seq. ID
                   uC-osflm202111a03b1
Method
                   BLASTX
NCBI GI
                   q1698582
BLAST score
                   652
E value
                   2.0e-68
Match length
                   158
% identity
NCBI Description (U60767) integral membrane protein OsNramp3 [Oryza sativa]
Seq. No.
                   416412
Seq. ID
                   uC-osflm202111a06b1
Method
                   BLASTX
NCBI GI
                   q1658313
BLAST score
                   303
E value
                   7.0e-28
                   55
Match length
% identity
                   96
NCBI Description (Y08987) osr40g2 [Oryza sativa]
Seq. No.
                   416413
Seq. ID
                   uC-osflm202111a07b1
Method
                   BLASTX
NCBI GI
                   g5762457
BLAST score
                   557
E value
                   3.0e-57
Match length
                   106
                   97
% identity
NCBI Description
                  (AF176040) ubiquitin-conjugating enzyme UBC2
                   [Mesembryanthemum crystallinum]
Seq. No.
                   416414
Seq. ID
                   uC-osflm202111a08b1
Method
                   BLASTX
NCBI GI
                   g3023713
BLAST score
                   538
E value
                   4.0e-66
```

% identity NCBI Description ENOLASE (2-PHOSPHOGLYCERATE DEHYDRATASE) (2-PHOSPHO-D-GLYCERATE HYDRO-LYASE) (OSE1) >qi 780372 (U09450) enolase [Oryza sativa] 416415 Seq. No. uC-osflm202111a10b1 Seq. ID Method BLASTX NCBI GI q4512653 BLAST score 342 E value 2.0e-32 Match length 90 % identity NCBI Description (AC007048) unknown protein [Arabidopsis thaliana] 416416 Seq. No. uC-osflm202111a12b1 Seq. ID Method BLASTX NCBI GI q1658313 BLAST score 424 E value 6.0e-42 Match length 79 % identity 51 NCBI Description (Y08987) osr40g2 [Oryza sativa] Seq. No. 416417 Seq. ID uC-osflm202111b02b1 Method BLASTX NCBI GI g5091552 BLAST score 317 E value 5.0e-29 Match length 165 % identity 45 NCBI Description (AC007067) T10024.21 [Arabidopsis thaliana] Seq. No. 416418 uC-osflm202111b03b1 Seq. ID Method BLASTX NCBI GI q4455338 BLAST score 284 E value 3.0e-25 Match length 165 % identity 40 NCBI Description (AL035525) putative protein [Arabidopsis thaliana] Seq. No. 416419 uC-osflm202111b06b1 Seq. ID Method BLASTX NCBI GI g320618 BLAST score 648 E value 6.0e-68 Match length 148 % identity 84 NCBI Description chlorophyll a/b-binding protein I precursor - rice >gi_218172_dbj_BAA00536_ (D00641) type I light-harvesting chlorophyll a/b-binding protein [Oryza sativa] >gi 227611 prf 1707316A chlorophyll a/b binding protein 1

[Oryza sativa]

Seq. No. 416420

Seq. ID uC-osflm202111b07b1

Method BLASTX
NCBI GI g3845469
BLAST score 377
E value 4.0e-36
Match length 148
% identity 49

NCBI Description (AL021046) phenylalanyl-trna synthetase beta chain

cytoplasmic [Schizosaccharomyces pombe]

Seq. No. 416421

Seq. ID uC-osflm202111b11b1

Method BLASTN
NCBI GI g1449931
BLAST score 168
E value 1.0e-89
Match length 168
% identity 100

NCBI Description Oryza sativa sucrose phosphate synthase gene, complete cds

Seq. No. 416422

Seq. ID uC-osflm202111b12b1

Method BLASTX
NCBI GI g3738284
BLAST score 262
E value 1.0e-22
Match length 103
% identity 51

NCBI Description (AC005309) unknown protein [Arabidopsis thaliana]

Seq. No. 416423

Seq. ID uC-osflm202111d01b1

Method BLASTX
NCBI GI g3914212
BLAST score 346
E value 2.0e-32
Match length 157
% identity 44

NCBI Description 5-OXOPROLINASE (5-OXO-L-PROLINASE) (PYROGLUTAMASE)

(5-OPASE) >gi 1732065 (U70825) 5-oxo-L-prolinase [Rattus

norvegicus]

Seq. No. 416424

Seq. ID uC-osflm202111d02b1

Method BLASTX
NCBI GI g1352440
BLAST score 627
E value 2.0e-65
Match length 108
% identity 100

NCBI Description EUKARYOTIC TRANSLATION INITIATION FACTOR 4E (EIF-4E)

(EIF4E) (MRNA CAP-BINDING PROTEIN) (EIF-4F 25 KD SUBUNIT)

(EIF-4F P26 SUBUNIT) >gi 1002915 (U34597) p26 [Oryza

satival

Seq. No.

Seq. ID

416430

uC-osflm202111d08b1

416425 Seq. No. uC-osflm202111d03b1 Seq. ID Method BLASTX NCBI GI g2384760 BLAST score 743 6.0e-79 E value Match length 144 % identity 99 NCBI Description (AF016897) GDP dissociation inhibitor protein OsGDI2 [Oryza sativa] Seq. No. 416426 Seq. ID uC-osflm202111d04b1 Method BLASTX q4982509 NCBI GI BLAST score 511 E value 7.0e-52Match length 123 % identity 82 NCBI Description (AC000107) F17F8.15 [Arabidopsis thaliana] 416427 Seq. No. Seq. ID uC-osflm202111d05b1 Method BLASTX g4335715 NCBI GI BLAST score 379 E value 3.0e - 36Match length 142 % identity 52 NCBI Description (AC006248) putative immediate-early salicylate-induced glucosyltransferase [Arabidopsis thaliana] Seq. No. 416428 Seq. ID uC-osflm202111d06b1 Method BLASTN NCBI GI q4097337 BLAST score 352 E value 0.0e + 00Match length 417 % identity 99 NCBI Description Oryza sativa metallothionein-like protein mRNA, complete Seq. No. 416429 Seq. ID uC-osflm202111d07b1 Method BLASTX NCBI GI q2388580 BLAST score 795 E value 4.0e-85 Match length 157 % identity 88 NCBI Description (AC000098) Similar to Sequence 10 from patent 5477002 (gb_1253956). [Arabidopsis thaliana]

NCBI GI

E value

BLAST score

g543711

4.0e-78

735

```
Method
                  BLASTX
NCBI GI
                  q4127456
BLAST score
                  248
E value
                   5.0e-21
Match length
                   94
                   60
% identity
NCBI Description (AJ010818) Cpn21 protein [Arabidopsis thaliana]
Seq. No.
                   416431
Seq. ID
                  uC-osflm202111d09b1
Method
                  BLASTX
NCBI GI
                  q3402282
BLAST score
                  150
E value
                   1.0e-09
Match length
                  92
                   38
% identity
                 (AJ000997) proline-rich protein [Solanum tuberosum]
NCBI Description
Seq. No.
                   416432
Seq. ID
                  uC-osflm202111d10b1
Method
                  BLASTX
NCBI GI
                  q3789954
BLAST score
                   340
E value
                   7.0e-32
Match length
                  105
% identity
                   68
                  (AF094776) chlorophyll a/b-binding protein precursor [Oryza
NCBI Description
                  sativa]
                   416433
Seq. No.
Seq. ID
                   uC-osflm202111d12b1
Method
                  BLASTX
NCBI GI
                   g1632822
                  572
BLAST score
E value
                   4.0e-59
Match length
                   140
% identity
                   80
NCBI Description
                  (Y08962) transmembrane protein [Oryza sativa] >gi 1667594
                   (U77297) transmembrane protein [Oryza sativa]
Seq. No.
                   416434
Seq. ID
                  uC-osflm202111e03b1
Method
                  BLASTX
NCBI GI
                  g2760362
BLAST score
                   422
E value
                  2.0e-41
Match length
                  116
                   73
% identity
NCBI Description (AF016511) 15.9 kDa subunit of RNA polymerase II
                   [Arabidopsis thaliana]
                   416435
Seq. No.
Seq. ID
                  uC-osflm202111e06b1
                  BLASTX
Method
```

Match length 151 99 % identity

NCBI Description 14-3-3-LIKE PROTEIN S94 >qi 419796 pir S30927 14-3-3 protein homolog - rice >gi 303859 dbj BAA03711 (D16140)

brain specific protein [Oryza sativa]

Seq. No. 416436

Seq. ID uC-osflm202111e07b1

Method BLASTX NCBI GI g283004 BLAST score 446 E value 3.0e-44Match length 136 % identity 37

NCBI Description DNA-binding protein Gt-2 - rice >gi 20249 emb CAA48328

(X68261) gt-2 [Oryza sativa]

416437 Seq. No.

Seq. ID uC-osflm202111e08b1

Method BLASTX NCBI GI g547712 BLAST score 506 E value 3.0e-51 Match length 100 % identity 96

EUKARYOTIC INITIATION FACTOR 4A (EIF-4A) NCBI Description

>gi_542153_pir__ \$38358 translation initiation factor eIF-4A - rice >gi_303844_dbj_BAA02152_ (D12627) eukaryotic

initiation factor 4A [Oryza sativa]

416438 Seq. No.

uC-osflm202111f01b1 Seq. ID

Method BLASTX NCBI GI g5733874 290 BLAST score E value 6.0e-26 134 Match length 48 % identity

NCBI Description (AC007932) F11A17.8 [Arabidopsis thaliana]

Seq. No. 416439

Seq. ID uC-osflm202111f02b1

Method BLASTX NCBI GI g2055230 BLAST score 200 E value 2.0e-15 Match length 121 % identity 40

NCBI Description (AB000130) SRC2 [Glycine max]

Seq. No. 416440

Seq. ID uC-osflm202111f03b1

Method BLASTX NCBI GI g3758859 BLAST score 201 E value 2.0e-15 Match length 114

% identity NCBI Description (Z98551) predicted using hexExon; MAL3P6.7 (PFC0730w), Hypothetical protein, len: 222 aa [Plasmodium falciparum] Seq. No. 416441 Seq. ID uC-osflm202111f04b1 Method BLASTX NCBI GI g5733874 BLAST score 290 E value 7.0e-26 Match length 134 % identity 48 NCBI Description (AC007932) F11A17.8 [Arabidopsis thaliana] Seq. No. 416442 Seq. ID uC-osflm202111f06b1 Method BLASTX NCBI GI g5915822 BLAST score 438 E value 3.0e-43Match length 152 % identity 54 NCBI Description CYTOCHROME P450 79A1 (CYTOCHROME P450TYR) >gi 2130096 pir S68203 cytochrome P450tyr - sorqhum >gi 984543 (U32624) cytochrome P-450 [Sorghum bicolor] Seq. No. 416443 uC-osflm202111f07b1 Seq. ID Method BLASTX NCBI GI q3885888 BLAST score 299 E value 3.0e-27 Match length 105 % identity 64 NCBI Description (AF093632) high mobility group protein [Oryza sativa] Seq. No. 416444 Seq. ID uC-osflm202111f09b1 Method BLASTX NCBI GI g4239891 BLAST score 473 E value 2.0e-47 Match length 106 % identity NCBI Description (AB016804) NADP-malic enzyme [Aloe arborescens] Seq. No. 416445 Seq. ID uC-osflm202111f10b1 Method BLASTX NCBI GI q6056399 BLAST score 186 E value 1.0e-13 Match length 128 % identity 40 (AC009324) AP2 domain containing protein RAP2.12 NCBI Description

[Arabidopsis thaliana]

Seq. No. 416446 Seq. ID uC-osflm202111f11b1 Method BLASTX NCBI GI q1076746 BLAST score 356 E value 6.0e-57 Match length 150 80 % identity NCBI Description heat shock protein 70 - rice (fragment) >gi_763160_emb_CAA47948_ (X67711) heat shock protein 70 [Oryza sativa] 416447 Seq. No. Seq. ID uC-osflm202111g03b1 Method BLASTX NCBI GI q3850621 BLAST score 273 E value 5.0e-24Match length 118 % identity 51 NCBI Description (Y15382) putative RNA binding protein [Arabidopsis thaliana] Seq. No. 416448 uC-osflm202111g06b1 Seq. ID Method BLASTX NCBI GI g6016151 BLAST score 723 E value 1.0e-76 Match length 150 95 % identity IMMUNOGLOBULIN BINDING PROTEIN HOMOLOG 3 PRECURSOR (HEAT NCBI Description SHOCK PROTEIN 70 HOMOLOG 3) >gi 1575130 (U58209) lumenal binding protein cBiPe3 [Zea mays] Seq. No. 416449 Seq. ID uC-osflm202111g07b1 Method BLASTN NCBI GI g2149018 BLAST score 59 E value 3.0e-2491 Match length 91 % identity NCBI Description Oryza sativa putative ADP-glucose pyrophosphorylase subunit SH2 and putative NADPH-dependent reductase A1 genes, complete cds 416450 Seq. No. Seq. ID uC-osflm202111q09b1 BLASTX Method NCBI GI g2995990 BLAST score 181 E value 2.0e-13 Match length 95 % identity NCBI Description (AF053746) dormancy-associated protein [Arabidopsis

thaliana] >gi 2995992 (AF053747) dormancy-associated

protein [Arabidopsis thaliana] Seq. No. 416451 Seq. ID uC-osflm202111g11b1 Method BLASTX NCBI GI g5454208 BLAST score 247 E value 7.0e-21 Match length 169 % identity 6 NCBI Description (AC005698) T3P18.22 [Arabidopsis thaliana] Seq. No. 416452 Seq. ID uC-osflm202111h01b1 Method BLASTX NCBI GI g5281021 BLAST score 227 E value 2.0e-30 108 Match length % identity 60 NCBI Description (Z97339) hypothetical protein [Arabidopsis thaliana] 416453 Seq. No. Seq. ID uC-osflm202111h02b1 Method BLASTX NCBI GI q4588003 BLAST score 434 E value 7.0e-43 Match length 124 % identity 69

NCBI Description (AF085279) hypothetical EIF-2-Alpha [Arabidopsis thaliana]

Seq. No. 416454

Seq. ID uC-osflm202111h04b1

Method BLASTN
NCBI GI g4091009
BLAST score 102
E value 4.0e-50
Match length 352
% identity 90

NCBI Description Oryza sativa anther-specific protein gene, complete cds

Seq. No. 416455

Seq. ID uC-osflm202111h07b1

Method BLASTX
NCBI GI g2494174
BLAST score 547
E value 4.0e-56
Match length 112
% identity 93

NCBI Description GLUTAMATE DECARBOXYLASE 1 (GAD 1) >gi_497979 (U10034)

glutamate decarboxylase [Arabidopsis thaliana]

Seq. No. 416456

Seq. ID uC-osflm202112a04b1

Method BLASTX NCBI GI g81601

BLAST score 266 E value 3.0e-23Match length 105 59 % identity NCBI Description chaperonin 60 beta - Arabidopsis thaliana Seq. No. 416457 Seq. ID uC-osflm202112a07b1 Method BLASTX NCBI GI g1709619 BLAST score 692 E value 4.0e-73 Match length 161 % identity 81 PROTEIN DISULFIDE ISOMERASE PRECURSOR (PDI) NCBI Description >gi_2146814_pir S69181 protein disulfide isomerase (EC 5.3.4.1) precursor - maize >gi_625148 (L39014) protein disulfide isomerase [Zea mays] Seq. No. 416458 uC-osflm202112a10b1 Seq. ID Method BLASTX NCBI GI g4164149 BLAST score 397 E value 6.0e-39 Match length 83 % identity 93 NCBI Description (AB014056) iron-superoxide dismutase [Oryza sativa] Seq. No. 416459 Seq. ID uC-osflm202112a12b1 Method BLASTX NCBI GI g1931631 BLAST score 308 E value 2.0e-28 Match length 87 71 % identity NCBI Description (U93561) glutamate dehydrogenase [Zea mays] Seq. No. 416460 Seq. ID uC-osflm202112b03b1 Method BLASTX NCBI GI g4586027 BLAST score 305 E value 9.0e-28 Match length 72 % identity NCBI Description (AC007109) putative ribosomal protein L14 [Arabidopsis thaliana]

Seq. No. 416461

Seq. ID uC-osflm202112b04b1

Method BLASTX
NCBI GI g2695929
BLAST score 144
E value 6.0e-09
Match length 47

Seq. No.

416467

```
% identity
NCBI Description (AJ222778) putative thiol protease [Hordeum vulgare]
                   416462
Seq. No.
                  uC-osflm202112b07b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3297810
BLAST score
                  182
E value
                  1.0e-13
Match length
                  92
                  38
% identity
NCBI Description (AL031032) putative protein [Arabidopsis thaliana]
Seq. No.
                   416463
Seq. ID
                  uC-osflm202112b09b1
Method
                  BLASTN
NCBI GI
                  g5091597
BLAST score
                  239
E value
                  1.0e-132
Match length
                  333
% identity
                  96
NCBI Description Oryza sativa chromosome 1 BAC 10A19I, complete sequence
Seq. No.
                   416464
Seq. ID
                  uC-osflm202112b10b1
                  BLASTX
Method
NCBI GI
                  q6006848
BLAST score
                  287
E value
                   3.0e - 34
Match length
                  124
% identity
                   63
NCBI Description (AC009540) unknown protein, 5' partial [Arabidopsis
                  thaliana]
                  416465
Seq. No.
Seq. ID
                  uC-osflm202112b12b1
Method
                  BLASTX
NCBI GI
                  q3023713
BLAST score
                  460
                  4.0e-46
E value
Match length
                  91
% identity
                  100
NCBI Description ENOLASE (2-PHOSPHOGLYCERATE DEHYDRATASE)
                   (2-PHOSPHO-D-GLYCERATE HYDRO-LYASE) (OSE1) >gi 780372
                   (U09450) enolase [Oryza sativa]
Seq. No.
                  416466
Seq. ID
                  uC-osflm202112c03b1
Method
                  BLASTN
NCBI GI
                  g2662342
BLAST score
                  120
E value
                  3.0e-61
Match length
                  132
% identity
                  98
NCBI Description Oryza sativa mRNA for EF-1 alpha, complete cds
```

```
Seq. ID
                   uC-osflm202112c04b1
Method
                   BLASTX
NCBI GI
                   g115577
BLAST score
                   419
                   2.0e-41
E value
Match length
                   89
                   88
% identity
NCBI Description PHOSPHOENOLPYRUVATE CARBOXYLASE, HOUSEKEEPING ISOZYME
                   (PEPCASE) >gi_348536_pir__S28614 phosphoenolpyruvate carboxylase (EC 4.1.1.31) - sugarcane hybrid H32-8560
                   >gi 169844 (M86661) phosphoenolpyruvate carboxylase
                   [Saccharum sp.]
Seq. No.
                   416468
Seq. ID
                   uC-osflm202112c08b1
                   BLASTN
Method
NCBI GI
                   g218144
BLAST score
                   84
E value
                   1.0e-39
Match length
                   84
% identity
                   100
NCBI Description Rice mRNA for ATP/ADP translocator, complete cds
Seq. No.
                   416469
Seq. ID
                   uC-osflm202112c09b1
Method
                   BLASTN
NCBI GI
                   q3789951
BLAST score
                   162
E value
                   3.0e - 86
Match length
                   178
% identity
                   98
NCBI Description Oryza sativa chlorophyll a/b-binding protein presursor
                   (Cab27) mRNA, nuclear gene encoding chloroplast protein,
                   complete cds
                   416470
Seq. No.
Seq. ID
                   uC-osflm202112d03b1
Method
                   BLASTX
NCBI GI
                   g1729971
BLAST score
                   336
E value
                   2.0e-31
Match length
                   103
% identity
                   69
NCBI Description TONOPLAST INTRINSIC PROTEIN, GAMMA (GAMMA TIP)
                   (AQUAPORIN-TIP) >gi 1076745 pir S52004 gamma-Tip protein -
                   rice >gi_473997 dbj BAA05017 (D25534) gamma-Tip [Oryza
                   sativa]
Seq. No.
                   416471
Seq. ID
                   uC-osflm202112d06b1
Method
                   BLASTX
NCBI GI
                   g2854070
BLAST score
                   164
E value
                   2.0e-17
Match length
                   95
% identity
```

NCBI Description (AF044914) putative histone deacetylase [Arabidopsis

thaliana]

Seq. No. 416472

Seq. ID uC-osflm202112d10b1

Method BLASTX
NCBI GI g417360
BLAST score 259
E value 3.0e-22
Match length 116
% identity 46

NCBI Description HIGH MOBILITY GROUP-LIKE NUCLEAR PROTEIN 2

>gi_2131280_pir__S67767 high mobility group-like protein

NHP2 - yeast (Saccharomyces cerevisiae)

>gi_666101_emb_CAA40885_ (X57714) high mobility group-like

nuclear protein 2 [Saccharomyces cerevisiae]

>gi_1429348_emb_CAA67483_ (X99000) high-mobility-group-like

protein [Saccharomyces cerevisiae]

>gi_1431346_emb_CAA98786_ (Z74256) ORF YDL208w

[Saccharomyces cerevisiae]

Seq. No. 416473

Seq. ID uC-osflm202112e03b1

Method BLASTX
NCBI GI g2104949
BLAST score 522
E value 4.0e-53
Match length 129
% identity 74

NCBI Description (U96716) MAP kinase-like protein [Selaginella lepidophylla]

Seq. No. 416474

Seq. ID uC-osflm202112e04b1

Method BLASTX
NCBI GI g1136120
BLAST score 523
E value 2.0e-53
Match length 104
% identity 92

NCBI Description (X91806) alpha-tubulin [Oryza sativa]

Seq. No. 416475

Seq. ID uC-osflm202112e05b1

Method BLASTX
NCBI GI g3169172
BLAST score 451
E value 9.0e-45
Match length 172
% identity 47

NCBI Description (AC004401) putative serine carboxypeptidase I [Arabidopsis

thaliana] >gi_3445214_gb_AAC32444.1 (AC004786) putative

serine carboxypeptidase I [Arabidopsis thaliana]

Seq. No. 416476

Seq. ID uC-osflm202112e06b1

Method BLASTX NCBI GI g3660471 BLAST score 384

Match length

105

E value 3.0e-46Match length 121 % identity 71 NCBI Description (AJ001809) succinate dehydrogenase flavoprotein alpha subunit [Arabidopsis thaliana] Seq. No. 416477 Seq. ID uC-osflm202112e07b1 Method BLASTX NCBI GI g6041837 BLAST score 205 E value 6.0e-16 Match length 49 % identity 71 NCBI Description (AC009853) hypothetical protein [Arabidopsis thaliana] Seq. No. 416478 Seq. ID uC-osflm202112e08b1 Method BLASTX NCBI GI g3023713 BLAST score 641 E value 4.0e-67 Match length 133 % identity 92 NCBI Description ENOLASE (2-PHOSPHOGLYCERATE DEHYDRATASE) (2-PHOSPHO-D-GLYCERATE HYDRO-LYASE) (OSE1) >gi 780372 (U09450) enolase [Oryza sativa] Seq. No. 416479 Seq. ID uC-osflm202112e09b1 Method BLASTX NCBI GI g3913018 BLAST score 690 E value 8.0e-73Match length 142 % identity 99 NCBI Description FRUCTOSE-BISPHOSPHATE ALDOLASE, CHLOROPLAST PRECURSOR (ALDP) >gi_218155_dbj_BAA02730_ (D13513) chloroplastic aldolase [Oryza sativa] Seq. No. 416480 Seq. ID uC-osflm202112f03b1 Method BLASTX NCBI GI g5733874 BLAST score 225 E value 3.0e-18 92 Match length % identity 42 NCBI Description (AC007932) F11A17.8 [Arabidopsis thaliana] Seq. No. 416481 Seq. ID uC-osflm202112f04b1 Method BLASTX NCBI GI g3319355 BLAST score 480 E value 3.0e-48

% identity NCBI Description (AF077407) similar to chaperonin containing TCP-1 complex gamma chain [Arabidopsis thaliana] Seq. No. 416482 Seq. ID uC-osflm202112f05b1 Method BLASTX NCBI GI g3915847 777 BLAST score E value 5.0e-83 Match length 158 % identity 93 NCBI Description 40S RIBOSOMAL PROTEIN S2 >gi 2335095 (AC002339) putative 40S ribosomal protein S2 [Arabidopsis thaliana] Seq. No. 416483 uC-osflm202112f07b1 Seq. ID BLASTX Method NCBI GI g3721942 BLAST score 415 E value 8.0e-41 Match length 109 71 % identity NCBI Description (AB018248) chitinase [Oryza sativa] Seq. No. 416484 uC-osflm202112f12b1 Seq. ID Method BLASTX NCBI GI g4585142 BLAST score 301 E value 2.0e-27 Match length 122 % identity 49 NCBI Description (AF088276) NADPH oxidase; gp91; phox homolog [Lycopersicon esculentum] 416485 Seq. No. Seq. ID uC-osflm202112g03b1 Method BLASTX NCBI GI g5690010 BLAST score 289 E value 9.0e-26 Match length 120 % identity 50 NCBI Description (AJ132472) Family 3 Glycoside Hydrolase [Ruminococcus flavefaciens] 416486 Seq. No. Seq. ID uC-osflm202112g04b1 Method BLASTX NCBI GI g1350986 BLAST score 160 E value 1.0e-10 Match length 33 % identity 91 NCBI Description 40S RIBOSOMAL PROTEIN S3A (CYC07 PROTEIN) >gi 483431 dbj BAA05059 (D26060) cyc07 [Oryza sativa]

% identity

Seq. No. 416487 Seq. ID uC-osflm202112q05b1 Method BLASTX NCBI GI g3335355 BLAST score 205 E value 2.0e-16 Match length 88 % identity 22 NCBI Description (AC004512) Match to polyubiquitin DNA gb L05401 from A. thaliana. Contains insertion of mitochondrial NADH dehydrogenase gb_X82618 and gb_X98301. May be a pseudogene with an expressed insert. EST gb AA586248 comes from this region. [Arabi 416488 Seq. No. Seq. ID uC-osflm202112q07b1 Method BLASTX NCBI GI g1519249 BLAST score 598 E value 4.0e-62 Match length 123 % identity 99 NCBI Description (U65956) GF14-b protein [Oryza sativa] Seq. No. 416489 uC-osflm202112q08b1 Seq. ID Method BLASTX NCBI GI g4753658 BLAST score 568 E value 1.0e-58 Match length 158 71 % identity NCBI Description (AL049751) putative protein [Arabidopsis thaliana] Seq. No. 416490 Seq. ID uC-osflm202112g10b1 Method BLASTX NCBI GI g231509 BLAST score 350 E value 1.0e-56 Match length 138 80 % identity NCBI Description ACTIN DEPOLYMERIZING FACTOR (ADF) >gi 419809 pir S30935 actin-depolymerizing factor - trumpet lily >gi 22748 emb CAA78483 (Z14110) actin depolymerizing factor [Lilium longiflorum] Seq. No. 416491 Seq. ID uC-osflm202112q11b1 Method BLASTX NCBI GI g3608481 473 BLAST score E value 2.0e-47 Match length 116

54441

NCBI Description (AF088913) ribosomal protein L27a [Petunia x hybrida]

Method

NCBI GI

BLASTX

g3337091

Seq. No. 416492 Seq. ID uC-osflm202112g12b1 Method BLASTX NCBI GI g4584546 BLAST score 500 E value 1.0e-50 Match length 140 % identity 62 NCBI Description (AL049608) putative protein [Arabidopsis thaliana] 416493 Seq. No. uC-osflm202112h01b1 Seq. ID Method BLASTX NCBI GI q136640 BLAST score 624 E value 3.0e-65 Match length 123 % identity 93 NCBI Description UBIQUITIN-CONJUGATING ENZYME E2-17 KD (UBIQUITIN-PROTEIN LIGASE) (UBIQUITIN CARRIER PROTEIN) >gi 170785 (M62720) ubiquitin carrier protein [Triticum aestivum] Seq. No. 416494 Seq. ID uC-osflm202112h05b1 Method BLASTX NCBI GI q1174745 BLAST score 753 E value 4.0e-80 Match length 158 % identity 90 TRIOSEPHOSPHATE ISOMERASE, CHLOROPLAST PRECURSOR (TIM) NCBI Description >gi_1363523_pir__S53761 triose-phosphate isomerase (EC 5.3.1.1) precursor, chloroplast - rye >gi 609262 emb CAA83533 (Z32521) triosephosphate isomerase [Secale cereale] >gi 1095494 prf 2109226B triosephosphate isomerase [Secale cereale] 416495 Seq. No. Seq. ID uC-osflm202112h06b1 Method BLASTX NCBI GI g1174745 200 BLAST score E value 8.0e-16 Match length 45 % identity NCBI Description TRIOSEPHOSPHATE ISOMERASE, CHLOROPLAST PRECURSOR (TIM) >gi 1363523 pir S53761 triose-phosphate isomerase (EC 5.3.1.1) precursor, chloroplast - rye >gi 609262 emb CAA83533 (Z32521) triosephosphate isomerase [Secale cereale] >gi 1095494 prf 2109226B triosephosphate isomerase [Secale cereale] 416496 Seq. No. Seq. ID uC-osflm202112h07b1

```
BLAST score
                   154
E value
                   3.0e-10
Match length
                   80
% identity
                   42
                  (AB016204) polygalacturonase inhibitor (PGIP) [Citrus
NCBI Description
                   unshiu]
Seq. No.
                   416497
Seq. ID
                   uC-osflm202112h08b1
Method
                   BLASTX
NCBI GI
                   q1170937
BLAST score
                   656
E value
                   5.0e-69
Match length
                   127
% identity
                   97
NCBI Description S-ADENOSYLMETHIONINE SYNTHETASE 1 (METHIONINE
                   ADENOSYLTRANSFERASE 1) (ADOMET SYNTHETASE 1)
                   >gi_450549_emb_CAA81481_ (Z26867) S-adenosyl methionine
                   synthetase [Oryza sativa]
Seq. No.
                   416498
Seq. ID
                   uC-osflm202112h09b1
Method
                   BLASTX
NCBI GI
                   q4587519
BLAST score
                   298
E value
                   6.0e-27
Match length
                   130
% identity
                   66
                   (AC007060) Strong similarity to F19I3.7 gi 3033380 putative
NCBI Description
                   coatomer epsilon subunit from Arabidopsis Thaliana BAC
                   gb_AC004238. ESTs gb_Z17908, gb_AA728673, gb_N96555,
                   gb H76335, gb AA712463, gb W43247, gb T45611, g
Seq. No.
                   416499
Seq. ID
                   uC-osflm202112h10b1
Method
                   BLASTX
NCBI GI
                   g543711
BLAST score
                   548
E value
                   3.0e-56
Match length
                   116
                   96
% identity
NCBI Description 14-3-3-LIKE PROTEIN S94 >gi_419796_pir__S30927 14-3-3 protein homolog - rice >gi_303859_dbj_BAA03711_ (D16140)
                   brain specific protein [Oryza satīva]
Seq. No.
                   416500
Seq. ID
                   uC-osflm202112h11b1
Method
                   BLASTX
NCBI GI
                   q131773
BLAST score
                   606
E value
                   6.0e-63
Match length
                   143
                   88
% identity
```

>gi_82724_pir__B30097 ribosomal protein S14 (clone MCH2) -

NCBI Description 40S RIBOSOMAL PROTEIN S14 (CLONE MCH2)

maize

Seq. No.

Seq. ID

416506

uC-osflm202113a05b1

```
Seq. No.
                  416501
Seq. ID
                  uC-osflm202112h12b1
                  BLASTX
Method
NCBI GI
                  g2833382
BLAST score
                  814
E value
                  2.0e-87
Match length
                  165
% identity
                  98
NCBI Description GRANULE-BOUND GLYCOGEN (STARCH) SYNTHASE PRECURSOR
                  >gi_532287_dbj_BAA01272_ (D10472) glucosyl transferase
                  [Oryza glaberrima]
                  416502
Seq. No.
Seq. ID
                  uC-osflm202113a01b1
Method
                  BLASTX
NCBI GI
                  g300265
BLAST score
                  523
E value
                  2.0e-53
Match length
                  120
% identity
                  88
NCBI Description HSP68=68 kda heat-stress DnaK homolog [Lycopersicon
                  peruvianum=tomatoes, Peptide Mitochondrial Partial, 580 aa]
                  416503
Seq. No.
                  uC-osflm202113a02b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g66298
BLAST score
                  241
E value
                  2.0e-20
Match length
                  96
                  59
% identity
NCBI Description catalase (EC 1.11.1.6) - rice >gi 20192 emb CAA43814
                  (X61626) catalase [Oryza sativa]
Seq. No.
                  416504
Seq. ID
                  uC-osflm202113a03b1
Method
                  BLASTN
NCBI GI
                  g3318614
BLAST score
                  181
E value
                  3.0e-97
Match length
                  193
% identity
                  98
NCBI Description Oryza sativa mRNA for mitochondrial phosphate transporter,
                  complete cds
                  416505
Seq. No.
                  uC-osflm202113a04b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3928150
BLAST score
                  206
E value
                  1.0e-16
Match length
                  60
% identity
NCBI Description (AJ131049) hypothetical protein [Cicer arietinum]
```

```
Method
                  BLASTX
NCBI GI
                  g3128218
BLAST score
                  170
E value
                  7.0e-12
                  39
Match length
% identity
                  85
NCBI Description (AC004077) putative end13 protein [Arabidopsis thaliana]
                  416507
Seq. No.
Seq. ID
                  uC-osflm202113a07b1
Method
                  BLASTX
NCBI GI
                  g6041808
BLAST score
                  185
E value
                  1.0e-13
                  33
Match length
                  85
% identity
NCBI Description (AC009755) unknown protein [Arabidopsis thaliana]
Seq. No.
                  416508
Seq. ID
                  uC-osflm202113a08b1
Method
                  BLASTX
NCBI GI
                  g3559805
BLAST score
                  302
E value
                  2.0e-27
Match length
                  86
% identity
                  62
NCBI Description (AJ006787) putative phytochelatin synthetase [Arabidopsis
                  thaliana]
                  416509
Seq. No.
Seq. ID
                  uC-osflm202113b03b1
Method
                  BLASTN
NCBI GI
                  g5679837
BLAST score
                  417
E value
                  0.0e + 00
Match length
                  515
% identity
                  98
NCBI Description Oryza sativa chromosome 4 BAC 11332 genomic sequences
Seq. No.
                  416510
Seq. ID
                  uC-osflm202113b04b1
Method
                  BLASTX
NCBI GI
                  g1167836
BLAST score
                  438
E value
                  3.0e-43
Match length
                  129
% identity
                  58
NCBI Description (Z68893) protein with incomplete signal sequence [Holcus
                  lanatus]
Seq. No.
                  416511
Seq. ID
                  uC-osflm202113b05b1
Method
                  BLASTX
NCBI GI
                  q6091756
BLAST score
                  173
E value
                  6.0e-25
Match length
                  132
```

% identity NCBI Description (AC009327) putative peroxidase [Arabidopsis thaliana] 416512 Seq. No. uC-osflm202113b08b1 Seq. ID Method BLASTX NCBI GI g1332579 BLAST score 670 E value 2.0e-70 Match length 141 % identity 10 NCBI Description (X98063) polyubiquitin [Pinus sylvestris] Seq. No. 416513 uC-osflm202113b09b1 Seq. ID Method BLASTN NCBI GI g5091597 BLAST score 204 E value 1.0e-111 Match length 303 % identity 98 NCBI Description Oryza sativa chromosome 1 BAC 10A19I, complete sequence Seq. No. 416514 Seq. ID uC-osflm202113b10b1 Method BLASTX NCBI GI g3024122 BLAST score 551 E value 3.0e-67 Match length 143 96 % identity S-ADENOSYLMETHIONINE SYNTHETASE 2 (METHIONINE NCBI Description ADENOSYLTRANSFERASE 2) (ADOMET SYNTHETASE 2) >gi 1778821 (U82833) S-adenosyl-L-methionine synthetase [Oryza sativa] 416515 Seq. No. Seq. ID uC-osflm202113b11b1 Method BLASTX NCBI GI g320618 BLAST score 253 E value 1.0e-26 85 Match length 78 % identity NCBI Description chlorophyll a/b-binding protein I precursor - rice >gi_218172_dbj_BAA00536_ (D00641) type I light-harvesting chlorophyll a/b-binding protein [Oryza sativa] >gi 227611 prf 1707316A chlorophyll a/b binding protein 1 [Oryza sativa] Seq. No. 416516 Seq. ID uC-osflm202113c01b1 Method BLASTX

NCBI GI g2119278
BLAST score 260
E value 2.0e-22
Match length 102
% identity 61

Method

BLASTN

```
NCBI Description tubulin beta-1 chain - rice
Seq. No.
                   416517
Seq. ID
                   uC-osflm202113c09b1
Method
                  BLASTX
NCBI GI
                  q1321627
BLAST score
                  203
E value
                   9.0e-16
Match length
                  42
% identity
                  86
                  (D83656) thylakoid-bound ascorbate peroxidase [Cucurbita
NCBI Description
                  sp.]
Seq. No.
                  416518
Seq. ID
                  uC-osflm202113d02b1
Method
                  BLASTN
NCBI GI
                  g2780745
BLAST score
                  150
E value
                  1.0e-78
Match length
                  342
% identity
                  96
                  Oryza sativa mRNA for plastid RNA polymerase sigma factor,
NCBI Description
                  complete cds
Seq. No.
                  416519
Seq. ID
                  uC-osflm202113d07b1
Method
                  BLASTX
NCBI GI
                  q3063460
BLAST score
                  376
E value
                  5.0e-36
Match length
                  98
% identity
                  68
NCBI Description (AC003981) F22013.22 [Arabidopsis thaliana]
Seq. No.
                  416520
Seq. ID
                  uC-osflm202113d08b1
Method
                  BLASTN
NCBI GI
                  g607894
BLAST score
                  383
E value
                  0.0e+00
Match length
                  496
% identity
                  99
NCBI Description Oryza sativa IR54 anther specific (RTS2) gene, complete cds
Seq. No.
                  416521
Seq. ID
                  uC-osflm202113d09b1
Method
                  BLASTX
NCBI GI
                  q1076737
BLAST score
                  719
E value
                  3.0e-76
Match length
                  132
% identity
                  99
NCBI Description beta-tubulin R1623 - rice
Seq. No.
                  416522
Seq. ID
                  uC-osflm202113d11b1
```

NCBI GI g2773153 BLAST score 455 0.0e + 00E value Match length 478 % identity 99 NCBI Description Oryza sativa abscisic acid- and stress-inducible protein (Asr1) mRNA, complete cds Seq. No. 416523 uC-osflm202113d12b1 Seq. ID Method BLASTX NCBI GI g1151244 BLAST score 291 E value 4.0e-26 Match length 94 % identity 62 NCBI Description (U43377) GTP-binding protein [Arabidopsis thaliana] 416524 Seq. No. Seq. ID uC-osflm202113e01b1Method BLASTX NCBI GI q1532171 BLAST score 282 E value 5.0e-25 Match length 145 % identity 41 NCBI Description (U63815) AT.I.24-9 gene product [Arabidopsis thaliana] 416525 Seq. No. uC-osflm202113e02b1 Seq. ID Method BLASTX NCBI GI g1362086 BLAST score 247 E value 7.0e-21 Match length 69 % identity 70 5-methyltetrahydropteroyltriglutamate--homocysteine NCBI Description S-methyltransferase (EC 2.1.1.14) - Madagascar periwinkle >gi_2129919_pir _S65957 5-methyltetrahydropteroyltriglutamate--homocysteine S-methyltransferase (EC 2.1.1.14) - Madagascar periwinkle >gi 886471 emb CAA58474 (X83499) methionine synthase [Catharanthus roseus] Seq. No. 416526 Seq. ID uC-osflm202113e03b1 Method BLASTX NCBI GI g4371290 BLAST score 489 E value 3.0e-49134 Match length 63 % identity

NCBI Description (AC006260) unknown protein [Arabidopsis thaliana]

Seq. No. 416527

Seq. ID uC-osflm202113e04b1

Method BLASTX

Seq. No.

```
NCBI GI
                  q136739
BLAST score
                  342
E value
                  5.0e - 32
                  78
Match length
% identity
NCBI Description
                  UTP--GLUCOSE-1-PHOSPHATE URIDYLYLTRANSFERASE (UDP-GLUCOSE
                  PYROPHOSPHORYLASE) (UDPGP) >gi_67061_pir__XNPOU
                  UTP--glucose-1-phosphate uridylyltransferase (EC 2.7.7.9) -
                  potato >gi_218001_dbj_BAA00570_ (D00667) UDP-glucose
                  pyrophosphorylase precursor [Solanum tuberosum]
Seq. No.
Seq. ID
                  uC-osflm202113e05b1
Method
                  BLASTX
NCBI GI
                  a5360953
BLAST score
                  238
E value
                  3.0e - 33
Match length
                  104
% identity
NCBI Description (AJ225059) v-ATPase subunit D [Arabidopsis thaliana]
Seq. No.
                  416529
Seq. ID
                  uC-osflm202113e06b1
Method
                  BLASTX
NCBI GI
                  g1709129
BLAST score
                  295
E value
                  2.0e-26
Match length
                  101
% identity
                  60
NCBI Description
                  GLYCOGEN SYNTHASE KINASE-3 HOMOLOG MSK-3
                  >gi_481018_pir__S37642 protein kinase MSK-3 (EC 2.7.1.-) -
                  alfalfa >gi_313148_emb_CAA48472 (X68409) protein kinase
                  [Medicago sativa]
                  416530
Seq. No.
Seq. ID
                  uC-osflm202113e07b1
Method
                  BLASTX
NCBI GI
                  q3421104
BLAST score
                  613
E value
                  9.0e-64
Match length
                  133
% identity
                 (AF043531) 20S proteasome beta subunit PBB2 [Arabidopsis
NCBI Description
                  thaliana]
                  416531
Seq. No.
Seq. ID
                  uC-osflm202113e08b1
Method
                  BLASTX
NCBI GI
                  q974782
BLAST score
                  700
E value
                  5.0e-74
Match length
                  164
% identity
                  81
NCBI Description (Z49150) cobalamine-independent methionine synthase
                  [Solenostemon scutellarioides]
```

Seq. ID uC-osflm202113e09b1 Method BLASTX NCBI GI q1054843 BLAST score 408 E value 1.0e-39 Match length 131 % identity 58 NCBI Description (X92847) D12 oleate desaturase [Solanum commersonii] Seq. No. 416533 Seq. ID uC-osflm202113e10b1 Method BLASTX NCBI GI q4467099 BLAST score 397 E value 5.0e-67 Match length 163 % identity 85 NCBI Description (AL035538) glycine hydroxymethyltransferase like protein [Arabidopsis thaliana] Seq. No. 416534 Seq. ID uC-osflm202113f01b1 Method BLASTX NCBI GI q2739374 BLAST score 569 E value 1.0e-58 Match length 169 % identity 66 NCBI Description (AC002505) hypothetical protein [Arabidopsis thaliana] Seq. No. 416535 Seq. ID uC-osflm202113f02b1 Method BLASTX NCBI GI g132105 BLAST score 798 E value 2.0e-85 Match length 168 % identity 90 NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR (RUBISCO SMALL SUBUNIT C) >gi_68094_pir__RKRZS9 ribulose-bisphosphate carboxylase (\overline{EC} 4.1.1.39) small chain precursor (clone pOSSS1139) - rice >gi 218208 dbj BAA00538 (D00643) small subunit of ribulose-1,5-bisphosphate carboxylase (RuBPC) [Oryza sativa] >gi 2407283 (AF017364) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa] >gi_226375_prf__1508256A ribulose bisphosphate carboxylase S [Oryza sativa] Seq. No. 416536 Seq. ID uC-osflm202113f03b1 Method BLASTX NCBI GI q4769012 BLAST score 724 E value 8.0e-77

Match length 157 % identity 89

NCBI Description (AF143746) CER1 [Oryza sativa]

```
Seq. No.
                   416537
Seq. ID
                  uC-osflm202113f05b1
Method
                  BLASTX
NCBI GI
                   g733458
BLAST score
                  678
E value
                   2.0e-71
Match length
                  144
% identity
                  88
NCBI Description
                  (U23190) chlorophyll a/b-binding apoprotein CP24 precursor
                   [Zea mays]
                  416538
Seq. No.
Seq. ID
                  uC-osflm202113f07b1
Method
                  BLASTX
NCBI GI
                  g3135543
BLAST score
                  361
E value
                  2.0e-39
Match length
                  126
% identity
                   72
NCBI Description (AF062393) aquaporin [Oryza sativa]
Seq. No.
                   416539
                  uC-osflm202113f08b1
Seq. ID
Method
                  BLASTX
NCBI GI
                   q542058
BLAST score
                   339
E value
                   1.0e-31
Match length
                  161
% identity
                   43
NCBI Description HSR203J protein - common tobacco >gi_444002_emb_CAA54393_
                   (X77136) HSR203J [Nicotiana tabacum]
Seq. No.
                   416540
Seq. ID
                   uC-osflm202113f10b1
Method
                  BLASTX
NCBI GI
                   g444790
BLAST score
                   252
E value
                   4.0e-26
Match length
                  139
                   49
% identity
NCBI Description nucleotide translocator [Arabidopsis thaliana]
                   416541
Seq. No.
Seq. ID
                   uC-osflm202113f11b1
Method
                  BLASTN
NCBI GI
                   g2920319
                  56
BLAST score
E value
                   1.0e-22
Match length
                  108
% identity
                   88
NCBI Description Oryza sativa mRNA for glutamyl-tRNA reductase, complete cds
Seq. No.
                   416542
Seq. ID
                   uC-osflm202113g02b1
Method
                   BLASTX
NCBI GI
                   q1332579
```

BLAST score 463 E value 6.0e-72 Match length 155 % identity 10

NCBI Description (X98063) polyubiquitin [Pinus sylvestris]

Seq. No. 416543

Seq. ID uC-osflm202113g04b1

Method BLASTX
NCBI GI g2842493
BLAST score 440
E value 1.0e-43
Match length 149
% identity 58

NCBI Description (AL021749) predicted protein [Arabidopsis thaliana]

Seq. No. 416544

Seq. ID uC-osflm202113g05b1

Method BLASTX
NCBI GI g1657859
BLAST score 221
E value 3.0e-18
Match length 56
% identity 68

NCBI Description (U73218) chlorophyll a/b-binding protein WCAB precursor

[Triticum aestivum]

Seq. No. 416545

Seq. ID uC-osflm202113g07b1

Method BLASTX
NCBI GI g6016151
BLAST score 647
E value 8.0e-68
Match length 131
% identity 96

NCBI Description IMMUNOGLOBULIN BINDING PROTEIN HOMOLOG 3 PRECURSOR (HEAT

SHOCK PROTEIN 70 HOMOLOG 3) >gi_1575130 (U58209) lumenal

binding protein cBiPe3 [Zea mays]

Seq. No. 416546

Seq. ID uC-osflm202113g08b1

Method BLASTX
NCBI GI g548605
BLAST score 595
E value 1.0e-61
Match length 133
% identity 89

NCBI Description PHOTOSYSTEM I REACTION CENTRE SUBUNIT X PRECURSOR

(LIGHT-HARVESTING COMPLEX I 7 KD PROTEIN) (PSI-K)

>gi_539055_pir__A48527 photosystem I protein psaK precursor - barley >gi_304220 (L12707) photosystem I PSI-K subunit

[Hordeum vulgare]

Seq. No. 416547

Seq. ID uC-osflm202113g09b1

Method BLASTX NCBI GI g2570505

```
BLAST score
                   695
                   2.0e-73
E value
                  155
Match length
                   90
% identity
NCBI Description
                  (AF022735) proteasome component [Oryza sativa]
                   416548
Seq. No.
                  uC-osflm202113g11b1
Seq. ID
Method
                  BLASTX
                  g320618
NCBI GI
BLAST score
                   468
                   8.0e-47
E value
Match length
                   133
                   72
% identity
                  chlorophyll a/b-binding protein I precursor - rice
NCBI Description
                   >gi_218172_dbj_BAA00536_ (D00641) type I light-harvesting
                   chlorophyll a/b-binding protein [Oryza sativa]
                   >gi_227611_prf__1707316A chlorophyll a/b binding protein 1
                   [Oryza satīva]
Seq. No.
                   416549
                   uC-osflm202113h03b1
Seq. ID
Method
                   BLASTX
                   g3785989
NCBI GI
BLAST score
                   611
E value
                   2.0e-63
                   152
Match length
% identity
NCBI Description (AC005560) unknown protein [Arabidopsis thaliana]
Seq. No.
                   416550
Seq. ID
                   uC-osflm202113h07b1
Method
                   BLASTX
NCBI GI
                   q3646373
BLAST score
                   704
E value
                   2.0e-74
Match length
                   145
% identity
                   92
NCBI Description (AJ011078) RGP1 protein [Oryza sativa]
Seq. No.
                   416551
                   uC-osflm202120a02b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g4006887
BLAST score
                   265
E value
                   4.0e-23
                   82
Match length
% identity
NCBI Description (299708) putative protein [Arabidopsis thaliana]
Seq. No.
                   416552
                   uC-osflm202120a03b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g131388
BLAST score
                   508
E value
                   2.0e-51
Match length
                   142
```

Method

BLASTX

% identity OXYGEN-EVOLVING ENHANCER PROTEIN 1 PRECURSOR (OEE1) (33 KD NCBI Description SUBUNIT OF OXYGEN EVOLVING SYSTEM OF PHOTOSYSTEM II) (33 KD THYLAKOID MEMBRANE PROTEIN) >gi 100831 pir S16260 photosystem II oxygen-evolving complex protein 1 - common wheat x Sanduri wheat >gi_21844_emb_CAA40670_ (X57408) 33kDa oxygen evolving protein of photosystem II [Triticum aestivum] Seq. No. 416553 Seq. ID uC-osflm202120a04b1 Method BLASTX NCBI GI q123593 BLAST score 576 E value 1.0e-59 Match length 119 97 % identity NCBI Description HEAT SHOCK 70 KD PROTEIN >gi 82697 pir A25089 heat shock protein 70 - maize Seq. No. 416554 Seq. ID uC-osflm202120a08b1 Method BLASTX NCBI GI q112802 BLAST score 589 E value 5.0e-61 Match length 149 77 % identity NCBI Description 4-COUMARATE--COA LIGASE >gi_82454_pir__JU0311 4-coumarate--CoA ligase (EC 6.2.1.12) - rice >gi 20161 emb CAA36850 (X52623) 4-coumarate-CoA ligase [Oryza sativa] Seq. No. 416555 Seq. ID uC-osflm202120a09b1 Method BLASTX NCBI GI q1944573 BLAST score 477 E value 7.0e-48Match length 107 86 % identity NCBI Description (Z49146) phenylalanine ammonia-lyase [Hordeum vulgare] Seq. No. 416556 Seq. ID uC-osflm202120a10b1 Method BLASTX NCBI GI g1922938 BLAST score 529 E value 7.0e-54Match length 152 % identity NCBI Description (AC000106) Similar to Caenorhabditis hypothetical protein CO7A9.11 (gb Z29094). [Arabidopsis thaliana] Seq. No. 416557 uC-osflm202120a12b1 Seq. ID

NCBI GI g4587571 BLAST score 179 E value 6.0e-13Match length 118 % identity (AC006550) Belongs to the PF 01027 Uncharacterized protein NCBI Description family UPF0005 with 7 transmembrane domains. [Arabidopsis thaliana] 416558 Seq. No. Seq. ID uC-osflm202120b04b1 Method BLASTX NCBI GI q1345504 BLAST score 151 E value 8.0e-10 Match length 52 58 % identity NCBI Description (X74756) ATAF2 [Arabidopsis thaliana] Seq. No. 416559 uC-osflm202120c01b1 Seq. ID Method BLASTX NCBI GI q1928960 BLAST score 471 E value 4.0e-47Match length 114 % identity NCBI Description (U92286) pyrroline-5-carboxylate synthetase [Actinidia deliciosa] Seq. No. 416560 Seq. ID uC-osflm202120c03b1 BLASTX Method NCBI GI g3450889 BLAST score 502 E value 1.0e-50 178 Match length 59 % identity NCBI Description (AF083890) 19S proteosome subunit 9 [Arabidopsis thaliana] Seq. No. 416561 Seq. ID uC-osflm202120c04b1 BLASTX Method NCBI GI g231503 BLAST score 791 E value 1.0e-84 Match length 160 96 % identity NCBI Description ACTIN 97 >gi_100417_pir__S20098 actin - potato >gi 21544 emb CAA39280 (X55751) actin [Solanum tuberosum]

Seq. No. 416562

Seq. ID uC-osflm202120c06b1

Method BLASTX
NCBI GI g2293566
BLAST score 854
E value 5.0e-92

Match length 167 % identity 98

NCBI Description (AF012896) ADP-ribosylation factor 1 [Oryza sativa]

Seq. No. 416563

Seq. ID uC-osflm202120c09b1

Method BLASTX
NCBI GI g3023713
BLAST score 339
E value 8.0e-32
Match length 104
% identity 69

NCBI Description ENOLASE (2-PHOSPHOGLYCERATE DEHYDRATASE)

(2-PHOSPHO-D-GLYCERATE HYDRO-LYASE) (OSE1) >gi 780372

(U09450) enolase [Oryza sativa]

Seq. No. 416564

Seq. ID uC-osflm202120c10b1

Method BLASTX
NCBI GI g3023713
BLAST score 391
E value 2.0e-57
Match length 126
% identity 94

NCBI Description ENOLASE (2-PHOSPHOGLYCERATE DEHYDRATASE)

(2-PHOSPHO-D-GLYCERATE HYDRO-LYASE) (OSE1) >gi_780372

(U09450) enolase [Oryza sativa]

Seq. No. 416565

Seq. ID uC-osflm202120c11b1

Method BLASTX
NCBI GI g3023713
BLAST score 661
E value 2.0e-69
Match length 147
% identity 90

NCBI Description ENOLASE (2-PHOSPHOGLYCERATE DEHYDRATASE)

(2-PHOSPHO-D-GLYCERATE HYDRO-LYASE) (OSE1) >gi 780372

(U09450) enolase [Oryza sativa]

Seq. No. 416566

Seq. ID uC-osflm202120c12b1

Method BLASTX
NCBI GI g4417304
BLAST score 334
E value 4.0e-31
Match length 88
% identity 69

NCBI Description (AC006446) putative beta-1,4-mannosyl-glycoprotein

beta-1,4-N-acetylglucosaminyltransferase [Arabidopsis

thaliana]

Seq. No. 416567

Seq. ID uC-osflm202120d01b1

Method BLASTX
NCBI GI g2293566
BLAST score 810

```
7.0e-87
E value
                  157
Match length
                  100
% identity
                 (AF012896) ADP-ribosylation factor 1 [Oryza sativa]
NCBI Description
                  416568
Seq. No.
                  uC-osflm202120d03b1
Seq. ID
                  BLASTX
Method
NCBI GI
                  g1363504
BLAST score
                  925
                  1.0e-100
E value
Match length
                  177
% identity
NCBI Description aspartic proteinase (EC 3.4.-.-) L5 - rice (fragment)
                  416569
Seq. No.
                  uC-osflm202120d04b1
Seq. ID
                  BLASTX
Method
NCBI GI
                  q2832683
BLAST score
                  420
E value
                  4.0e-41
Match length
                  103
                  77
% identity
NCBI Description (AL021712) putative protein [Arabidopsis thaliana]
                  416570
Seq. No.
                  uC-osflm202120d06b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q451193
BLAST score
                   383
E value
                  8.0e-37
Match length
                  102
                   76
% identity
                  (L28008) wali7 [Triticum aestivum]
NCBI Description
                  >gi_1090845_prf__2019486B wali7 gene [Triticum aestivum]
                   416571
Seq. No.
                  uC-osflm202120d08b1
Seq. ID
Method
                  BLASTX
                  g3258575
NCBI GI
BLAST score
                   304
                  1.0e-27
E value
                  131
Match length
                   55
% identity
NCBI Description (U89959) Hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   416572
                   uC-osflm202120d10b1
Seq. ID
                   BLASTX
Method
NCBI GI
                   g1169238
BLAST score
                   612
E value
                   1.0e-63
                  152
Match length
                   76
% identity
                  GLUTAMATE DECARBOXYLASE (GAD) >gi 1076648 pir_ A48767
NCBI Description
                   glutamate decarboxylase (EC 4.1.1.15), calmodulin-binding -
```

garden petunia >gi 294112 (L16797) glutamate decarboxylase

[Petunia hybrida] >gi_309680 (L16977) glutamate decarboxylase [Petunia hybrida]

Seq. No. 416573

Seq. ID uC-osflm202120d12b1

Method BLASTX
NCBI GI g1711507
BLAST score 611
E value 1.0e-63
Match length 119
% identity 97

NCBI Description SIGNAL RECOGNITION PARTICLE 19 KD PROTEIN (SRP19)

>qi 624221 (U19030) signal recognition particle 19 kDa

protein subunit SRP19 [Oryza sativa]

Seq. No. 416574

Seq. ID uC-osflm202120e04b1

Method BLASTX
NCBI GI g2129538
BLAST score 417
E value 8.0e-41
Match length 105
% identity 76

% identity 76
NCBI Description AT103 protein - Arabidopsis thaliana >gi_1033195 (U38232)

AT103 [Arabidopsis thaliana]

Seq. No. 416575

Seq. ID uC-osflm202120e06b1

Method BLASTX
NCBI GI g1710807
BLAST score 529
E value 6.0e-54
Match length 121
% identity 88

NCBI Description RUBISCO SUBUNIT BINDING-PROTEIN ALPHA SUBUNIT PRECURSOR (60

KD CHAPERONIN ALPHA SUBUNIT) (CPN-60 ALPHA) >gi_1185390

(U21105) alphacpn60 [Pisum sativum]

Seq. No. 416576

Seq. ID uC-osflm202120e08b1

Method BLASTX
NCBI GI g2129578
BLAST score 395
E value 2.0e-38
Match length 130
% identity 59

NCBI Description dTDP-glucose 4-6-dehydratases homolog - Arabidopsis

thaliana >gi_928932_emb_CAA89205_ (Z49239) homolog of dTDP-glucose 4-6-dehydratases [Arabidopsis thaliana] >gi_1585435_prf__2124427B diamide resistance gene

[Arabidopsis thaliana]

Seq. No. 416577

Seq. ID uC-osflm202120e10b1

Method BLASTX
NCBI GI g1362086
BLAST score 657



E value 5.0e-69 Match length 139 % identity 88

5-methyltetrahydropteroyltriglutamate--homocysteine NCBI Description

S-methyltransferase (EC 2.1.1.14) - Madagascar periwinkle

>gi 2129919 pir S65957

5-methyltetrahydropteroyltriglutamate--homocysteine

S-methyltransferase (EC 2.1.1.14) - Madagascar periwinkle

>gi_886471_emb_CAA58474_ (X83499) methionine synthase

[Catharanthus roseus]

416578 Seq. No.

uC-osflm202120e12b1 Seq. ID

BLASTX Method NCBI GI a3618310 BLAST score 408 E value 6.0e-40Match length 79 % identity

NCBI Description (AB001883) zinc finger protein [Oryza sativa]

416579 Seq. No.

Seq. ID uC-osflm202120f01b1

Method BLASTX NCBI GI q1729971 BLAST score 401 E value 4.0e-39 Match length 110 % identity 74

NCBI Description TONOPLAST INTRINSIC PROTEIN, GAMMA (GAMMA TIP)

(AQUAPORIN-TIP) >gi_1076745_pir__S52004_gamma-Tip_protein -

rice >gi 473997 dbj BAA05017 (D25534) gamma-Tip [Oryza

sativa]

Seq. No. 416580

Seq. ID uC-osflm202120f04b1

BLASTX Method NCBI GI g2191150 BLAST score 479 E value 1.0e-48 Match length 129 % identity 81

NCBI Description (AF007269) similar to mitochondrial carrier family

[Arabidopsis thaliana]

Seq. No. 416581

uC-osflm202120f08b1 Seq. ID

BLASTX Method NCBI GI q2497543 BLAST score 480 E value 3.0e-48 Match length 123 77 % identity

NCBI Description PYRUVATE KINASE, CYTOSOLIC ISOZYME >gi_542061_pir S41379

pyruvate kinase - common tobacco >gi 444023 emb CAA82628

(Z29492) pyruvate kinase [Nicotiana tabacum]

Seq. No. 416582

Seq. ID uC-osflm202120f10b1

Method BLASTX
NCBI GI g548485
BLAST score 274
E value 5.0e-24
Match length 131
% identity 47

NCBI Description POLYGALACTURONASE INHIBITOR PRECURSOR (POLYGALACTURONASE-INHIBITING PROTEIN)

>gi_478677_pir__S23764 polygalacturanase-inhibiting protein
precursor - kidney bean >gi_21029_emb_CAA46016_ (X64769)
polygalacturanase-inhibiting protein [Phaseolus vulgaris]

Seq. No. 416583

Seq. ID uC-osflm202120g01b1

Method BLASTX
NCBI GI g462243
BLAST score 371
E value 2.0e-35
Match length 79
% identity 95

NCBI Description HISTONE H4 >gi_421921_pir__S32769 histone H4 - tomato

>gi_297150_emb_CAA48923 (X69179) histone H4 [Lycopersicon esculentum] >gi_297152_emb_CAA48924 (X69180) histone H4 [Lycopersicon esculentum] >gi_2746721 (AF038387) histone H4

[Capsicum annuum]

Seq. No. 416584

Seq. ID uC-osflm202120g02b1

Method BLASTX
NCBI GI g283008
BLAST score 442
E value 9.0e-44
Match length 138
% identity 54

NCBI Description sucrose synthase (EC 2.4.1.13) - rice

>qi 20366 emb CAA46017 (X64770) sucrose synthase [Oryza

sativa]

Seq. No. 416585

Seq. ID uC-osflm202120g03b1

Method BLASTX
NCBI GI g1076746
BLAST score 299
E value 7.0e-53
Match length 113
% identity 90

NCBI Description heat shock protein 70 - rice (fragment)

>gi 763160 emb CAA47948 (X67711) heat shock protein 70

[Oryza sativa]

Seq. No. 416586

Seq. ID uC-osflm202120g06b1

Method BLASTN
NCBI GI g902200
BLAST score 407

E value 0.0e+00
Match length 459
% identity 49

NCBI Description Z.mays complete chloroplast genome

Seq. No. 416587

Seq. ID uC-osflm202120g07b1

Method BLASTX
NCBI GI g3649776
BLAST score 225
E value 2.0e-18
Match length 52
% identity 87

NCBI Description (AJ011302) phosphoenolpyruvate-carboxylase [Vicia faba]

Seq. No. 416588

Seq. ID uC-osflm202120h03b1

Method BLASTN
NCBI GI g2662344
BLAST score 157
E value 5.0e-83
Match length 161
% identity 99

NCBI Description Oryza sativa mRNA for EF-1 alpha, complete cds

Seq. No. 416589

Seq. ID uC-osflm202120h04b1

Method BLASTX
NCBI GI g6093736
BLAST score 331
E value 9.0e-31
Match length 151
% identity 47

NCBI Description PECTINESTERASE 1 PRECURSOR (PECTIN METHYLESTERASE 1) (PE 1)

>gi_1076365_pir__S51370 pectinesterase (EC 3.1.1.11) PME1
precursor - Arabidopsis thaliana >gi_2129666_pir__JC4778
pectinesterase (EC 3.1.1.11) 1 - Arabidopsis thaliana
>gi_550306_emb_CAA57275_ (X81585) ATPME1 [Arabidopsis

thaliana] >gi_903895 (U25649) ATPME1 precursor [Arabidopsis thaliana] >gi_6056393_gb_AAF02857.1_AC009324_6 (AC009324)

Pectinesterase 1 [Arabidopsis thaliana]

Seq. No. 416590

Seq. ID uC-osflm202120h07b1

Method BLASTX
NCBI GI g3080436
BLAST score 261
E value 1.0e-22
Match length 69
% identity 68

NCBI Description (AL022605) putative protein [Arabidopsis thaliana]

Seq. No. 416591

Seq. ID uC-osflm202120h09b1

Method BLASTX
NCBI GI g3201554
BLAST score 488

4.0e-49 E value Match length 158 59 % identity (AJ006501) beta-D-glucosidase [Tropaeolum majus] NCBI Description 416592 Seq. No. uC-osflm202120h10b1 Seq. ID BLASTX Method NCBI GI q2231312 BLAST score 189 E value 3.0e-14 88 Match length % identity NCBI Description (U75603) AtRab18 [Arabidopsis thaliana] 416593 Seq. No. uC-osflm202120h11b1 Seq. ID BLASTX Method NCBI GI g2459424 BLAST score 423 2.0e-41 E value Match length 158 % identity NCBI Description (AC002332) unknown protein [Arabidopsis thaliana] Seq. No. 416594 uC-osroM202001a02a1 Seq. ID BLASTX Method NCBI GI g2078386 BLAST score 503 6.0e-51 E value 117 Match length 83 % identity NCBI Description (U96623) glyceraldehyde-3-phosphate-dehydrogenase [Selaginella lepidophylla] 416595 Seq. No. uC-osroM202001a05b1 Seq. ID Method BLASTX NCBI GI g542157 612 BLAST score 9.0e-64 E value 138 Match length 87 % identity NCBI Description ribosomal 5S RNA-binding protein - Rice 416596 Seq. No. uC-osroM202001a06b1 Seq. ID BLASTX Method NCBI GI g5912299 674 BLAST score 5.0e-71E value 142 Match length % identity NCBI Description (AJ133787) gigantea homologue [Oryza sativa]

54462

416597

Seq. No.

```
uC-osroM202001a07b1
Seq. ID
                  BLASTX
Method
NCBI GI
                  q6016685
BLAST score
                  252
                  1.0e-21
E value
Match length
                  90
                  56
% identity
NCBI Description (AC009991) hypothetical protein [Arabidopsis thaliana]
                  416598
Seq. No.
                  uC-osroM202001a08a1
Seq. ID
                  BLASTX
Method
                  q113377
NCBI GI
                  159
BLAST score
                   1.0e-10
E value
                  50
Match length
                   66
% identity
NCBI Description ALCOHOL DEHYDROGENASE 2 >gi_82671_pir__A23084 alcohol
                  dehydrogenase (EC 1.1.1.1) 2 - maize
                  >gi 22137_emb_CAA26001_ (X01965) Adh2-N (aa 1-379) [Zea
                  mays]
                   416599
Seq. No.
                   uC-osroM202001a08b1
Seq. ID
                   BLASTX
Method
                   g113385
NCBI GI
                   672
BLAST score
                   2.0e-73
E value
                   146
Match length
                   95
% identity
NCBI Description ALCOHOL DEHYDROGENASE 3 >gi 82349_pir S04040 alcohol
                   dehydrogenase (EC 1.1.1.1) 3 - barley
                   >gi 18886_emb_CAA31231_ (X12734) alcohol dehydrogenase
                   [Hordeum vulgare]
Seq. No.
                   416600
                   uC-osroM202001a09a1
Seq. ID
                   BLASTX
Method
                   q399942
NCBI GI
                   198
BLAST score
                   2.0e-18
E value
                   78
Match length
                   76
 % identity
NCBI Description CHLOROPLAST STROMA 70 KD HEAT SHOCK-RELATED PROTEIN
                   PRECURSOR >gi 421881 pir S32818 heat shock protein, 70K,
                   chloroplast - garden pea >gi_169023 (L03299) 70 kDa heat
                   shock protein [Pisum sativum] >gi 871515_emb_CAA49147_
                   (X69213) Psst70 (stress 70 protein) [Pisum sativum]
                   416601
 Seq. No.
                   uC-osroM202001a09b1
 Seq. ID
                   BLASTX
 Method
                   g399942
 NCBI GI
                   804
 BLAST score
                   3.0e-86
 E value
Match length
                   164
                   96
 % identity
```

NCBI Description CHLOROPLAST STROMA 70 KD HEAT SHOCK-RELATED PROTEIN

PRECURSOR >gi_421881_pir__S32818 heat shock protein, 70K, chloroplast - garden pea >gi_169023 (L03299) 70 kDa heat shock protein [Pisum sativum] >gi_871515_emb_CAA49147_(X69213) Psst70 (stress 70 protein) [Pisum sativum]

Seq. No. 416602

Seq. ID uC-osroM202001a12b1

Method BLASTN
NCBI GI g394735
BLAST score 354
E value 0.0e+00
Match length 450
% identity 95

NCBI Description Rice lip19 mRNA for basic/leucine zipper protein

Seq. No. 416603

Seq. ID uC-osroM202001b02a1

Method BLASTX
NCBI GI g3242785
BLAST score 502
E value 7.0e-51
Match length 131
% identity 66

NCBI Description (AF055355) respiratory burst oxidase protein C [Arabidopsis

thaliana]

Seq. No. 416604

Seq. ID uC-osroM202001b02b1

Method BLASTX
NCBI GI g3242783
BLAST score 359
E value 5.0e-34
Match length 164
% identity 46

NCBI Description (AF055354) respiratory burst oxidase protein B [Arabidopsis

thaliana]

Seq. No. 416605

Seq. ID uC-osroM202001b03a1

Method BLASTN
NCBI GI g1051257
BLAST score 35
E value 5.0e-10
Match length 47
% identity 94

NCBI Description Hordeum vulgare vacuolar ATPase catalytic subunit mRNA,

partial cds

Seq. No. 416606

Seq. ID uC-osroM202001b03b1

Method BLASTX
NCBI GI g1352830
BLAST score 800
E value 9.0e-86
Match length 158
% identity 99

VACUOLAR ATP SYNTHASE CATALYTIC SUBUNIT A (V-ATPASE 69 KD NCBI Description SUBUNIT) >gi_1049253 (U36436) vacuolar ATPase 69 kDa subunit [Zea mays] 416607 Seq. No. uC-osroM202001b04a1 Seq. ID Method BLASTX g3868857 NCBI GI 378 BLAST score 3.0e-36 E value 158 Match length % identity 54 (AB013886) RAV1 [Arabidopsis thaliana] NCBI Description 416608 Seq. No. uC-osroM202001b06b1 Seq. ID BLASTX Method NCBI GI q135191 382 BLAST score 9.0e-37 E value 122 Match length 58 % identity TRYPTOPHANYL-TRNA SYNTHETASE (TRYPTOPHAN--TRNA LIGASE) NCBI Description (TRPRS) (IFP53) >gi_107990_pir__A41706 tryptophan--tRNA ligase homolog - human >gi_308 $\overline{21}$ _emb_CAA42545_ (X59892) 471 aa polypeptide (gamma2) [Homo sapiens] >gi_184657 (M77804) transfer RNA-Trp synthetase [Homo sapiens] 416609 Seq. No. uC-osroM202001b07b1 Seq. ID BLASTX Method g2781347 NCBI GI 399 BLAST score 1.0e-40 E value 142 Match length 59 % identity NCBI Description (AC003113) F2401.3 [Arabidopsis thaliana] 416610 Seq. No. uC-osroM202001b08a1 Seq. ID BLASTX Method NCBI GI g1173286 434 BLAST score 7.0e-43E value 122 Match length 71 % identity NCBI Description 40S RIBOSOMAL PROTEIN S9 >gi_112274_pir__S21497 ribosomal protein S9 - rat >gi_57143 emb CAA47013 (X66370) ribosomal protein S9 [Rattus norvegicus] Seq. No. 416611 uC-osroM202001b08b1 Seq. ID Method BLASTX NCBI GI g1351017 182 BLAST score

54465

3.0e-13

42

E value Match length

```
79
% identity
                  40S RIBOSOMAL PROTEIN S9 (S4) >gi_629697_pir__S45375
NCBI Description
                  ribosomal protein S4 - common tobacco (fragment)
                  >gi_443960_emb_CAA78463_ (Z14085) RIBOSOMAL PROTEIN S4
                  [Nicotiana tabacum]
                  416612
Seq. No.
                  uC-osroM202001b11a1
Seq. ID
                  BLASTX
Method
                  g3127892
NCBI GI
                  246
BLAST score
                  7.0e-21
E value
                  51
Match length
                  88
% identity
                 (AJ006025) acyl-coA synthetase [Cicer arietinum]
NCBI Description
                  416613
Seq. No.
                  uC-osroM202001b11b1
Seq. ID
                  BLASTX
Method
                  g1617270
NCBI GI
BLAST score
                  367
                  5.0e - 35
E value
                  99
Match length
                  63
% identity
NCBI Description (X94624) acyl-CoA synthetase [Brassica napus]
                  416614
Seq. No.
                  uC-osroM202001b12a1
Seq. ID
                  BLASTX
Method
NCBI GI
                  q1362086
BLAST score
                   225
                   2.0e-18
E value
                   52
Match length
% identity
                   5-methyltetrahydropteroyltriglutamate--homocysteine
NCBI Description
                   S-methyltransferase (EC 2.1.1.14) - Madagascar periwinkle
                   >gi 2129919 pir S65957
                   5-methyltetrahydropteroyltriglutamate--homocysteine
                   S-methyltransferase (EC 2.1.1.14) - Madagascar periwinkle
                   >gi 886471 emb CAA58474 (X83499) methionine synthase
                   [Catharanthus roseus]
                   416615
Seq. No.
                   uC-osroM202001b12b1
Seq. ID
                   BLASTX
Method
NCBI GI
                   g1362086
BLAST score
                   571
                   7.0e-59
E value
                   149
Match length
                   74
% identity
                   \verb§5-methyltetrahydropteroyltriglutamate--homocysteine
NCBI Description
                   S-methyltransferase (EC 2.1.1.14) - Madagascar periwinkle
                   >gi_2129919_pir__S65957
                   5-methyltetrahydropteroyltriglutamate--homocysteine
                   S-methyltransferase (EC 2.1.1.14) - Madagascar periwinkle
                   >gi 886471 emb CAA58474 (X83499) methionine synthase
```

[Catharanthus roseus]

416616 Seq. No. Seq. ID uC-osroM202001c01b1 Method BLASTX NCBI GI q2257756 BLAST score 215 5.0e-17 E value 55 Match length % identity 78 (U82815) nucleolar histone deacetylase HD2-p39 [Zea mays] NCBI Description >gi 3650466 (AF026917) histone deacetylase HD2-p39 [Zea mays] 416617 Seq. No. Seq. ID uC-osroM202001c02a1 BLASTX Method q4972051 NCBI GI 225 BLAST score 1.0e-26 E value Match length 90 % identity 71 (AL078470) serine/threonine-specific kinase like protein NCBI Description [Arabidopsis thaliana] 416618 Seq. No. Seq. ID uC-osroM202001c03b1 BLASTX Method NCBI GI a1168489 BLAST score 317 1.0e-37 E value Match length 140 54 % identity ADP-RIBOSYLATION FACTOR >gi 727191 (M54910) NCBI Description ADP-ribosylation factor [Candida albicans] Seq. No. 416619 uC-osroM202001c04b1 Seq. ID BLASTX Method NCBI GI q3785975 BLAST score 458 E value 1.0e-45 Match length 165 38 % identity NCBI Description (AC005560) hypothetical protein [Arabidopsis thaliana] Seq. No. 416620 uC-osroM202001c05b1 Seq. ID BLASTXMethod NCBI GI g3582333 BLAST score 168 E value 1.0e-15 Match length 119 % identity NCBI Description (AC005496) hypothetical protein [Arabidopsis thaliana] Seq. No. 416621 Seq. ID uC-osroM202001c07b1

BLASTX Method q2191136 NCBI GI 177 BLAST score E value 1.0e-12 98 Match length 44 % identity (AF007269) Similar to UTP-Glucose Glucosyltransferase; NCBI Description coded for by A. thaliana cDNA T46230; coded for by A. thaliana cDNA H76538; coded for by A. thaliana cDNA H76290 [Arabidopsis thaliana] 416622 Seq. No. uC-osroM202001c08a1 Seq. ID BLASTX Method NCBI GI q4680193 BLAST score 456 2.0e-45E value Match length 91 98 % identity NCBI Description (AF111710) putative farnesyl pyrophosphate synthase [Oryza sativa subsp. indica] 416623 Seq. No. Seq. ID uC-osroM202001c08b1 BLASTX Method NCBI GI q4680193 BLAST score 479 5.0e-48E value Match length 174 60 % identity NCBI Description (AF111710) putative farnesyl pyrophosphate synthase [Oryza sativa subsp. indica] 416624 Seq. No. Seq. ID uC-osroM202001c10a1 Method BLASTX q2959732 NCBI GI 147 BLAST score 3.0e-09 E value Match length 31 % identity 81 (Y13649) homologous to GATA-binding transcription factors NCBI Description [Arabidopsis thaliana] >gi_4895246_gb_AAD32831.1_AC007659_13 (AC007659) putative GATA-binding transcription factor [Arabidopsis thaliana] 416625 Seq. No. uC-osroM202001c11b1 Seq. ID BLASTX Method NCBI GI q2499114 677 BLAST score E value 3.0e-71Match length 163 78 % identity NCBI Description VACUOLAR ASSEMBLY PROTEIN VPS41 HOMOLOG >gi 1839240

(U86663) aVps41p [Arabidopsis thaliana]

```
Seq. No.
                  416626
                  uC-osroM202001d01a1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4519936
BLAST score
                  253
E value
                  1.0e-21
                  71
Match length
% identity
                  70
NCBI Description (AB019186) RPR1 [Oryza sativa]
Seq. No.
                  416627
                  uC-osroM202001d01b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4519936
BLAST score
                  431
E value
                  2.0e-42
Match length
                  129
                  69
% identity
NCBI Description (AB019186) RPR1 [Oryza sativa]
                  416628
Seq. No.
Seq. ID
                  uC-osroM202001d03a1
Method
                  BLASTX
NCBI GI
                  g829283
BLAST score
                  257
E value
                  2.0e-30
                  75
Match length
% identity
                  99
NCBI Description (Z15018) heat shock protein hsp82 [Oryza sativa]
                  416629
Seq. No.
                  uC-osroM202001d03b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g417154
                  708
BLAST score
E value
                  6.0e-75
                  140
Match length
                  99
% identity
NCBI Description HEAT SHOCK PROTEIN 82 >gi 100685 pir S25541 heat shock
                  protein 82 - rice (strain Taichung Native One)
                  >gi_20256_emb_CAA77978_ (Z11920) heat shock protein 82
                  (HSP82) [Oryza sativa]
                  416630
Seq. No.
Seq. ID
                  uC-osroM202001d07b1
                  BLASTX
Method
NCBI GI
                  q730510
                  852
BLAST score
E value
                  1.0e-91
Match length
                  170
% identity
                  98
NCBI Description RAS-RELATED PROTEIN RIC1 >gi 542150 pir S38740 GTP-binding
                  protein - rice >gi 432607 gb AAB28535 (S66160) ras-related
                  GTP binding protein possessing GTPase activity=ric1 [Oryza
                  sativa=rice, var. Yamahoushi, callus, Peptide, 202 aa]
```

[Oryza sativa]

416631 Seq. No. uC-osroM202001d08a1 Seq. ID Method BLASTN g167107 NCBI GI BLAST score 39 2.0e-12 E value Match length 162 86 % identity

NCBI Description Hordeum vulgare vacuolar ATPase B subunit isoform mRNA,

complete cds

Seq. No. 416632

Seq. ID uC-osroM202001d08b1

Method BLASTX
NCBI GI g2493131
BLAST score 733
E value 8.0e-78
Match length 151
% identity 97

NCBI Description VACUOLAR ATP SYNTHASE SUBUNIT B ISOFORM 1 (V-ATPASE B

SUBUNIT) >gi_167108 (L11862) vacuolar ATPase B subunit

[Hordeum vulgare]

Seq. No. 416633

Seq. ID uC-osroM202001d09a1

Method BLASTN
NCBI GI g516838
BLAST score 297
E value 1.0e-166
Match length 329
% identity 98

NCBI Description Rice mRNA for catalase, complete cds

Seq. No. 416634

Seq. ID uC-osroM202001d09b1

Method BLASTX
NCBI GI g1705629
BLAST score 1052
E value 1.0e-115
Match length 189
% identity 100

NCBI Description CATALASE ISOZYME B (CAT-B) >gi 516839_dbj_BAA05494_

(D26484) catalase [Oryza sativa]

Seq. No. 416635

Seq. ID uC-osroM202001d10a1

Method BLASTN
NCBI GI g2662344
BLAST score 91
E value 2.0e-43
Match length 279
% identity 86

NCBI Description Oryza sativa mRNA for EF-1 alpha, complete cds

Seq. No. 416636

Seq. ID uC-osroM202001d10b1

Method BLASTX

```
NCBI GI
                   q2662343
BLAST score
                   760
E value
                   5.0e-81
Match length
                   148
                   99
% identity
NCBI Description (D63581) EF-1 alpha [Oryza sativa]
                   416637
Seq. No.
                   uC-osroM202001d11a1
Seq. ID
Method
                   BLASTX
NCBI GI
                   q480669
BLAST score
                   197
E value
                   4.0e-15
Match length
                   44
% identity
                   86
NCBI Description NADPH--ferrihemoprotein reductase (EC 1.6.2.4) - Jerusalem
                   artichoke (fragment) >gi_1359894 emb_CAA81210 (Z26251)
                   NADPH-ferrihemoprotein reductase [Helianthus tuberosus]
Seq. No.
                   416638
                   uC-osroM202001d11b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2580499
BLAST score
                   695
E value
                   2.0e-73
Match length
                   173
                   73
% identity
NCBI Description (U67186) NADPH: ferrihemoprotein oxidoreductase
                   [Eschscholzia californica]
                   416639
Seq. No.
Seq. ID
                   uC-osroM202001d12b1
Method
                   BLASTX
NCBI GI
                   q1731146
                   295
BLAST score
                   1.0e-26
E value
                   85
Match length
                   61
% identity
NCBI Description HYPOTHETICAL 42.1 KD PROTEIN ZK1307.9 IN CHROMOSOME III
                   >gi_3881615_emb_CAA87435.1_ (Z47358) similar to YJU2 protein; cDNA EST yk645d5.3 comes from this gene
                   [Caenorhabditis elegans]
Seq. No.
                   416640
                   uC-osroM202001e01a1
Seq. ID
Method
                   BLASTX
NCBI GI
                   q1161167
BLAST score
                   276
E value
                   2.0e-24
                   106
Match length
% identity
NCBI Description (L42466) ethylene-forming enzyme [Picea glauca]
Seq. No.
                   416641
                   uC-osroM202001e01b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   q4454019
```

```
BLAST score
                        152
                        9.0e-17
     E value
Match length
                        111
     % identity
                        42
                       (AL035396) SRG1-like protein [Arabidopsis thaliana]
     NCBI Description
                        416642
     Seq. No.
                        uC-osroM202001e02a1
     Seq. ID
     Method
                        BLASTX
                        q2425101
     NCBI GI
     BLAST score
                        261
     E value
                        1.0e-22
     Match length
                        56
                        93
     % identity
     NCBI Description (AF019743) cationic peroxidase [Oryza sativa]
                        416643
     Seq. No.
                        uC-osroM202001e02b1
     Seq. ID
                        BLASTX
     Method
     NCBI GI
                        g2425101
                        807
     BLAST score
                        2.0e-86
     E value
     Match length
                        163
                        97
     % identity
                       (AF019743) cationic peroxidase [Oryza sativa]
     NCBI Description
                        416644
     Seq. No.
                        uC-osroM202001e03b1
     Seq. ID
                        BLASTX
     Method
     NCBI GI
                        g4063746
     BLAST score
                        503
     E value
                        7.0e-51
     Match length
                        134
     -% identity
                        71
                       (AC005851) nodulin-like protein [Arabidopsis thaliana]
   NCBI Description
                        416645
      Seq. No.
                        uC-osroM202001e04a1
     Seq. ID
     Method
                        BLASTN
                        g1815625
      NCBI GI
      BLAST score
                        38
                        8.0e-12
      E value
     Match length
                        50
                        94
      % identity
      NCBI Description Oryza sativa metallothionein-like type 1 (OsMT-1) mRNA,
                        complete cds
                        416646
      Seq. No.
                        uC-osroM202001e04b1
      Seq. ID
                        BLASTN
      Method
      NCBI GI
                        g2647937
      BLAST score
                        42
      E value
                        4.0e-14
      Match length
                        66
      % identity
                        91
      NCBI Description Hordeum vulgare DNA for plant metallothionein-like protein,
                        complete cds
```

```
416647
Seq. No.
Seq. ID
                  uC-osroM202001e05b1
Method
                  BLASTX
NCBI GI
                  q5020215
BLAST score
                  211
                  1.0e-16
E value
                  98
Match length
                  49
% identity
                  (AF149917) acyl CoA reductase [Simmondsia chinensis]
NCBI Description
                  >gi 5020217 gb AAD38040.1 AF149918 1 (AF149918) acyl CoA
                  reductase [synthetic construct]
                  416648
Seq. No.
Seq. ID
                  uC-osroM202001e06a1
                  BLASTX
Method
NCBI GI
                  q3157934
BLAST score
                  240
                  2.0e-24
E value
Match length
                  87
% identity
                  67
                  (AC002131) Similar to hypothetical protein F09E5.8
NCBI Description
                  gb U37429 from C. elegans. ESTs gb T42019 and gb N97000
                  come from this gene. [Arabidopsis thaliana]
Seq. No.
                  416649
Seq. ID
                  uC-osroM202001e06b1
Method
                  BLASTX
NCBI GI
                  g3157934
BLAST score
                  521
E value
                  5.0e-53
Match length
                  145
% identity
                  71
NCBI Description
                  (AC002131) Similar to hypothetical protein F09E5.8
                  gb U37429 from C. elegans. ESTs gb T42019 and gb N97000
                  come from this gene. [Arabidopsis thaliana]
                  416650
Seq. No.
Seq. ID
                  uC-osroM202001e07b1
Method
                  BLASTX
                  g2959324
NCBI GI
BLAST score
                  740
                  1.0e-78
E value
                  174
Match length
% identity
                  82
NCBI Description (Y15224) Importin alpha-like protein [Arabidopsis thaliana]
                  416651
Seq. No.
Seq. ID
                  uC-osroM202001e08b1
                  BLASTX
Method
NCBI GI
                  g4512653
BLAST score
                  279
E value
                  1.0e-24
                  73
Match length
% identity
```

NCBI Description (AC007048) unknown protein [Arabidopsis thaliana]

```
416652
Seq. No.
                  uC-osroM202001e09b1
Seq. ID
                  BLASTX
Method
                  g3004565
NCBI GI
BLAST score
                  199
                  2.0e-15
E value
                  62
Match length
                  60
% identity
NCBI Description (AC003673) putative protein kinase [Arabidopsis thaliana]
                  416653
Seq. No.
                  uC-osroM202001e10a1
Seq. ID
                  BLASTN
Method
                  g4104219
NCBI GI
                  53
BLAST score
                  7.0e-21
E value
                  69
Match length
                  94
% identity
NCBI Description Lolium perenne caffeic acid O-methyltransferase (OMT1)
                  mRNA, complete cds
                  416654
Seq. No.
                  uC-osroM202001e10b1
Seq. ID
                  BLASTN
Method
                  g4104219
NCBI GI
                  53
BLAST score
E value
                  7.0e-21
                  69
Match length
                  94
% identity
NCBI Description Lolium perenne caffeic acid O-methyltransferase (OMT1)
                  mRNA, complete cds
                  416655
Seq. No.
                  uC-osroM202001e11b1
Seq. ID
                  BLASTX
Method
NCBI GI
                  q1362086
BLAST score
                  621
                   9.0e-65
E value
                  156
Match length
% identity
                   5-methyltetrahydropteroyltriglutamate--homocysteine
NCBI Description
                   S-methyltransferase (EC 2.1.1.14) - Madagascar periwinkle
                  >gi_2129919_pir__S65957
                   5-methyltetrahydropteroyltriglutamate--homocysteine
                   S-methyltransferase (EC 2.1.1.14) - Madagascar periwinkle
                   >gi_886471_emb_CAA58474_ (X83499) methionine synthase
                   [Catharanthus roseus]
                   416656
Seq. No.
                   uC-osroM202001e12a1
Seq. ID
Method
                  BLASTN
NCBI GI
                   g452233
                  250
BLAST score
                   1.0e-138
E value
                  282
Match length
                   97
% identity
NCBI Description Rice Cht-2 gene for endochitinase, complete cds
```

416657 Seq. No. uC-osroM202001e12b1 Seq. ID BLASTX Method g1076740 NCBI GI 495 BLAST score 6.0e-50 E value 166 Match length 57 % identity chitinase (EC 3.2.1.14) - rice >gi_407472_emb_CAA40107 NCBI Description (X56787) chitinase [Oryza sativa] >gi_500616_dbj_BAA03750_ (D16222) endochitinase [Oryza sativa] >gi 742301_prf__2009354A chitinase [Oryza sativa] 416658 Seq. No. uC-osroM202001f01a1 Seq. ID BLASTX Method q5734636 NCBI GI 180 BLAST score 4.0e-13 E value 48 Match length 65 % identity (AP000391) Similar to putative lipase (AC006232) [Oryza NCBI Description sativa] 416659 Seq. No. uC-osroM202001f01b1 Seq. ID Method BLASTX g5734634 NCBI GI 207 BLAST score 3.0e-16 E value Match length 86 45 % identity NCBI Description (AP000391) Similar to putative lipase (AC006232) [Oryza sativa] Seq. No. 416660 uC-osroM202001f06b1 Seq. ID BLASTX Method q2702279 NCBI GI 556 BLAST score 4.0e-58 E value 132 Match length % identity (AC003033) putative phosphate transporter [Arabidopsis NCBI Description thaliana] >gi 2780345 dbj BAA24280_ (AB000093) inorganic phosphate transporter [Arabidopsis thaliana] >gi_2914691 (AC003974) putative phosphate transporter [Arabidopsis thaliana] 416661 Seq. No. uC-osroM202001f08a1 Seq. ID Method BLASTX NCBI GI g4646206 BLAST score 507 2.0e-51 E value Match length 119

NCBI Description

oleracea]

% identity (AC007230) Contains similarity to gb_D13630 KIAA0005 gene NCBI Description from Homo sapiens. ESTs gb T45345, gb T21086, gb R90360, gb T20468, gb T45191 and gb AI100459 come from this gene. [Arabidopsis thaliana] 416662 Seq. No. Seq. ID uC-osroM202001f08b1 Method BLASTX NCBI GI q4646206 BLAST score 337 2.0e-31 E value Match length 80 72 % identity (AC007230) Contains similarity to gb_D13630 KIAA0005 gene NCBI Description from Homo sapiens. ESTs gb_T45345, gb_T21086, gb_R90360, gb T20468, gb T45191 and gb_AI100459 come from this gene. [Arabidopsis thaliana] Seq. No. 416663 uC-osroM202001f09a1 Seq. ID BLASTX Method NCBI GI q584752 BLAST score 180 4.0e-13 E value Match length 85 45 % identity NCBI Description AMINOPEPTIDASE N (ALPHA-AMINOACYLPEPTIDE HYDROLASE) >gi_281454_pir__S27532 aminopeptidase N - Caulobacter crescentus (fragment) >gi 144272 (M91449) aminopeptidase N [Caulobacter crescentus] 416664 Seq. No. uC-osroM202001f09b1 Seq. ID Method BLASTX NCBI GI q1168446 275 BLAST score 4.0e-24 E value 160 Match length 39 % identity NCBI Description AMINOPEPTIDASE N (ALPHA-AMINOACYLPEPTIDE HYDROLASE) >gi 1073840 pir__F64132 aminopeptidase N (pepN) homolog -Haemophilus influenzae (strain Rd KW20) >gi_1574460 (U32835) aminopeptidase N (pepN) [Haemophilus influenzae Rd] 416665 Seq. No. uC-osroM202001f11a1 Seq. ID BLASTX Method g3413511 NCBI GI 173 BLAST score 3.0e-13 E value 46 Match length % identity (AJ000265) glucose-6-phosphate isomerase [Spinacia

416666 Seq. No. uC-osroM202001f11b1 Seq. ID Method BLASTX q3413511 NCBI GI 210 BLAST score 2.0e-16 E value Match length 60 60 % identity (AJ000265) glucose-6-phosphate isomerase [Spinacia NCBI Description oleracea] 416667 Seq. No. uC-osroM202001f12b1 Seq. ID BLASTX Method NCBI GI q82496 221 BLAST score 7.0e-18 E value 122 Match length 48 % identity NCBI Description phenylalanine ammonia-lyase (EC 4.3.1.5) - rice 416668 Seq. No. uC-osroM202001g02a1 Seq. ID Method BLASTX NCBI GI q4760370 BLAST score 182 3.0e-13E value Match length 66 52 % identity (AF082565) ATP dependent copper transporter [Arabidopsis NCBI Description thaliana] >gi 4760380 gb AAD29115.1 (AF091112) ATP dependent copper transporter [Arabidopsis thaliana] Seq. No. 416669 uC-osroM202001g05b1 Seq. ID BLASTX Method q4325372 NCBI GI 223 BLAST score 5.0e-18 E value 103 Match length % identity 46 (AF128396) contains similarity to protein disulfide NCBI Description isomerases [Arabidopsis thaliana] Seq. No. 416670 uC-osroM202001g06a1 Seq. ID BLASTX Method g3421413 NCBI GI 771 BLAST score 2.0e-82 E value 147 Match length 100 % identity (AF081922) protein phosphatase 2A 55 kDa B regulatory NCBI Description subunit [Oryza sativa] >gi_3421415 (AF081923) protein phosphatase 2A 55 kDa B regulatory subunit [Oryza sativa]

54477

416671

Seq. No.

uC-osroM202001g06b1 Seq. ID BLASTN Method NCBI GI q3421412 BLAST score 269 1.0e-149 E value Match length 371 100 % identity NCBI Description Oryza sativa protein phosphatase 2A 55 kDa B regulatory subunit gene, complete cds 416672 Seq. No. uC-osroM202001g07b1 Seq. ID BLASTX Method q5729706 NCBI GI BLAST score 216 2.0e-17 E value 86 Match length 38 % identity NCBI Description (AC007927) unknown protein [Arabidopsis thaliana] 416673 Seq. No. uC-osroM202001g08a1 Seq. ID Method BLASTX NCBI GI g1729971 222 BLAST score E value 2.0e-31 72 Match length % identity 97 NCBI Description TONOPLAST INTRINSIC PROTEIN, GAMMA (GAMMA TIP) (AQUAPORIN-TIP) >gi_1076745_pir__S52004 gamma-Tip protein rice >gi 473997 dbj BAA05017 (D25534) gamma-Tip [Oryza sativa] 416674 Seq. No. Seq. ID uC-osroM202001g08b1 Method BLASTX q1729971 NCBI GI 554 BLAST score 8.0e-57 E value 156 Match length 73 % identity NCBI Description TONOPLAST INTRINSIC PROTEIN, GAMMA (GAMMA TIP) (AQUAPORIN-TIP) >gi 1076745 pir_S52004 gamma-Tip protein rice >gi 473997 dbj_BAA05017_ (D25534) gamma-Tip [Oryza sativa] 416675 Seq. No. uC-osroM202001g12a1 Seq. ID BLASTX Method g129591 NCBI GI 242 BLAST score 2.0e-20 E value 45 Match length % identity NCBI Description PHENYLALANINE AMMONIA-LYASE >gi 295824 emb CAA34226

(X16099) phenylalanine ammonia-Tyase [Oryza sativa]

```
416676
Seq. No.
                  uC-osroM202001g12b1
Seq. ID
                  BLASTX
Method
NCBI GI
                  g82496
                  742
BLAST score
                  7.0e-79
E value
                  164
Match length
                  88
% identity
                  phenylalanine ammonia-lyase (EC 4.3.1.5) - rice
NCBI Description
                   416677
Seq. No.
                  uC-osroM202001h01a1
Seq. ID
                   BLASTN
Method
                   g1220121
NCBI GI
                   34
BLAST score
                   2.0e-09
E value
                   58
Match length
                   90
% identity
                  Nicotiana tabacum mRNA for S-adenosyl-L-homocysteine
NCBI Description
                   hydrolase, complete cds >gi_2172113_dbj_E03902 E03902 A
                   gene involved in tobacco flower bud formation
                   416678
Seq. No.
                   uC-osroM202001h01b1
Seq. ID
Method
                   BLASTX
                   q1710841
NCBI GI
BLAST score
                   553
                   7.0e-57
E value
Match length
                   121
% identity
                   86
                  ADENOSYLHOMOCYSTEINASE (S-ADENOSYL-L-HOMOCYSTEINE
NCBI Description
                   HYDROLASE) (ADOHCYASE) >gi_758247_emb_CAA56278_ (X79905)
                   S-adenosylhomocysteine hydrolase [Phalaenopsis sp.]
                   416679
Seq. No.
                   uC-osroM202001h02a1
Seq. ID
                   BLASTX
Method
NCBI GI
                   g6006867
                   335
BLAST score
E value
                   3.0e - 31
Match length
                   96
% identity
                   71
NCBI Description (AC009540) unknown protein [Arabidopsis thaliana]
                   416680
Seq. No.
                   uC-osroM202001h02b1
Seq. ID
Method
                   BLASTX
                   q6006867
NCBI GI
                   164
BLAST score
                   1.0e-20
E value
                   63
Match length
% identity
                  (AC009540) unknown protein [Arabidopsis thaliana]
NCBI Description
```

416681

BLASTX

uC-osroM202001h03b1

Seq. No. Seq. ID

Method

```
g1518540
NCBI GI
                  521
BLAST score
                  4.0e-53
E value
                  112
Match length
                  88
% identity
                 (U53418) UDP-glucose dehydrogenase [Glycine max]
NCBI Description
Seq. No.
                  416682
                  uC-osroM202001h06a1
Seq. ID
                  BLASTX
Method
                  g3757527
NCBI GI
                  238
BLAST score
                  7.0e-20
E value
Match length
                  50
% identity
                  76
                  (AC005167) putative ribosomal protein L27 [Arabidopsis
NCBI Description
                  thaliana]
                   416683
Seq. No.
                  uC-osroM202001h06b1
Seq. ID
                  BLASTX
Method
NCBI GI
                   g3757527
                   262
BLAST score
E value
                   1.0e-22
Match length
                  59
% identity
                   85
NCBI Description (AC005167) putative ribosomal protein L27 [Arabidopsis
                   thaliana]
                   416684
Seq. No.
                   uC-osroM202001h07b1
Seq. ID
                   BLASTX
Method
                   g2444271
NCBI GI
                   298
BLAST score
                   7.0e-27
E value
                   97
Match length
                   56
% identity
NCBI Description (AF019637) putative amino acid or GABA permease
                   [Arabidopsis thaliana]
                   416685
Seq. No.
Seq. ID
                   uC-osroM202001h09b1
                   BLASTX
Method
NCBI GI
                   g5080777
                   265
BLAST score
                   5.0e-23
E value
                   103
Match length
                   46
 % identity
NCBI Description (AC007576) Unknown protein [Arabidopsis thaliana]
                   416686
 Seq. No.
 Seq. ID
                   uC-osroM202001h10a1
                   BLASTX
 Method
 NCBI GI
                   q4678332
 BLAST score
                   191
                   2.0e-14
 E value
```

60

Match length

NCBI GI

```
% identity
                   (AL049658) putative peptide transporter [Arabidopsis
NCBI Description
                   thaliana]
                   416687
Seq. No.
                   uC-osroM202001h10b1
Seq. ID
                   BLASTX
Method
NCBI GI
                   q4678332
                   250
BLAST score
E value
                   3.0e-21
                   117
Match length
% identity
                   43
                   (AL049658) putative peptide transporter [Arabidopsis
NCBI Description
                   thalianal
                   416688
Seq. No.
                   uC-osroM202001h11a1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g584892
                   315
BLAST score
                   6.0e-29
E value
Match length
                   62
% identity
                   90
                   SERINE CARBOXYPEPTIDASE I PRECURSOR (CARBOXYPEPTIDASE C)
NCBI Description
                   >gi_629805_pir__S43516 serine carboxypeptidase I - rice
>gi_409580_dbj_BAA04510_ (D17586) serine carboxypeptidase I
                    [Oryza sativa]
                   416689
Seq. No.
                   uC-osroM202001h11b1
Seq. ID
                   BLASTX
Method
                   g584892
NCBI GI
                   936
BLAST score
E value
                   1.0e-101
Match length
                   175
                   99
% identity
NCBI Description SERINE CARBOXYPEPTIDASE I PRECURSOR (CARBOXYPEPTIDASE C)
                   >gi 629805_pir__S43516 serine carboxypeptidase I - rice
                    >qi 409580 dbj BAA04510 (D17586) serine carboxypeptidase I
                    [Oryza sativa]
                    416690
Seq. No.
Seq. ID
                   uC-osroM202003a01a2
                   BLASTX
Method
NCBI GI
                   g1203832
                   531
BLAST score
                    1.0e-54
E value
Match length
                    144,
                    78
% identity
                   (U46003) beta-D-glucan exohydrolase, isoenzyme ExoII
NCBI Description
                    [Hordeum vulgare] >gi_1588407_prf__2208395A beta-D-glucan
                    exohydrolase [Hordeum vulgare]
                    416691
Seq. No.
Seq. ID
                    uC-osroM202003a10a2
Method
                    BLASTX
```

54481

g2342676

```
152
BLAST score
                  2.0e-10
E value
                  38
Match length
                  71
% identity
                   (AC000106) Strong similarity to Oryza NADPH oxidase
NCBI Description
                  (gb_X93301). [Arabidopsis thaliana]
                  416692
Seq. No.
                  uC-osroM202003b01a2
Seq. ID
                  BLASTX
Method
                  q2462828
NCBI GI
BLAST score
                  222
                  6.0e-18
E value
                  74
Match length
                  54
% identity
                  (AF000657) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                  416693
Seq. No.
                  uC-osroM202003b02a2
Seq. ID
                  BLASTX
Method
                  g6015059
NCBI GI
                   274
BLAST score
                   8.0e-30
E value
                   72
Match length
                   100
% identity
NCBI Description ELONGATION FACTOR 1-ALPHA (EF-1-ALPHA) >gi_2996096
                   (AF030517) translation elongation factor-1 alpha; EF-1
                   alpha [Oryza sativa]
                   416694
Seq. No.
                   uC-osroM202003b05a2
Seq. ID
                   BLASTX
Method
                   g2150002
NCBI GI
                   438
BLAST score
                   2.0e-43
E value
Match length
                   125
% identity
                   66
NCBI Description (AF000940) ribonuclease [Hordeum vulgare]
                   416695
Seq. No.
                   uC-osroM202003b07a2
Seq. ID
                   BLASTX
Method
NCBI GI
                   g4680207
                   211
BLAST score
                   7.0e-17
E value
Match length
                   112
 % identity
                   40
                  (AF114171) disease resistance protein RPM1 homolog [Sorghum
NCBI Description
                   bicolor]
                   416696
 Seq. No.
                   uC-osroM202003b11a2
 Seq. ID
                   BLASTX
 Method
                   g3132310
 NCBI GI
                   163
 BLAST score
                   8.0e-15
 E value
                   58
 Match length
```

% identity (AB012228) phosphoenolpyruvate carboxylase [Zea mays] NCBI Description 416697 Seq. No. uC-osroM202003c01a2 Seq. ID BLASTX Method q5668813 NCBI GI 211 BLAST score 4.0e-20 E value 140 Match length 42 % identity (AC007519) Similar to gb_X77136 HSR203J protein from NCBI Description Nicotiana tabacum and is a member of the PF_00135 Carboxylesterase family. ESTs gb_Z25688 and gb_F14025 come from this gene. [Arabidopsis thaliana] 416698 Seq. No. uC-osroM202003c03a2 Seq. ID BLASTX Method q729135 NCBI GI 172 BLAST score 6.0e-14E value 51 Match length 82 % identity CAFFEIC ACID 3-O-METHYLTRANSFERASE NCBI Description (S-ADENOSYSL-L-METHIONINE: CAFFEIC ACID 3-O-METHYLTRANSFERASE) (COMT) >gi_283034_pir__S28612 catechol O-methyltransferase (EC $\overline{2}.1.1.6$) - $\overline{\text{maize}}$ >gi_168532 (M73235) O-methyltransferase [Zea mays] 416699 Seq. No. uC-osroM202003c05a2 Seq. ID BLASTN Method q20280 NCBI GI 197 BLAST score 1.0e-107 E value Match length 315 97 % identity NCBI Description Rice gene for phenylalanine ammonia-lyase (EC 4.3.1.5) 416700 Seq. No. uC-osroM202003c06a2 Seq. ID BLASTX Method g3881138 NCBI GI 202 BLAST score 1.0e-15 E value Match length 75 % identity NCBI Description (AL023846) Y52B11C.1 [Caenorhabditis elegans] 416701 Seq. No. uC-osroM202003c08a2 Seq. ID BLASTX Method g1783312 NCBI GI 147 BLAST score 3.0e-09 E value

54483

50

Match length

% identity (X98520) receptor-like kinase [Brassica oleracea] NCBI Description 416702 Seq. No. uC-osroM202003c12a2 Seq. ID BLASTX Method q3702326 NCBI GI 300 BLAST score E value 3.0e-27 68 Match length 76 % identity (AC005397) hypothetical protein [Arabidopsis thaliana] NCBI Description 416703 Seq. No. uC-osroM202003d01a2 Seq. ID BLASTX Method q6006867 NCBI GI 389 BLAST score 1.0e-37 E value 107 Match length 72 % identity (AC009540) unknown protein [Arabidopsis thaliana] NCBI Description 416704 Seq. No. uC-osroM202003d04a2 Seq. ID BLASTX Method q462195 NCBI GI 270 BLAST score 9.0e-24 E value Match length 52 98 % identity PROTEIN TRANSLATION FACTOR SUI1 HOMOLOG (GOS2 PROTEIN) NCBI Description >gi_100682_pir___S21636 GOS2 protein - rice >gi_20238 emb_CAA36190_ (X51910) GOS2 [Oryza sativa]
>gi_3789950 (AF094774) translation initiation factor [Oryza sativa] 416705 Seq. No. uC-osroM202003d09a2 Seq. ID BLASTX Method g2130073 NCBI GI 407 BLAST score 1.0e-39 E value 80 Match length 99 % identity fructose-bisphosphate aldolase (EC 4.1.2.13) isoenzyme C-1, NCBI Description cytosolic - rice >gi_786178_dbj_BAA08845_ (D50307) aldolase C-1 [Oryza sativa] $> \overline{gi}$ 7909 $\overline{70}$ d \overline{bj} BAA08830 (D50301) aldolase C-1 [Oryza sativa] 416706 Seq. No. uC-osroM202003d10a2 Seq. ID BLASTN Method q4996645 NCBI GI BLAST score 167 6.0e-89 E value 264 Match length

% identity NCBI Description Oryza sativa mRNA for Dof zinc finger protein, complete cds 416707 Seq. No. uC-osroM202003e03a2 Seq. ID BLASTX Method q5281051 NCBI GI BLAST score 228 1.0e-18 E value 54 Match length 80 % identity (AL080318) stress-induced protein stil-like protein NCBI Description [Arabidopsis thaliana] 416708 Seq. No. uC-osroM202003e05a2 Seq. ID BLASTN Method q1421729 NCBI GI 74 BLAST score 3.0e - 33E value 166 Match length 88 % identity Zea mays T cytoplasm male sterility restorer factor 2 (rf2) NCBI Description mRNA, complete cds 416709 Seq. No. uC-osroM202003e06a2 Seq. ID BLASTX Method g4982479 NCBI GI 318 BLAST score E value 3.0e-29Match length 102 60 % identity (AF069441) predicted protein of unknown function NCBI Description [Arabidopsis thaliana] 416710 Seq. No. uC-osroM202003e08a2 Seq. ID BLASTN Method g786131 NCBI GI 72 BLAST score 4.0e-32 E value 119 Match length 91 % identity NCBI Description Oryza sativa root-specific RCc3 mRNA, complete cds Seq. No. 416711 uC-osroM202003e09a2 Seq. ID BLASTX Method g3287693 NCBI GI 300 BLAST score 3.0e-27 E value 76 Match length % identity (AC003979) Similar to LIM17 gene product gb 1653769 from NCBI Description the genome of Synechocystis sp. gb_D90916. [Arabidopsis

54485

thaliana]

```
Seq. No.
                  416712
                  uC-osroM202003e11a2
Seq. ID
Method
                  BLASTX
NCBI GI
                  g168570
BLAST score
                  184
E value
                  2.0e-13
Match length
                  48
% identity
NCBI Description (M95077) phenylalanine ammonia lyase [Zea mays]
Seq. No.
                  416713
                  uC-osroM202003e12a2
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1617274
BLAST score
                  162
E value
                  6.0e-11
Match length
                  49
% identity
                  65
NCBI Description (Z72152) AMP-binding protein [Brassica napus]
                  416714
Seq. No.
                  uC-osroM202003f02a2
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2702280
BLAST score
                  163
                  4.0e-11
E value
Match length
                  32
                  100
% identity
NCBI Description (AC003033) photomorphogenesis repressor COP1 [Arabidopsis
                  thaliana]
                  416715
Seq. No.
                  uC-osroM202003f05a2
Seq. ID
Method
                  BLASTX
NCBI GI
                  q120668
                  248
BLAST score
                  8.0e-30
E value
                  91
Match length
                  77
% identity
NCBI Description GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC
                  >gi_82399_pir__A24159 glyceraldehyde-3-phosphate
                  dehydrogenase (EC 1.2.1.12), cytosolic - barley (fragment)
                  >qi 167044 (M36650) glyceraldehyde-3-phosphate
                  dehydrogenase [Hordeum vulgare] >gi_225347 prf 1301218A
                  dehydrogenase, glyceraldehydephosphate [Hordeum vulgare var.
                  distichum]
                  416716
Seq. No.
                  uC-osroM202003f10a2
Seq. ID
                  BLASTX
Method
                  g4539293
NCBI GI
                  298
BLAST score
                  7.0e-27
E value
Match length
                  103
% identity
NCBI Description (AL049480) putative membrane transporter [Arabidopsis
```

thaliana]

416717 Seq. No. uC-osroM202003g01a2 Seq. ID BLASTX Method g97330 NCBI GI 149 BLAST score 4.0e-10 E value 62 Match length 42 % identity formate dehydrogenase A - Wolinella succinogenes NCBI Description >gi 48507_emb_CAA37989_ (X54057) formate dehydrogenase [Wolinella succinogenes] 416718 Seq. No. uC-osroM202003q02a2 Seq. ID BLASTN Method g460988 NCBI GI 281 BLAST score 1.0e-157 E value 289 Match length 99 % identity NCBI Description O.sativa (Arborio) Beta Tubulin mRNA, clone OSTB-34 416719 Seq. No. uC-osroM202003g05a2 Seq. ID BLASTX Method g2065531 NCBI GI 146 BLAST score 5.0e-09 E value 73 Match length 45 % identity (U78526) endo-1,4-beta-glucanase [Lycopersicon esculentum] NCBI Description 416720 Seq. No. uC-osroM202003g07a2 Seq. ID Method BLASTX NCBI GI q4895183 387 BLAST score 3.0e - 37E value 104 Match length % identity 66 (AC007661) hypothetical protein [Arabidopsis thaliana] NCBI Description 416721 Seq. No. uC-osroM202003g09a2 Seq. ID Method BLASTX NCBI GI q4731374 BLAST score 339 9.0e - 32E value Match length 85 72 % identity (AF133839) papain-like cysteine protease [Sandersonia NCBI Description aurantiaca]

54487

416722

uC-osroM202003h04a2

Seq. No.

Seq. ID

BLASTN Method g2113846 NCBI GI 92 BLAST score 6.0e-44E value 188 Match length 87 % identity Hordeum vulgare mRNA for hypothetical protein, partial, NCBI Description clone WL5 416723 Seq. No. uC-osroM202003h05a2 Seq. ID BLASTN Method NCBI GI q3789947 154 BLAST score 5.0e-81 E value Match length 222 97 % identity NCBI Description Oryza sativa translation initiation factor 5A (eIF-5A) mRNA, complete cds 416724 Seq. No. uC-osroM202003h10a2 Seq. ID BLASTX Method q1709563 NCBI GI BLAST score 581 1.0e-61 E value Match length 139 91 % identity NCBI Description PHENYLALANINE AMMONIA-LYASE >gi_2130081_pir__S66313 phenylalanine ammonia-lyase (EC 4.3.1.5) - rice >gi_871494_emb_CAA61198_ (X87946) phenylalanine ammonia-lyase [Oryza sativa] 416725 Seq. No. uC-osroM202004a01b1 Seq. ID Method BLASTX NCBI GI q4760700 246 BLAST score 7.0e-21E value Match length 74 % identity NCBI Description (AB024437) peroxidase 1 [Scutellaria baicalensis] 416726 Seq. No.

Seq. ID uC-osroM202004a05b1

Method BLASTX
NCBI GI g2494175
BLAST score 547
E value 5.0e-69
Match length 166
% identity 87

NCBI Description GLUTAMATE DECARBOXYLASE 2 (GAD 2) >gi_1184960 (U46665)

glutamate decarboxylase 2 [Arabidopsis thaliana]

>gi_1236619 (U49937) glutamate decarboxylase [Arabidopsis

thaliana]

Seq. No. 416727

BLAST score

E value

288

4.0e-26

```
uC-osroM202004a07b1
Seq. ID
                  BLASTX
Method
                  a1084461
NCBI GI
BLAST score
                  475
E value
                  1.0e-47
                  133
Match length
                  71
% identity
NCBI Description RCc3 protein - rice >gi_786132 (L27208) RCc3 [Oryza sativa]
                  416728
Seq. No.
                  uC-osroM202004a08a2
Seq. ID
                  BLASTX
Method
NCBI GI
                  g3551958
BLAST score
                  149
                   2.0e-09
E value
Match length
                  44
                   61
% identity
                  (AF082032) senescence-associated protein 12 [Hemerocallis
NCBI Description
                  hybrid cultivar]
Seq. No.
                   416729
                   uC-osroM202004a08b1
Seq. ID
                   BLASTX
Method
NCBI GI
                   g2708750
BLAST score
                   149
                   2.0e-09
E value
                   110
Match length
                   35
% identity
                  (AC003952) putative physical impedence protein [Arabidopsis
NCBI Description
                   thaliana]
                   416730
Seq. No.
                   uC-osroM202004a10a2
Seq. ID
                   BLASTN
Method
NCBI GI
                   g5410347
BLAST score
                   54
E value
                   2.0e-21
Match length
                   130
% identity
                   85
NCBI Description Sorghum bicolor BAC clone 110K5, partial sequence
Seq. No.
                   416731
                   uC-osroM202004a10b1
Seq. ID
                   BLASTN
Method
NCBI GI
                   g5410347
BLAST score
                   94
E value
                   4.0e-45
                   408
Match length
                   86
% identity
NCBI Description Sorghum bicolor BAC clone 110K5, partial sequence
Seq. No.
                   416732
                   uC-osroM202004a12a2
Seq. ID
                   BLASTX
Method
                   g84439
NCBI GI
```

Match length 81 % identity 67

NCBI Description translation elongation factor eEF-2 - Caenorhabditis

elegans >gi_156279 (M86959) elongation factor

[Caenorhabditis elegans]

Seq. No. 416733

Seq. ID uC-osroM202004a12b1

Method BLASTX
NCBI GI g2494246
BLAST score 334
E value 2.0e-31
Match length 108
% identity 62

NCBI Description ELONGATION FACTOR 2 (EF-2) >gi 1184958 (U46663) elongation

factor 2 [Gallus gallus]

Seq. No. 416734

Seq. ID uC-osroM202004b01a2

Method BLASTX
NCBI GI g3132310
BLAST score 757
E value 1.0e-80
Match length 170
% identity 91

NCBI Description (AB012228) phosphoenolpyruvate carboxylase [Zea mays]

Seq. No. 416735

Seq. ID uC-osroM202004b02a2

Method BLASTX
NCBI GI g1170937
BLAST score 195
E value 6.0e-15
Match length 34
% identity 100

NCBI Description S-ADENOSYLMETHIONINE SYNTHETASE 1 (METHIONINE

ADENOSYLTRANSFERASE 1) (ADOMET SYNTHETASE 1)

>gi_450549_emb_CAA81481_ (Z26867) S-adenosyl methionine

synthetase [Oryza sativa]

Seq. No. 416736

Seq. ID uC-osroM202004b02b1

Method BLASTX
NCBI GI g1170937
BLAST score 558
E value 2.0e-61
Match length 133
% identity 91

NCBI Description S-ADENOSYLMETHIONINE SYNTHETASE 1 (METHIONINE

ADENOSYLTRANSFERASE 1) (ADOMET SYNTHETASE 1)

>gi_450549_emb_CAA81481_ (Z26867) S-adenosyl methionine

synthetase [Oryza sativa]

Seq. No. 416737

Seq. ID uC-osroM202004b04b1

Method BLASTX NCBI GI g4775270

Seq. ID

```
BLAST score
                   379
E value
                   2.0e-36
Match length
                   81
% identity
                   86
NCBI Description (AJ131214) SF2/ASF-like splicing modulator Srp30
                   [Arabidopsis thaliana]
Seq. No.
                   416738
                   uC-osroM202004b05a2
Seq. ID
Method
                   BLASTX
NCBI GI
                   g120668
BLAST score
                   269
E value
                   1.0e-23
                   57
Match length
% identity
                   89
NCBI Description
                   GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC
                   >gi_82399_pir__A24159 glyceraldehyde-3-phosphate
dehydrogenase (EC 1.2.1.12), cytosolic - barley (fragment)
                   >gi 167044 (M36650) glyceraldehyde-3-phosphate
                   dehydrogenase [Hordeum vulgare] >gi 225347 prf 1301218A
                   dehydrogenase, glyceraldehydephosphate [Hordeum vulgare var.
                   distichum]
                   416739
Seq. No.
Seq. ID
                   uC-osroM202004b05b1
Method
                   BLASTX
NCBI GI
                   g1184774
BLAST score
                   668
E value
                   3.0e-70
Match length
                   157
% identity
                   82
NCBI Description (U45856) cytosolic glyceroldehyde-3-phosphate dehydrogenase
                   GAPC3 [Zea mays]
                   416740
Seq. No.
Seq. ID
                   uC-osroM202004b06a2
Method
                   BLASTX
NCBI GI
                   g2913891
BLAST score
                   241
E value
                   3.0e-20
Match length
                   47
% identity
                   100
NCBI Description (AB011367) LIP9 [Oryza sativa]
                   416741
Seq. No.
Seq. ID
                   uC-osroM202004b06b1
Method
                   BLASTX
NCBI GI
                   q1657843
BLAST score
                   188
E value
                   5.0e-14
Match length
                   52
                   75
% identity
NCBI Description
                  (U73210) cold acclimation protein WCOR410b [Triticum
                   aestivum]
Seq. No.
                   416742
```

54491

uC-osroM202004b07b1

Method BLASTX
NCBI GI g2739381
BLAST score 565
E value 4.0e-58
Match length 163
% identity 64

NCBI Description (AC002505) putative patatin [Arabidopsis thaliana]

Seq. No. 416743

Seq. ID uC-osroM202004b09b1

Method BLASTX
NCBI GI g1514643
BLAST score 415
E value 1.0e-40
Match length 142
% identity 51

NCBI Description (Z70524) PDR5-like ABC transporter [Spirodela polyrrhiza]

Seq. No. 416744

Seq. ID uC-osroM202004b10a2

Method BLASTN
NCBI GI g3850815
BLAST score 371
E value 0.0e+00
Match length 500
% identity 98

NCBI Description Oryza sativa mRNA for U2 snRNP auxiliary factor, small

subunit 35b

Seq. No. 416745

Seq. ID uC-osroM202004b10b1

Method BLASTX
NCBI GI g3850816
BLAST score 679
E value 2.0e-71
Match length 126
% identity 99

NCBI Description (Y18348) U2 snRNP auxiliary factor, small subunit [Oryza

sativa]

Seq. No. 416746

Seq. ID uC-osroM202004b11b1

Method BLASTX
NCBI GI g3152598
BLAST score 232
E value 3.0e-19
Match length 113
% identity 50

NCBI Description (AC002986) Contains similarity to C2-HC type zinc finger

protein C.e-MyT1 gb U67079 from C. elegans and to

hypersensitivity-related gene 201 isolog T28M21.14 from A.

thaliana BAC gb AF002109. [Arabidopsis thaliana]

Seq. No. 416747

Seq. ID uC-osroM202004b12a2

Method BLASTN NCBI GI g218144

```
BLAST score
                   325
                   0.0e+00
E value
Match length
                   388
% identity
                   96
NCBI Description Rice mRNA for ATP/ADP translocator, complete cds
                   416748
Seq. No.
Seq. ID
                   uC-osroM202004b12b1
Method
                  BLASTX
NCBI GI
                   q485517
BLAST score
                   411
E value
                   3.0e-40
Match length
                  91
% identity
                   89
NCBI Description ADP, ATP carrier protein - rice
Seq. No. Seq. ID
                   416749
                   uC-osroM202004c01a2
Method
                  BLASTX
NCBI GI
                   g1203832
BLAST score
                   531
E value
                   3.0e-54
Match length
                   140
% identity
                   74
NCBI Description
                  (U46003) beta-D-glucan exohydrolase, isoenzyme ExoII
                   [Hordeum vulgare] >gi 1588407 prf 2208395A beta-D-glucan
                   exohydrolase [Hordeum vulgare]
                   416750
Seq. No.
Seq. ID
                   uC-osroM202004c01b1
Method
                   BLASTX
NCBI GI
                   g4490704
BLAST score
                   188
E value
                   6.0e-18
                  116
Match length
% identity
                   42
NCBI Description (AL035680) putative protein [Arabidopsis thaliana]
Seq. No.
                   416751
Seq. ID
                   uC-osroM202004c03a2
                   BLASTX
Method
NCBI GI
                   g1097876
BLAST score
                   149
E value
                   2.0e-09
Match length
                   105
                   39
% identity
NCBI Description peroxidase: ISOTYPE=RPN [Oryza sativa]
                   416752
Seq. No.
Seq. ID
                   uC-osroM202004c03b1
Method
                   BLASTX
NCBI GI
                   g2829914
BLAST score
                   279
E value
                   1.0e-24
Match length
                   106
% identity
NCBI Description (AC002291) putative peroxidase [Arabidopsis thaliana]
```

Seq. ID

```
Seq. No.
                  416753
Seq. ID
                  uC-osroM202004c04b1
Method
                  BLASTX
NCBI GI
                  g2738752
BLAST score
                  302
E value
                  3.0e-27
Match length
                  77
% identity
                  78
NCBI Description (AF016306) sulfate permease [Zea mays]
Seq. No.
                  416754
Seq. ID
                  uC-osroM202004c05b1
Method
                  BLASTX
NCBI GI
                  q1352830
BLAST score
                  725
E value
                  6.0e-77
Match length
                  148
% identity
                  98
NCBI Description
                  VACUOLAR ATP SYNTHASE CATALYTIC SUBUNIT A (V-ATPASE 69 KD
                  SUBUNIT) >gi_1049253 (U36436) vacuolar ATPase 69 kDa
                  subunit [Zea mays]
Seq. No.
                  416755
Seq. ID
                  uC-osroM202004c07a2
Method
                  BLASTX
NCBI GI
                  q4490704
BLAST score
                  295
E value
                  2.0e-26
Match length
                  71
                  77
% identity
NCBI Description (AL035680) putative protein [Arabidopsis thaliana]
Seq. No.
                  416756
Seq. ID
                  uC-osroM202004c07b1
Method
                  BLASTX
NCBI GI
                  q4490704
BLAST score
                  571
E value
                  8.0e-59
Match length
                  140
                  76
% identity
NCBI Description (AL035680) putative protein [Arabidopsis thaliana]
Seq. No.
                  416757
Seq. ID
                  uC-osroM202004c09a2
Method
                  BLASTX
NCBI GI
                  g5921189
BLAST score
                  325
E value
                  5.0e-30
Match length
                  164
% identity
                  45
                 CYTOCHROME P450 71C4 >gi_550542_emb_CAA57425_ (X81831)
NCBI Description
                  cytochrome P450 [Zea mays] >gi 1850903 emb CAA72196
                  (Y11368) cytochrome p450 [Zea mays]
Seq. No.
                  416758
```

54494

uC-osroM202004c09b1

Method BLASTX
NCBI GI g584861
BLAST score 155
E value 3.0e-10
Match length 58
% identity 55

NCBI Description CYTOCHROME P450 71A2 (CYPLXXIA2) (P-450EG4)

>gi_480396_pir__S36806 cytochrome P450 71A2 - eggplant
>gi_408140_emb_CAA50645_ (X71654) P450 hydroxylase [Solanum melongena] >gi_441185_dbj_BAA03635_ (D14990) Cytochrome

P-450EG4 [Solanum melongena]

Seq. No. 416759

Seq. ID uC-osroM202004c10a2

Method BLASTX
NCBI GI g4646206
BLAST score 662
E value 2.0e-69
Match length 154
% identity 84

NCBI Description (AC007230) Contains similarity to gb_D13630 KIAA0005 gene

from Homo sapiens. ESTs gb_T45345, gb_T21086, gb_R90360, gb_T20468, gb_T45191 and gb_AI100459 come from this gene.

[Arabidopsis thaliana]

Seq. No. 416760

Seq. ID uC-osroM202004c10b1

Method BLASTX
NCBI GI g4646206
BLAST score 604
E value 1.0e-62
Match length 159
% identity 69

NCBI Description (AC007230) Contains similarity to gb_D13630 KIAA0005 gene

from Homo sapiens. ESTs gb_T45345, gb_T21086, gb_R90360, gb_T20468, gb_T45191 and gb_AI100459 come from this gene.

[Arabidopsis thaliana]

Seq. No. 416761

Seq. ID uC-osroM202004d02b1

Method BLASTX
NCBI GI g4155128
BLAST score 160
E value 1.0e-10
Match length 65
% identity 48

NCBI Description (AE001491) putative 3-HYDROXYACID DEHYDROGENASE

[Helicobacter pylori J99]

Seq. No. 416762

Seq. ID uC-osroM202004d03a2

Method BLASTX
NCBI GI g549986
BLAST score 303
E value 1.0e-27
Match length 63
% identity 92

NCBI Description

tremula]

```
NCBI Description
                  (U13149) possible apospory-associated protein [Pennisetum
                   ciliare]
                   416763
Seq. No.
Seq. ID
                   uC-osroM202004d03b1
Method
                   BLASTX
NCBI GI
                   g2262170
BLAST score
                   254
E value
                   1.0e-21
Match length
                   115
% identity
                   50
NCBI Description (AC002329) predicted glycosyl hydrolase [Arabidopsis
                   thalianal
Seq. No.
                   416764
Seq. ID
                   uC-osroM202004d04a2
Method
                   BLASTX
NCBI GI
                   g3297818
BLAST score
                   304
E value
                   1.0e-27
Match length
                  99
% identity
                   60
NCBI Description (AL031032) putative protein [Arabidopsis thaliana]
Seq. No.
                   416765
Seq. ID
                   uC-osroM202004d08a2
Method
                  BLASTX
NCBI GI
                  g4335747
BLAST score
                  144
E value
                   8.0e-09
Match length
                  35
% identity
                   86
NCBI Description (AC006284) putative A3 protein [Vigna unguiculata]
                   (integral membrane protein) [Arabidopsis thaliana]
Seq. No.
                  416766
Seq. ID
                  uC-osroM202004d08b1
Method
                  BLASTX
NCBI GI
                  g4406756
BLAST score
                  562
E value
                  9.0e-58
Match length
                  140
% identity
                  77
NCBI Description
                 (AC006836) putative integral membrane protein A3
                  [Arabidopsis thaliana]
Seq. No.
                  416767
Seq. ID
                  uC-osroM202004d09b1
Method
                  BLASTX
NCBI GI
                  g3511285
BLAST score
                  187
E value
                  7.0e-14
Match length
                  43
% identity
                  72
```

(AF081534) cellulose synthase [Populus alba x Populus

Method

NCBI GI

BLAST score

BLASTX

144

g3746059

Seq. No. 416768 Seq. ID uC-osroM202004d10b1 Method BLASTX NCBI GI g3941480 BLAST score 150 E value 2.0e-09 Match length 38 % identity 74 NCBI Description (AF062894) putative transcription factor [Arabidopsis thaliana] Seq. No. 416769 Seq. ID uC-osroM202004d11a2 Method BLASTN NCBI GI g394735 BLAST score 488 E value 0.0e+00Match length 519 % identity 99 NCBI Description Rice lip19 mRNA for basic/leucine zipper protein Seq. No. 416770 Seq. ID uC-osroM202004d11b1 Method BLASTN NCBI GI g394735 BLAST score 486 E value 0.0e+00 Match length 539 % identity 98 NCBI Description Rice lip19 mRNA for basic/leucine zipper protein Seq. No. 416771 uC-osroM202004d12a2 Seq. ID Method BLASTX NCBI GI q2576361 BLAST score 218 E value 2.0e-17 Match length 52 % identity 67 NCBI Description (U39782) lysine and histidine specific transporter [Arabidopsis thaliana] Seq. No. 416772 Seq. ID uC-osroM202004d12b1 Method BLASTX NCBI GI q2213629 BLAST score 519 E value 9.0e-53 Match length 123 % identity 75 NCBI Description (AC000103) F21J9.21 [Arabidopsis thaliana] Seq. No. 416773 Seq. ID uC-osroM202004e02a2

```
E value
                    8.0e-09
 Match length
                    59
 % identity
 NCBI Description
                    (AC005311) putative cysteinyl-tRNA synthetase [Arabidopsis
                    thaliana] >gi_4432812_gb_AAD20662_ (AC006593) putative
                    cysteinyl-tRNA synthetase [Arabidopsis thaliana]
 Seq. No.
                    416774
 Seq. ID
                    uC-osroM202004e02b1
Method
                    BLASTX
NCBI GI
                    q3746059
BLAST score
                    147
E value
                    4.0e-09
Match length
                    66
 % identity
NCBI Description
                   (AC005311) putative cysteinyl-tRNA synthetase [Arabidopsis
                    thaliana] >gi_4432812_gb_AAD20662_ (AC006593) putative
                    cysteinyl-tRNA synthetase [Arabidopsis thaliana]
Seq. No.
                    416775
Seq. ID
                    uC-osroM202004e04a2
Method
                    BLASTX
NCBI GI
                    q2130073
BLAST score
                    358
E value
                    7.0e-34
Match length
                    69
% identity
                    100
NCBI Description
                   fructose-bisphosphate aldolase (EC 4.1.2.13) isoenzyme C-1,
                    cytosolic - rice >gi_786178_dbj_BAA08845_ (D50307) aldolase
                   C-1 [Oryza sativa] >gi_790970_dbj_BAA08830_ (D50301)
                    aldolase C-1 [Oryza sativa]
Seq. No.
                    416776
Seq. ID
                   uC-osroM202004e04b1
Method
                   BLASTX
NCBI GI
                   g2130073
BLAST score
                   745
E value
                   3.0e-79
Match length
                   148
% identity
                   99
NCBI Description
                   fructose-bisphosphate aldolase (EC 4.1.2.13) isoenzyme C-1,
cytosolic - rice >gi_786178_dbj_BAA08845_ (D50307) aldolase
                   C-1 [Oryza sativa] >gi_790970_dbj_BAA08830_ (D50301)
                   aldolase C-1 [Oryza sativa]
Seq. No.
                   416777
Seq. ID
                   uC-osroM202004e06a2
Method
                   BLASTN
NCBI GI
                   g2331130
BLAST score
                   205
E value
                   1.0e-111
Match length
                   287
% identity
                   98
NCBI Description
                   Oryza sativa glycine-rich protein (OSGRP1) mRNA, complete
```

Seq. No. 416778

cds



uC-osroM202004e06b1 Seq. ID

Method BLASTN NCBI GI g2331130 BLAST score 202 1.0e-109 E value Match length 249 % identity 99

NCBI Description Oryza sativa glycine-rich protein (OSGRP1) mRNA, complete

Seq. No. 416779

Seq. ID uC-osroM202004e07a2

Method BLASTX NCBI GI g2190551 BLAST score 158 E value 1.0e-10 Match length 43 % identity 65

(AC001229) Similar to C. elegans hypothetical protein NCBI Description

K07C5.6 (gb Z71181). ESTs gb H36844, gb AA394956 come from

this gene. [Arabidopsis thaliana]

416780 Seq. No.

uC-osroM202004e07b1 Seq. ID

Method BLASTX NCBI GI g2190551 BLAST score 597 E value 6.0e-62 Match length 121 % identity

NCBI Description (AC001229) Similar to C. elegans hypothetical protein

K07C5.6 (gb_Z71181). ESTs gb_H36844,gb_AA394956 come from this gene. [Arabidopsis thaliana]

Seq. No. 416781

Seq. ID uC-osroM202004e08b1

Method BLASTX NCBI GI g417154 BLAST score 674 5.0e-71 E value Match length 139 % identity

NCBI Description HEAT SHOCK PROTEIN 82 >gi 100685 pir S25541 heat shock

protein 82 - rice (strain Taichung Native One)

>gi 20256 emb CAA77978 (Z11920) heat shock protein 82

(HSP82) [Oryza sativa]

Seq. No. 416782

uC-osroM202004e09a2 Seq. ID

Method BLASTN NCBI GI g4730883 BLAST score 435 E value 0.0e + 00Match length 497 % identity 96

NCBI Description Oryza sativa gene for alanine aminotransferase, complete

1

Seq. No. 416783

Seq. ID uC-osroM202004e09b1

Method BLASTX
NCBI GI g4730884
BLAST score 520
E value 3.0e-54
Match length 138
% identity 82

NCBI Description (AB007404) alanine aminotransferase [Oryza sativa]

>gi_4730886_dbj_BAA77261.1_ (AB007405) alanine

aminotransferase [Oryza sativa]

Seq. No. 416784

Seq. ID uC-osroM202004e11a2

Method BLASTN
NCBI GI g5926739
BLAST score 437
E value 0.0e+00
Match length 469
% identity 99

NCBI Description Oryza sativa mRNA for asparaginyl endopeptidase, complete

cds

Seq. No. 416785

Seq. ID uC-osroM202004e11b1

Method BLASTX
NCBI GI g5926740
BLAST score 485
E value 8.0e-49
Match length 104
% identity 86

NCBI Description (AB025310) asparaginyl endopeptidase [Oryza sativa]

Seq. No. 416786

Seq. ID uC-osroM202004e12a2

Method BLASTX
NCBI GI g4982499
BLAST score 165
E value 2.0e-11
Match length 42
% identity 74

NCBI Description (AC000107) F17F8.5 [Arabidopsis thaliana]

Seq. No. 416787

Seq. ID uC-osroM202004e12b1

Method BLASTX
NCBI GI g2827665
BLAST score 262
E value 1.0e-22
Match length 77
% identity 64

NCBI Description (AL021637) vacuolar sorting receptor-like protein

[Arabidopsis thaliana]

Seq. No. 416788

Seq. ID uC-osroM202004f01a2

```
BLASTX
 Method
 NCBI GI
                    q4210332
                    181
BLAST score
  E value
                    3.0e-13
                    37
 Match length
                    95
  % identity
 NCBI Description (AJ223803) 2-oxoglutarate dehydrogenase E2 subunit
                    [Arabidopsis thaliana]
                    416789
  Seq. No.
  Seq. ID
                    uC-osroM202004f01b1
 Method
                    BLASTX
                    q3219722
  NCBI GI
  BLAST score
                    150
  E value
                    2.0e-19
                    69
  Match length
  % identity
                    62
  NCBI Description (AF068740) dihydrolipoamide succinyltransferase; E2
                    [Pseudomonas putida]
                    416790
  Seq. No.
                    uC-osroM202004f02a2
  Seq. ID
 Method
                    BLASTX
  NCBI GI
                    g3024122
  BLAST score
                    623
  E value
                    5.0e-65
  Match length
                    119
                    99
  % identity
                    S-ADENOSYLMETHIONINE SYNTHETASE 2 (METHIONINE
  NCBI Description
                    ADENOSYLTRANSFERASE 2) (ADOMET SYNTHETASE 2) >gi 1778821
                    (U82833) S-adenosyl-L-methionine synthetase [Oryza sativa]
  Seq. No.
                    416791
  Seq. ID
                    uC-osroM202004f05b1
  Method
                    BLASTX
  NCBI GI
                    g4262167
  BLAST score
                    387
  E value
                    2.0e-37
  Match length
                    134
                    57
  % identity
  NCBI Description (AC005275) putative LRR receptor-linked protein kinase
                     [Arabidopsis thaliana]
                    416792
  Seq. No.
                    uC-osroM202004f06a2
  Seq. ID
  Method
                    BLASTX
  NCBI GI
                    g728809
  BLAST score
                    237
  E value
                    8.0e-20
  Match length
                    64
```

NCBI Description ADP, ATP CARRIER PROTEIN 2 PRECURSOR (ADP/ATP TRANSLOCASE 2)

(ADENINE NUCLEOTIDE TRANSLOCATOR 2) (ANT 2)

77

% identity

>gi_478810_pir__S29852 ADP,ATP carrier protein Arabidopsis thaliana >gi_16160_emb_CAA48579_ (X68592)
adenosine nucleotide translocator [Arabidopsis thaliana]



```
Seq. No.
                   416793
Seq. ID
                   uC-osroM202004f06b1
Method
                   BLASTX
NCBI GI
                   g728809
BLAST score
                   224
E value
                   3.0e-18
Match length
                   64
% identity
                   72
NCBI Description ADP, ATP CARRIER PROTEIN 2 PRECURSOR (ADP/ATP TRANSLOCASE 2)
                   (ADENINE NUCLEOTIDE TRANSLOCATOR 2) (ANT 2)
                   >gi_478810_pir__S29852 ADP,ATP carrier protein -
                   Arabidopsis thaliana >gi_16160_emb_CAA48579_ (X68592)
                   adenosine nucleotide translocator [Arabidopsis thaliana]
Seq. No.
                   416794
Seq. ID
                  uC-osroM202004f07a2
Method
                  BLASTX
NCBI GI
                  g3757529
BLAST score
                  185
E value
                  9.0e-14
Match length
                  63
% identity
                  52
NCBI Description (AC005167) tetracycline transporter-like protein
                   [Arabidopsis thaliana]
Seq. No.
                  416795
Seq. ID
                  uC-osroM202004f07b1
Method
                  BLASTX
NCBI GI
                  g2264382
BLAST score
                  230
E value
                  5.0e-19
Match length
                  85
% identity
                  49
NCBI Description (AC002354) putative tetracycline transporter-like protein
                  [Arabidopsis thaliana]
Seq. No.
                  416796
Seq. ID
                  uC-osroM202004f09a2
Method
                  BLASTX
NCBI GI
                  g3378652
BLAST score
                  241
E value
                  3.0e-20
Match length
                  49
% identity
NCBI Description
                  (AJ005039) CaM-1 [Nicotiana plumbaginifolia]
                  >gi_3378654 emb CAA06307 (AJ005040) CaM-2 [Nicotiana
                  plumbaginifolia]
Seq. No.
                  416797
Seq. ID
                  uC-osroM202004f09b1
Method
                  BLASTX
NCBI GI
                  g115511
```

Method BLASTX
NCBI GI g115511
BLAST score 727
E value 4.0e-77
Match length 149

% identity 64

NCBI Description CALMODULIN >gi 231682 sp P29612 CALM ORYSA CALMODULIN



>gi 71682 pir__MCBH calmodulin - barley >gi 100666 pir S24952 calmodulin 1 (clone lambda DASH) rice >gi_20188_emb_CAA78287_ (Z12827) calmodulin [Oryza sativa] >gi_167008 (M27303) calmodulin [Hordeum vulgare] >gi 170072 (L01431) calmodulin [Glycine max] >gi 310315 (L18913) calmodulin [Oryza sativa] >gi 506850 (L $\overline{2}$ 0691) calmodulin [Vigna radiata] >gi_1478370 bbs 176852 (S81594) auxin-regulated calmodulin, arCaM [Vigna radiata=mung bean, Wilczek, seedling, Peptide, 149 aa] [Vigna radiata] >gi 1742989 emb CAA70982 (Y09853) CaM protein [Cicer arietinum] >gi 1754991 (U48242) calmodulin TaCaM1-1 [Triticum aestīvum] >qi 1754993 (U48688) calmodulin TaCaM1-2 [Triticum aestivum] >qi 1754995 (U48689) calmodulin TaCaM1-3 [Triticum aestivum] >qi 1755003 (U48693) calmodulin TaCaM3-1 [Triticum aestīvum] >gi 1755005 (U49103) calmodulin TaCaM3-2 [Triticum aestivum] >gi_1755007 (U49104) calmodulin TaCaM3-3 [Triticum aestivum] >gi_1755009 (U49105) calmodulin TaCaM4-1 [Triticum aestīvum] >gi_3617842 (AF042840) calmodulin [Oryza sativa] >gi 226769 prf 1604476A calmodulin [Hordeum vulgare var. distichum] >gi 1583768 prf 2121384B calmodulin [Glycine max]

Seq. No. 416798

Seq. ID uC-osroM202004f11a2

Method BLASTX NCBI GI g4586025 BLAST score 298 E value 7.0e-27 Match length 66 % identity

NCBI Description (AC007109) putative succinyl-CoA-ligase beta subunit; 5'

partial [Arabidopsis thaliana]

Seq. No. 416799

uC-osroM202004f11b1 Seq. ID

Method BLASTX NCBI GI q3660469 BLAST score 546 E value 6.0e-56 Match length 135 % identity

NCBI Description (AJ001808) succinyl-CoA-ligase beta subunit [Arabidopsis

thaliana] >gi 4512693 gb AAD21746.1 (AC006569)

succinyl-CoA ligase beta subunit [Arabidopsis thaliana]

Seq. No. 416800

Seq. ID uC-osroM202004g02a2

Method BLASTX NCBI GI g1703380 BLAST score 150 E value 1.0e-09 Match length 28 % identity 100

NCBI Description ADP-RIBOSYLATION FACTOR >gi 1132483 dbj BAA04607 (D17760)

ADP-ribosylation factor [Oryza sativa]

```
Seq. No.
                  416801
                  uC-osroM202004q02b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1703380
BLAST score
                  284
E value
                  2.0e-25
Match length
                  76
                  78
% identity
NCBI Description ADP-RIBOSYLATION FACTOR >gi 1132483 dbj_BAA04607_ (D17760)
```

ADP-ribosylation factor [Oryza sativa]
Seq. No. 416802

Seq. ID uC-osroM202004g03a2
Method BLASTX
NCBI GI g3980397
BLAST score 142
E value 3.0e-09
Match length 41
% identity 63

NCBI Description (AC004561) putative protein phosphatase 2C [Arabidopsis

thaliana]

 Seq. No.
 416803

 Seq. ID
 uC-osroM202004g04a2

 Method
 BLASTN

Method BLASTN
NCBI GI g3550984
BLAST score 214
E value 1.0e-117
Match length 214
% identity 100

NCBI Description Oryza sativa mRNA for OsS5a, complete cds

Seq. No. 416804

Seq. ID uC-osroM202004g04b1

Method BLASTX
NCBI GI g3550985
BLAST score 716
E value 7.0e-76
Match length 157
% identity 89

NCBI Description (AB010740) OsS5a [Oryza sativa]

Seq. No. 416805

Seq. ID uC-osroM202004g05a2

Method BLASTN
NCBI GI g3377508
BLAST score 448
E value 0.0e+00
Match length 464
% identity 99

NCBI Description Oryza sativa auxin transport protein REH1 (REH1) mRNA,

complete cds

Seq. No. 416806

Seq. ID uC-osroM202004g05b1

Method BLASTX NCBI GI g3377509

```
BLAST score
                   552
E value
                  1.0e-56
                  122
Match length
                  87
% identity
                  (AF056027) auxin transport protein REH1 [Oryza sativa]
NCBI Description
                  416807
Seq. No.
                  uC-osroM202004g06a2
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3342802
                  412
BLAST score
                   3.0e-40
E value
                  80
Match length
                  96
% identity
                  (AF061838) putative cytosolic 6-phosphogluconate
NCBI Description
                  dehydrogenase [Zea mays]
                  416808
Seq. No.
                  uC-osroM202004g06b1
Seq. ID
                  BLASTX
Method
NCBI GI
                  g3342800
BLAST score
                   626
                   2.0e-65
E value
                  127
Match length
                   94
% identity
NCBI Description (AF061837) putative cytosolic 6-phosphogluconate
                  dehydrogenase [Zea mays]
                   416809
Seq. No.
                  uC-osroM202004q07b1
Seq. ID
                  BLASTX
                   g543867
                   532
                   2.0e-54
                   128
                   77
```

Method NCBI GI BLAST score E value Match length

% identity

NCBI Description ATP SYNTHASE GAMMA CHAIN, MITOCHONDRIAL PRECURSOR

>gi_1076684_pir__A47493 H+-transporting ATP synthase (EC

3.6.1.34) gamma chain precursor - sweet potato

>gi 303626 dbj BAA03526 (D14699) F1-ATPase gammma subunit

[Ipomoea batatas]

416810 Seq. No.

uC-osroM202004g08a2 Seq. ID

Method BLASTN NCBI GI q2647937 BLAST score 42 E value 3.0e-14 Match length 66 91 % identity

Hordeum vulgare DNA for plant metallothionein-like protein, NCBI Description

complete cds

416811 Seq. No.

uC-osroM202004g08b1 Seq. ID

Method BLASTX NCBI GI g2647938



BLAST score 163 E value 4.0e-11 Match length 56 % identity 57

NCBI Description (D50641) plant metallothionein-like protein [Hordeum

vulgare]

Seq. No. 416812

Seq. ID uC-osroM202004g12b1

Method BLASTX
NCBI GI g4008441
BLAST score 239
E value 5.0e-20
Match length 75
% identity 64

NCBI Description (AL034488) predicted using Genefinder; cDNA EST yk433c6.3

comes from this gene; cDNA EST EMBL:D72601 comes from this gene; cDNA EST EMBL:D75524 comes from this gene; cDNA EST

yk433c6.5 comes from this gene [Caenorhabditis ele

Seq. No. 416813

Seq. ID uC-osroM202004h05a2

Method BLASTX
NCBI GI g3819697
BLAST score 156
E value 2.0e-10
Match length 69
% identity 51

NCBI Description (AJ009608) BnMAP4K alpha1 [Brassica napus]

Seq. No. 416814

Seq. ID uC-osroM202004h05b1

Method BLASTX
NCBI GI g3819699
BLAST score 147
E value 4.0e-09
Match length 108
% identity 35

NCBI Description (AJ009609) BnMAP4K alpha2 [Brassica napus]

Seq. No. 416815

Seq. ID uC-osroM202004h10a2

Method BLASTX
NCBI GI g5926740
BLAST score 835
E value 9.0e-90
Match length 169
% identity 91

NCBI Description (AB025310) asparaginyl endopeptidase [Oryza sativa]

Seq. No. 416816

Seq. ID uC-osroM202004h10b1

Method BLASTX
NCBI GI g5926740
BLAST score 191
E value 2.0e-14
Match length 38



% identity 95

NCBI Description (AB025310) asparaginyl endopeptidase [Oryza sativa]

Seq. No. 416817

Seq. ID uC-osroM202005a01b1

Method BLASTX
NCBI GI g4099921
BLAST score 226
E value 2.0e-18
Match length 61
% identity 67

NCBI Description (U91982) EREBP-3 homolog [Stylosanthes hamata]

Seq. No. 416818

Seq. ID uC-osroM202005a03b1

Method BLASTX
NCBI GI g2245131
BLAST score 153
E value 7.0e-10
Match length 80
% identity 51

NCBI Description (297344) hypothetical protein [Arabidopsis thaliana]

Seq. No. 416819

Seq. ID uC-osroM202005a04b1

Method BLASTX
NCBI GI g2501647
BLAST score 439
E value 2.0e-43
Match length 144
% identity 56

NCBI Description UROPORPHYRINOGEN DECARBOXYLASE PRECURSOR (UPD)

>gi_1362120_pir__S55732 uroporphyrinogen decarboxylase -

common tobacco >gi_1009429_emb_CAA58040_ (X82833) uroporphyrinogen decarboxylase [Nicotiana tabacum]

Seq. No. 416820

Seq. ID uC-osroM202005a05b1

Method BLASTX
NCBI GI g1546692
BLAST score 198
E value 3.0e-15
Match length 66
% identity 55

NCBI Description (X98805) peroxidase ATP19a [Arabidopsis thaliana]

Seq. No. 416821

Seq. ID uC-osroM202005a06b1

Method BLASTX
NCBI GI g2576361
BLAST score 247
E value 3.0e-21
Match length 70
% identity 64

NCBI Description (U39782) lysine and histidine specific transporter

[Arabidopsis thaliana]



Seq. No. 416822 Seq. ID uC-osroM202005a11b1 BLASTX Method NCBI GI g3935175 BLAST score 291 E value 4.0e-26 Match length 77 71 % identity NCBI Description (AC004557) F17L21.18 [Arabidopsis thaliana] 416823 Seq. No. Seq. ID uC-osroM202005b03b1 Method BLASTX g3063694 NCBI GI BLAST score 349 E value 8.0e-33 Match length 160 % identity 49 NCBI Description (AL022537) putative protein [Arabidopsis thaliana] Seq. No. 416824 uC-osroM202005b04b1 Seq. ID Method BLASTX NCBI GI q401140 BLAST score 602 E value 2.0e-62 Match length 120 100 % identity NCBI Description SUCROSE SYNTHASE 2 (SUCROSE-UDP GLUCOSYLTRANSFERASE 2) >gi_20095_emb_CAA41774_ (X59046) sucrose-UDP glucosyltransferase (isoenzyme 2) [Oryza sativa] >gi 1587662 prf 2207194A sucrose synthase:ISOTYPE=2 [Oryza satīva] Seq. No. 416825 Seq. ID uC-osroM202005b06b1 Method BLASTX NCBI GI q129591 BLAST score 179 E value 5.0e-13 Match length 36 % identity 89 NCBI Description PHENYLALANINE AMMONIA-LYASE >gi 295824 emb CAA34226 (X16099) phenylalanine ammonia-lyase [Oryza sativa] Seq. No. 416826 Seq. ID uC-osroM202005b09b1 Method BLASTX

Method BLASTX
NCBI GI 94512667
BLAST score 619
E value 2.0e-64
Match length 156
% identity 77

NCBI Description (AC006931) putative MAP kinase [Arabidopsis thaliana]

Seq. No. 416827

Seq. ID uC-osroM202005b11b1



```
BLASTX
Method
NCBI GI
                  q4406759
BLAST score
                  360
                   4.0e-34
E value
Match length
                  172
                   48
% identity
NCBI Description
                 (AC006836) hypothetical protein [Arabidopsis thaliana]
                  416828
Seq. No.
                  uC-osroM202005c01b1
Seq. ID
Method
                  BLASTX
NCBI GI
                   g2425170
BLAST score
                   700
                   2.0e-74
E value
                  146
Match length
                   94
% identity
                  (AB003195) basic class III chitinase OsChib3b [Oryza
NCBI Description
                  sativa]
                   416829
Seq. No.
Seq. ID
                  uC-osroM202005c02b1
Method
                  BLASTX
NCBI GI
                   q82496
BLAST score
                   657
E value
                   6.0e-69
Match length
                  150
% identity
                   85
NCBI Description phenylalanine ammonia-lyase (EC 4.3.1.5) - rice
                   416830
Seq. No.
Seq. ID
                  uC-osroM202005c03b1
                  BLASTX
Method
NCBI GI
                   q2190542
BLAST score
                  228
E value
                   1.0e-18
Match length
                   131
% identity
NCBI Description (AC001229) F5I14.5 gene product [Arabidopsis thaliana]
Seq. No.
                   416831
Seq. ID
                  uC-osroM202005c05b1
Method
                  BLASTX
NCBI GI
                   g5103831
BLAST score
                   266
E value
                   4.0e-23
Match length
                   97
% identity
                   56
                   (AC007591) ESTs gb H37032, gb R6425, gb Z34651, gb N37268,
NCBI Description
                   gb AA713172 and gb Z34241 come from this gene. [Arabidopsis
                   thaliana]
```

Seq. No. 416832

Seq. ID uC-osroM202005c06b1

Method BLASTX
NCBI GI g4914319
BLAST score 440
E value 2.0e-43



Match length 168 % identity 57

NCBI Description (AC005489) F14N23.5 [Arabidopsis thaliana]

Seq. No. 416833

Seq. ID uC-osroM202005c08b1

Method BLASTX
NCBI GI g4218535
BLAST score 208
E value 2.0e-16
Match length 50
% identity 74

NCBI Description (AJ010829) GRAB1 protein [Triticum sp.]

Seq. No. 416834

Seq. ID uC-osroM202005c09b1

Method BLASTX
NCBI GI g5733874
BLAST score 325
E value 4.0e-30
Match length 84
% identity 75

NCBI Description (AC007932) F11A17.8 [Arabidopsis thaliana]

Seq. No. 416835

Seq. ID uC-osroM202005c11b1

Method BLASTX
NCBI GI g4755188
BLAST score 613
E value 9.0e-64
Match length 158
% identity 70

NCBI Description (AC007018) unknown protein [Arabidopsis thaliana]

Seq. No. 416836

Seq. ID uC-osroM202005d01b1

Method BLASTX
NCBI GI g3023816
BLAST score 322
E value 6.0e-35
Match length 97
% identity 80

NCBI Description GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC

>gi_968996 (U31676) glyceraldehyde-3-phosphate

dehydrogenase [Oryza sativa]

Seq. No. 416837

Seq. ID uC-osroM202005d03b1

Method BLASTX
NCBI GI g2055230
BLAST score 160
E value 8.0e-11
Match length 103
% identity 44

NCBI Description (AB000130) SRC2 [Glycine max]

Seq. No. 416838



Seq. ID uC-osroM202005d06b1

Method BLASTX NCBI GI q3522937 BLAST score 407 E value 1.0e-39 Match length 158 % identity 54

NCBI Description (AC004411) unknown protein [Arabidopsis thaliana]

416839 Seq. No.

Seq. ID uC-osroM202005d07b1

Method BLASTX NCBI GI q2662343 BLAST score 622 E value 6.0e-65 Match length 123 97 % identity

NCBI Description (D63581) EF-1 alpha [Oryza sativa]

Seq. No. 416840

Seq. ID uC-osroM202005d08b1

Method BLASTX NCBI GI q70642 BLAST score 607 E value 3.0e-63 Match length 125 % identity 21

NCBI Description ubiquitin precursor - Arabidopsis thaliana

>gi_17678_emb_CAA31331_ (X12853) polyubiquitin (AA 1 - 382)
[Arabidopsis thaliana] >gi_987519 (U33014) polyubiquitin
[Arabidopsis thaliana] >gi_226499_prf__1515347A

poly-ubiquitin [Arabidopsis thaliana]

416841 Seq. No.

Seq. ID uC-osroM202005d09b1

Method BLASTX NCBI GI q3318615 BLAST score 291 E value 9.0e-37 Match length 123 % identity

NCBI Description (AB016065) mitochondrial phosphate transporter [Oryza

sativa]

Seq. No. 416842

Seq. ID uC-osroM202005d10b1

Method BLASTX NCBI GI g3790100 BLAST score 520 E value 7.0e-53 Match length 129 % identity

NCBI Description (AF095520) pyrophosphate-dependent phosphofructokinase beta

subunit [Citrus X paradisi]

Seq. No. 416843

Seq. ID uC-osroM202005d11b1



Method BLASTX
NCBI GI g3152568
BLAST score 341
E value 7.0e-32
Match length 156
% identity 47

NCBI Description (AC002986) Similar to hypothetical protein product

gb_Z97337 from A. thaliana. EST gb_H76597 comes from this

gene. [Arabidopsis thaliana]

Seq. No. 416844

Seq. ID uC-osroM202005e03b1

Method BLASTX
NCBI GI g1321661
BLAST score 335
E value 1.0e-31
Match length 75
% identity 88

NCBI Description (D45423) ascorbate peroxidase [Oryza sativa]

Seq. No. 416845

Seq. ID uC-osroM202005e05b1

Method BLASTX
NCBI GI g5103807
BLAST score 354
E value 2.0e-33
Match length 113
% identity 58

NCBI Description (AC007591) Contains similarity to gb_AF014403 type-2

phosphatidic acid phosphatase alpha- $\overline{2}$ (PAP2_a2) from Homo sapiens. ESTs gb_T88254 and gb_AA394650 come from this

gene. [Arabidopsis thaliana]

Seq. No. 416846

Seq. ID uC-osroM202005e06b1

Method BLASTX
NCBI GI g729480
BLAST score 807
E value 2.0e-86
Match length 152
% identity 99

NCBI Description FERREDOXIN--NADP REDUCTASE, ROOT ISOZYME PRECURSOR (FNR)

>gi_435647_dbj_BAA04232 (D17410) ferredoxin-NADP+
reductase [Oryza sativa] >gi_902936_dbj_BAA07479.1_
(D38445) root ferredoxin-NADP+ reductase [Oryza sativa]
>gi_1096932_prf__2113196A ferredoxin-NADP oxidoreductase

[Oryza sativa]

Seq. No. 416847

Seq. ID uC-osroM202005e10b1

Method BLASTX
NCBI GI 94097948
BLAST score 366
E value 8.0e-35
Match length 127
% identity 59

NCBI Description (U72255) beta-1,3-glucanase precursor [Oryza sativa]

Seq. ID

Method

Seq. No.

416848

```
Seq. ID
                  uC-osroM202005f02b1
Method
                  BLASTX
NCBI GI
                  g1351856
BLAST score
                  311
E value
                  4.0e-29
Match length
                  62
% identity
                  95
NCBI Description
                  ACONITATE HYDRATASE, CYTOPLASMIC (CITRATE HYDRO-LYASE)
                   (ACONITASE) >gi_868003_dbj BAA06108 (D29629) aconitase
                   [Cucurbita sp.]
                  416849
Seq. No.
Seq. ID
                  uC-osroM202005f03b1
Method
                  BLASTX
NCBI GI
                  q5081779
BLAST score
                  266
E value
                  8.0e-24
Match length
                  58
% identity
                  86
NCBI Description (AF150630) cellulose synthase [Gossypium hirsutum]
Seq. No.
                  416850
Seq. ID
                  uC-osroM202005f05b1
Method
                  BLASTX
NCBI GI
                  q2342726
BLAST score
                  177
E value
                  1.0e-12
Match length
                  55
% identity
                  55
NCBI Description (AC002341) peroxidase isolog [Arabidopsis thaliana]
Seq. No.
                  416851
Seq. ID
                  uC-osroM202005f06b1
Method
                  BLASTX
NCBI GI
                  g3927825
BLAST score
                  539
E value
                  4.0e-55
Match length
                  130
% identity
                  80
NCBI Description
                  (AC005727) putative dTDP-glucose 4-6-dehydratase
                  [Arabidopsis thaliana]
Seq. No.
                  416852
Seq. ID
                  uC-osroM202005f07b1
Method
                  BLASTN
NCBI GI
                  g5777612
BLAST score
                  39
E value
                  1.0e-12
Match length
                  66
                  93
% identity
NCBI Description Oryza sativa chromosome 4 BAC q3037-207F1 complete genome
Seq. No.
                  416853
```

54513

uC-osroM202005f09b1

BLASTX



```
NCBI GI
                  q3337356
                  219
BLAST score
E value
                  3.0e-31
Match length
                  89
% identity
                  78
NCBI Description
                  (AC004481) putative protein transport protein SEC61 alpha
                  subunit [Arabidopsis thaliana]
Seq. No.
                  416854
                  uC-osroM202005f12b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q129591
BLAST score
                  432
E value
                  1.0e-42
Match length
                  112
% identity
                  76
NCBI Description PHENYLALANINE AMMONIA-LYASE >gi 295824 emb CAA34226
                   (X16099) phenylalanine ammonia-Tyase [Oryza sativa]
Seq. No.
                  416855
Seq. ID
                  uC-osroM202005g01b1
Method
                  BLASTX
NCBI GI
                  q1408222
BLAST score
                  263
E value
                  5.0e-23
Match length
                  84
% identity
                  65
NCBI Description (U60764) pathogenesis-related protein [Sorghum bicolor]
Seq. No.
                  416856
Seq. ID
                  uC-osroM202005g04b1
Method
                  BLASTX
NCBI GI
                  q4220462
BLAST score
                  666
E value
                  5.0e-70
Match length
                  162
                  77
% identity
NCBI Description
                  (AC006216) Strong similarity to gb Z50851 HD-zip (athb-8)
                  gene from Arabidopsis thaliana containing Homeobox PF 00046
                  and bZIP PF_00170 domains. [Arabidopsis thaliana]
Seq. No.
                  416857
Seq. ID
                  uC-osroM202005g05b1
Method
                  BLASTN
NCBI GI
                  g5257255
BLAST score
                  222
E value
                  1.0e-121
Match length
                  452
                  88
% identity
NCBI Description Oryza sativa genomic DNA, chromosome 8, clone:P0026F07
```

416858 Seq. No.

Seq. ID uC-osroM202005g06b1

Method BLASTX NCBI GI g4510375 BLAST score 142 E value 2.0e-23



```
Match length
% identity
NCBI Description
                   (AC007017) putative homeotic protein BEL1 [Arabidopsis
                   thaliana]
                   416859
Seq. No.
Seq. ID
                  uC-osroM202005g11b1
Method
                  BLASTX
NCBI GI
                   q3738324
BLAST score
                   206
E value
                   4.0e-16
Match length
                   68
% identity
                   54
                 (AC005170) GMP synthase-like protein [Arabidopsis thaliana]
NCBI Description
                   416860
Seq. No.
                  uC-osroM202005h04b1
Seq. ID
Method
                  BLASTN
NCBI GI
                   g2773153
BLAST score
                   57
E value
                   4.0e-23
Match length
                  207
% identity
                  86
NCBI Description Oryza sativa abscisic acid- and stress-inducible protein
                   (Asr1) mRNA, complete cds
                   416861
Seq. No.
Seq. ID
                  uC-osroM202005h05b1
Method
                  BLASTX
NCBI GI
                   g3522945
BLAST score
                  228
E value
                   1.0e-18
Match length
                  84
                   48
% identity
NCBI Description (AC004411) putative cytochrome P450 [Arabidopsis thaliana]
Seq. No.
                   416862
Seq. ID
                   uC-osroM202005h06b1
Method
                  BLASTN
NCBI GI
                  q5042437
BLAST score
                   92
E value
                   4.0e-44
                  147
Match length
% identity
                   91
NCBI Description Oryza sativa BAC T49B20 genomic sequence, complete sequence
Seq. No.
                   416863
                  uC-osroM202005h07b1
Seq. ID
                  BLASTX
Method
NCBI GI
                  q4521249
BLAST score
                  224
```

2.0e-21 E value 84 Match length 67 % identity

(AB013912) DNA helicase [Mus musculus] NCBI Description

Seq. No. 416864



Seq. ID uC-osroM202006a01b1
Method BLASTX
NCBI GI g1076668
BLAST score 338

E value 1.0e-31 Match length 69 % identity 87

NCBI Description NADH dehydrogenase (EC 1.6.99.3) - potato

>gi_639834_emb_CAA58823_ (X83999) NADH dehydrogenase

[Solanum tuberosum]

Seq. No. 416865

Seq. ID uC-osroM202006a02b1

Method BLASTX
NCBI GI g3776567
BLAST score 274
E value 3.0e-24
Match length 103
% identity 53

NCBI Description (AC005388) Strong similarity to F21B7.33 gi_2809264 from A.

thaliana BAC gb AC002560. EST gb N65119 comes from this

gene. [Arabidopsis thaliana]

Seq. No. 416866

Seq. ID uC-osroM202006a04b1

Method BLASTX
NCBI GI g401140
BLAST score 550
E value 2.0e-57
Match length 121
% identity 84

NCBI Description SUCROSE SYNTHASE 2 (SUCROSE-UDP GLUCOSYLTRANSFERASE 2)

>gi_20095_emb_CAA41774_ (X59046) sucrose-UDP
glucosyltransferase (isoenzyme 2) [Oryza sativa]

>gi 1587662 prf 2207194A sucrose synthase:ISOTYPE=2 [Oryza

satīva]

Seq. No. 416867

Seq. ID uC-osroM202006a06b1

Method BLASTX
NCBI GI g5738361
BLAST score 292
E value 2.0e-26
Match length 86
% identity 64

NCBI Description (AL021637) putative protein, fragment [Arabidopsis

thaliana]

Seq. No. 416868

Seq. ID uC-osroM202006a07b1

Method BLASTX
NCBI GI g2244899
BLAST score 257
E value 1.0e-23
Match length 82
% identity 73

NCBI Description (Z97338) UFD1 like protein [Arabidopsis thaliana]

Seq. No.

% identity

68

416869

```
Seq. ID
                     uC-osroM202006a12b1
Method
                     BLASTX
NCBI GI
                     q2641619
BLAST score
                     319
E value
                     1.0e-29
Match length
                     64
% identity
                     89
NCBI Description (AF032468) ubiquitin-conjugating enzyme protein E2 [Zea
                    mays]
                     416870
Seq. No.
Seq. ID
                    uC-osroM202006b02b1
Method
                    BLASTX
                    g4972062
NCBI GI
BLAST score
                     308
E value
                     6.0e-30
Match length
                    124
% identity
NCBI Description (AL078470) putative protein [Arabidopsis thaliana]
Seq. No.
                     416871
Seq. ID
                    uC-osroM202006b06b1
Method
                    BLASTX
NCBI GI
                    q2660670
BLAST score
                     610
E value
                    2.0e-63
Match length
                    167
% identity
                    70
NCBI Description (AC002342) putative Cu2+-transporting ATPase [Arabidopsis
                    thaliana]
                    416872
Seq. No.
Seq. ID
                    uC-osroM202006b07b1
Method
                    BLASTX
NCBI GI
                    q2499931
BLAST score
                    343
E value
                    4.0e-32
Match length
                    92
                    72
% identity
NCBI Description ADENINE PHOSPHORIBOSYLTRANSFERASE 2 (APRT)
                    >gi_2129534_pir__S71272 adenine phosphoribosyltransferase
(EC 2.4.2.7) - Arabidopsis thaliana
                    >gi_1321681_emb_CAA65609_ (X96866) adenine
phosphoribosyltransferase [Arabidopsis thaliana]
                    >gi_5902383_gb_AAD55485.1_AC009322_25 (AC009322) adenine phosphoribosyltransferase [Arabidopsis thaliana]
Seq. No.
                    416873
Seq. ID
                    uC-osroM202006b09b1
Method
                    BLASTX
NCBI GI
                    g571484
BLAST score
                    407
E value
                    1.0e-39
Match length
                    125
```

```
NCBI Description (U16727) peroxidase precursor [Medicago truncatula]

Seq. No. 416874
Seq. ID 416874
uC-osroM202006c03b1
```

Method BLASTX
NCBI GI g1171577
BLAST score 199
E value 1.0e-17
Match length 136
% identity 42

NCBI Description (X95343) hypersensitivity-related gene [Nicotiana tabacum]

Seq. No. 416875

Seq. ID uC-osroM202006c05b1

Method BLASTX
NCBI GI g2982301
BLAST score 146
E value 2.0e-09
Match length 84
% identity 37

NCBI Description (AF051235) YGL010w-like protein [Picea mariana]

Seq. No. 416876

Seq. ID uC-osroM202006c07b1

Method BLASTX
NCBI GI g3415117
BLAST score 147
E value 4.0e-09
Match length 86
% identity 43

NCBI Description (AF081203) villin 3 [Arabidopsis thaliana]

Seq. No. 416877

Seq. ID uC-osroM202006d01b1

Method BLASTX
NCBI GI g1136120
BLAST score 173
E value 2.0e-12
Match length 44
% identity 73

NCBI Description (X91806) alpha-tubulin [Oryza sativa]

Seq. No. 416878

Seq. ID uC-osroM202006d03b1

Method BLASTX
NCBI GI g5051781
BLAST score 310
E value 2.0e-28
Match length 120
% identity 53

NCBI Description (AL078637) transport inhibitor response-like protein

[Arabidopsis thaliana]

Seq. No. 416879

Seq. ID uC-osroM202006d04b1

Method BLASTX NCBI GI g3641837

```
BLAST score
                  313
                   6.0e-29
E value
                  95
Match length
                   67
% identity
                  (AL023094) Nonclathrin coat protein gamma-like protein
NCBI Description
                   [Arabidopsis thaliana]
                  416880
Seq. No.
                  uC-osroM202006d05b1
Seq. ID
                  BLASTX
Method
                  g5091555
NCBI GI
BLAST score
                  363
                  1.0e-34
E value
Match length
                  103
                  70
% identity
                 (AC007067) T10024.24 [Arabidopsis thaliana]
NCBI Description
                  416881
Seq. No.
                  uC-osroM202006d06b1
Seq. ID
                  BLASTX
Method
                  g283008
NCBI GI
                  549
BLAST score
                  2.0e-56
E value
                  134
Match length
                   83
% identity
                  sucrose synthase (EC 2.4.1.13) - rice
NCBI Description
                  >gi 20366 emb CAA46017 (X64770) sucrose synthase [Oryza
                  sativa]
                   416882
Seq. No.
Seq. ID
                   uC-osroM202006d08b1
Method
                  BLASTX
                   q445613
NCBI GI
BLAST score
                   142
E value
                   9.0e-09
Match length
                   41
% identity
NCBI Description ribosomal protein L7 [Solanum tuberosum]
                   416883
Seq. No.
Seq. ID
                   uC-osroM202006d09b1
Method
                  BLASTX
NCBI GI
                   g1688233
BLAST score
                   264
E value
                   4.0e-23
Match length
                   91
% identity
                   71
NCBI Description (U77655) DNA binding protein homolog [Solanum tuberosum]
Seq. No.
                   416884
                   uC-osroM202006d12b1
Seq. ID
Method
                  BLASTX
NCBI GI
                   g4006902
BLAST score
                   176
                   1.0e-12
E value
Match length
                  114
```

54519

34

% identity

E value

Match length

% identity

1.0e-67

158

78



```
NCBI Description (299708) putative protein [Arabidopsis thaliana]
Seq. No.
                   416885
Seq. ID
                   uC-osroM202006e01b1
                   BLASTX
Method
NCBI GI
                   q4678342
BLAST score
                   192
                   1.0e-14
E value
Match length
                   95
% identity
                   51
NCBI Description
                  (AL049659) lipase-like protein [Arabidopsis thaliana]
Seq. No.
                   416886
                   uC-osroM202006e02b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   a2499931
BLAST score
                   295
E value
                   1.0e-26
                   76
Match length
% identity
                   74
                   ADENINE PHOSPHORIBOSYLTRANSFERASE 2 (APRT)
NCBI Description
                   >gi_2129534_pir__S71272 adenine phosphoribosyltransferase
                   (EC 2.4.2.7) - Arabidopsis thaliana
                   >gi_1321681_emb_CAA65609_ (X96866) adenine
phosphoribosyltransferase [Arabidopsis thaliana]
                   >gi_5902383_gb_AAD55485.1_AC009322_25 (AC009322) adenine
                   phosphoribosyltransferase [Arabidopsis thaliana]
                   416887
Seq. No.
Seq. ID
                   uC-osroM202006f02b1
Method
                   BLASTX
NCBI GI
                   g4467153
BLAST score
                   361
E value
                   2.0e-34
Match length
                   108
% identity
NCBI Description
                   (AL035540) putative thaumatin-like protein [Arabidopsis
                   thaliana]
                   416888
Seq. No.
Seq. ID
                   uC-osroM202006f04b1
Method
                   BLASTX
NCBI GI
                   g5882745
BLAST score
                   669
E value
                   2.0e-70
Match length
                   174
                   69
% identity
NCBI Description (AC008263) F25A4.24 [Arabidopsis thaliana]
Seq. No.
                   416889
Seq. ID
                   uC-osroM202006f05b1
Method
                   BLASTX
NCBI GI
                   g1495251
BLAST score
                   645
```

Seq. ID

Method

NCBI GI



```
NCBI Description (Z70314) heat-shock protein [Arabidopsis thaliana]
                   416890
Seq. No.
Seq. ID
                   uC-osroM202006f06b1
Method
                   BLASTX
NCBI GI
                   g231536
BLAST score
                   148
E value
                   2.0e-09
Match length
                   49
% identity
                   55
NCBI Description CYTOSOL AMINOPEPTIDASE (LEUCINE AMINOPEPTIDASE) (LAP)
                   (LEUCYL AMINOPEPTIDASE) (PROLINE AMINOPEPTIDASE) (PROLYL
                   AMINOPEPTIDASE) >gi 99683 pir S22399 leucyl aminopeptidase
                   (EC 3.4.11.1) - Arabidopsis thaliana
                   >gi_16394_emb_CAA45040_ (X63444) leucine aminopeptidase
[Arabidopsis thaliana] >gi_4115380 (AC005967) putative
                   leucine aminopeptidase [Arabidopsis thaliana]
Seq. No.
                   416891
Seq. ID
                   uC-osroM202006f07b1
Method
                   BLASTX
NCBI GI
                   q4314370
BLAST score
                   152
E value
                   2.0e-11
Match length
                   68
                   55
% identity
NCBI Description (AC006340) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   416892
                   uC-osroM202006f08b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   q1168537
BLAST score
                   539
E value
                   3.0e-55
Match length
                   119
% identity
                   87
NCBI Description ASPARTIC PROTEINASE PRECURSOR >gi_82458_pir__JS0732
                   aspartic proteinase (EC 3.4.23.-) - rice
                   >gi_218143 dbj BAA02242 (D12777) aspartic proteinase
                   [Oryza sativa]
Seq. No.
                   416893
Seq. ID
                   uC-osroM202006f09b1
Method
                   BLASTX
NCBI GI
                   g1710780
BLAST score
                   490
E value
                   2.0e-49
Match length
                   137
% identity
                   71
                   40S RIBOSOMAL PROTEIN S9 (S7) >gi 1321917 emb CAA65433
NCBI Description
                   (X96613) cytoplasmic ribosomal protein S7 [Podospora
                   anserina]
                   416894
Seq. No.
```

uC-osroM202006f11b1

BLASTX

g6056193

```
BLAST score
                  408
E value
                  1.0e-46
Match length
                  110
% identity
                  83
NCBI Description (AC009400) transcription initiation factor IIB (TFIIB)
                  [Arabidopsis thaliana]
Seq. No.
                  416895
Seq. ID
                  uC-osroM202006f12b1
Method
                  BLASTX
NCBI GI
                  q4115337
BLAST score
                  773
E value
                  1.0e-82
Match length
                  158
% identity
                  18
NCBI Description (L81141) ubiquitin [Pisum sativum]
Seq. No.
                  416896
Seq. ID
                  uC-osroM202006g03a1
Method
                  BLASTX
NCBI GI
                  q21699
BLAST score
                  358
E value
                  5.0e-34
Match length
                  80
% identity
                  82
NCBI Description (X66013) cathepsin B [Triticum aestivum]
                  416897
Seq. No.
Seq. ID
                  uC-osroM202006q03b1
Method
                  BLASTX
NCBI GI
                  q4138583
BLAST score
                  547
E value
                  3.0e-56
Match length
                  128
% identity
                  85
NCBI Description (Y10821) plastidic ATP/ADP-transporter [Solanum tuberosum]
Seq. No.
                  416898
Seq. ID
                  uC-osroM202006q04b1
Method
                  BLASTX
NCBI GI
                  g1706260
BLAST score
                  535
E value
                  1.0e-54
Match length
                  116
% identity
                  90
NCBI Description CYSTEINE PROTEINASE 1 PRECURSOR >gi 2118131 pir S59597
                  cysteine proteinase 1 precursor - maize
                  >gi 643597 dbj BAA08244 (D45402) cysteine proteinase [Zea
                  mays]
                  416899
Seq. No.
Seq. ID
                  uC-osroM202006g08b1
Method
                  BLASTX
NCBI GI
                  g5734777
BLAST score
```

54522

532

153

3.0e-54

E value

Match length

E value

Match length

% identity

5.0e-19 134

43



```
% identity
NCBI Description (AC007980) 55212 [Arabidopsis thaliana]
Seq. No.
                   416900
Seq. ID
                   uC-osroM202006q09b1
Method
                   BLASTX
NCBI GI
                   q21695
BLAST score
                   354
E value
                   2.0e-33
Match length
                   107
% identity
                   64
NCBI Description (X66014) cathepsin B [Triticum aestivum]
                   416901
Seq. No.
Seq. ID
                   uC-osroM202006q11b1
Method
                   BLASTX
NCBI GI
                   q113385
BLAST score
                   424
E value
                   2.0e-45
Match length
                   95
                   100
% identity
                   ALCOHOL DEHYDROGENASE 3 >gi_82349_pir__S04040 alcohol dehydrogenase (EC 1.1.1.1) 3 - barley
NCBI Description
                   >gi_18886_emb_CAA31231_ (X12734) alcohol dehydrogenase
                   [Hordeum vulgare]
                   416902
Seq. No.
Seq. ID
                   uC-osroM202006h02b1
Method
                   BLASTX
NCBI GI
                   g3426039
BLAST score
                   449
E value
                   1.0e-44
Match length
                   120
% identity
                   68
NCBI Description (AC005168) unknown protein [Arabidopsis thaliana]
                   416903
Seq. No.
Seq. ID
                   uC-osroM202006h03b1
Method
                   BLASTX
NCBI GI
                   g1184774
BLAST score
                   293
E value
                   1.0e-26
Match length
                   84
% identity
                   68
                  (U45856) cytosolic glyceroldehyde-3-phosphate dehydrogenase
NCBI Description
                   GAPC3 [Zea mays]
Seq. No.
                   416904
                   uC-osroM202006h04b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3894159
BLAST score
                   231
```

NCBI Description (AC005312) hypothetical protein [Arabidopsis thaliana]



```
416905
Seq. No.
Seq. ID
                  uC-osroM202006h05b1
Method
                  BLASTN
NCBI GI
                  g415314
BLAST score
                  116
E value
                  2.0e-58
Match length
                  252
% identity
                  92
NCBI Description Rice mRNA for NADP dependent malic enzyme, complete cds
                  416906
Seq. No.
                  uC-osroM202006h08b1
Seq. ID
                  BLASTX
Method
NCBI GI
                  q4417286
BLAST score
                  239
E value
                  5.0e-20
                  78
Match length
% identity
                  60
NCBI Description (AC007019) putative shikimate kinase [Arabidopsis thaliana]
                  416907
Seq. No.
Seq. ID
                  uC-osroM202006h09b1
Method
                  BLASTX
NCBI GI
                  q3885888
BLAST score
                  160
E value
                  7.0e-11
                  78
Match length
% identity
                  50
NCBI Description (AF093632) high mobility group protein [Oryza sativa]
                  416908
Seq. No.
                  uC-osroM202006h10b1
Seq. ID
                  BLASTX
Method
NCBI GI
                  g3068809
BLAST score
                  275
E value
                  3.0e-24
Match length
                  94
                  59
% identity
NCBI Description (AF059295) Skp1 homolog [Arabidopsis thaliana]
Seq. No.
                  416909
Seq. ID
                  uC-osroM202006h11b1
Method
                  BLASTN
NCBI GI
                  g3641660
BLAST score
                  61
E value
                  5.0e-26
                  105
Match length
                  90
% identity
NCBI Description Oryza sativa Nrt2 mRNA for high affinity nitrate
                  transporter, complete cds
                  416910
Seq. No.
                  uC-osroM202007a02b1
```

Seq. ID

Method BLASTX NCBI GI g1169798 BLAST score 637 E value 1.0e-66



```
Match length 89

NCBI Description GLUCOSE-6-PHOSPHATE ISOMERASE, CYTOSOLIC B (GPI-B)

(PHOSPHOGLUCOSE ISOMERASE B) (PGI-B) (PHOSPHOHEXOSE
ISOMERASE B) (PHI-B) >gi_639686_dbj_BAA08149_ (D45218)

phosphoglucose isomerase (Pgi-b) [Oryza sativa]

Seq. No. 416911
Seq. ID uC-osroM202007a03a1
Method BLASTN
```

Method BLASTN
NCBI GI g20315
BLAST score 96
E value 4.0e-47
Match length 100
% identity 99

NCBI Description O.sativa DNA for rab 16D gene

Seq. No. 416912

Seq. ID uC-osroM202007a07a1

Method BLASTX
NCBI GI g129591
BLAST score 173
E value 3.0e-12
Match length 38
% identity 87

NCBI Description PHENYLALANINE AMMONIA-LYASE >gi_295824_emb_CAA34226_

(X16099) phenylalanine ammonia-lyase [Oryza sativa]

Seq. No. 416913

Seq. ID uC-osroM202007a07b1

Method BLASTX
NCBI GI g82496
BLAST score 636
E value 2.0e-66
Match length 142
% identity 87

NCBI Description phenylalanine ammonia-lyase (EC 4.3.1.5) - rice

Seq. No. 416914

Seq. ID uC-osroM202007a11b1

Method BLASTX
NCBI GI g4160280
BLAST score 299
E value 5.0e-27
Match length 100
% identity 54

NCBI Description (AJ006224) purple acid phosphatase [Ipomoea batatas]

Seq. No. 416915

Seq. ID uC-osroM202007a12b1

Method BLASTX
NCBI GI g2262113
BLAST score 163
E value 4.0e-11
Match length 93
% identity 42

NCBI Description (AC002343) unknown protein [Arabidopsis thaliana]



>gi_5668630_emb_CAB51645.1_ (AL109619) putative protein
[Arabidopsis thaliana]

Seq. No. 416916

Seq. ID uC-osroM202007b02a1

Method BLASTX
NCBI GI g2275202
BLAST score 529
E value 6.0e-54
Match length 157
% identity 62

NCBI Description (AC002337) acyl-CoA synthetase isolog [Arabidopsis

thaliana]

Seq. No. 416917

Seq. ID uC-osroM202007b03a1

Method BLASTX
NCBI GI g2501555
BLAST score 364
E value 1.0e-34
Match length 71
% identity 93

NCBI Description POSSIBLE APOSPORY-ASSOCIATED PROTEIN C >gi 549984 (U13148)

possible apospory-associated protein [Pennisetum ciliare]

Seq. No. 416918

Seq. ID uC-osroM202007b05a1

Method BLASTX
NCBI GI g1703380
BLAST score 205
E value 4.0e-16
Match length 40
% identity 93

NCBI Description ADP-RIBOSYLATION FACTOR >gi_1132483_dbj_BAA04607_ (D17760)

ADP-ribosylation factor [Oryza sativa]

Seq. No. 416919

Seq. ID uC-osroM202007b05b1

Method BLASTX
NCBI GI g1351974
BLAST score 490
E value 2.0e-49
Match length 97
% identity 98

NCBI Description ADP-RIBOSYLATION FACTOR >gi_1076788_pir__S49325

ADP-ribosylation factor - maize >gi_1076789_pir__S53486 ADP-ribosylation factor - maize >gi_556686_emb_CAA56351_

(X80042) ADP-ribosylation factor [Zea mays]

Seq. No. 416920

Seq. ID uC-osroM202007b06a1

Method BLASTX
NCBI GI g481477
BLAST score 404
E value 3.0e-39
Match length 95
% identity 15

Seq. No.

416925

```
NCBI Description ubiquitin precursor - rice >gi 416038 emb CAA53665
                   (X76064) polyubiquitin [Oryza sativa] >qi 1574944 (U37687)
                   polyubiquitin [Oryza sativa]
                   >gi_6013289_gb_AAF01315.1_AF184279_1 (AF184279)
                   polyubiquitin [Oryza sativa]
                   >gi_6013291_gb_AAF01316.1_AF184280_1 (AF184280)
                   polyubiquitin [Oryza sativa]
Seq. No.
                   416921
Seq. ID
                   uC-osroM202007b06b1
Method
                   BLASTX
NCBI GI
                   q82040
BLAST score
                   719
E value
                   3.0e-76
Match length
                   162
% identity
                   26
NCBI Description ubiquitin precursor - flax (fragment) >qi 168304 (M57895)
                   ubiquitin [Linum usitatissimum]
Seq. No.
                   416922
Seq. ID
                   uC-osroM202007b07a1
Method
                   BLASTX
NCBI GI
                   g1729868
BLAST score
                   506
E value
                   3.0e-51
Match length
                   163
% identity
                   64
NCBI Description PROBABLE T-COMPLEX PROTEIN 1, BETA SUBUNIT (TCP-1-BETA)
                   (CCT-BETA) >gi 1177337 emb CAA93213.1 (Z69239) probable
                   t-complex protein 1, beta subunit [Schizosaccharomyces
                   pombe]
                   416923
Seq. No.
Seq. ID
                   uC-osroM202007b07b1
Method
                   BLASTX
NCBI GI
                   q549056
BLAST score
                   295
E value
                   1.0e-26
Match length
                   90
                   67
% identity
NCBI Description T-COMPLEX PROTEIN 1, BETA SUBUNIT (TCP-1-BETA) (CCT-BETA)
                   >gi 631651 pir S43059 CCT (chaperonin containing TCP-1)
                   beta chain - mouse >gi 468546 emb CAA83428 (Z31553) CCT (chaperonin containing TCP-1) beta subunit [Mus musculus]
Seq. No.
                   416924
Seq. ID
                   uC-osroM202007b08a1
Method
                   BLASTX
NCBI GI
                   g6056419
BLAST score
                   199
E value
                   3.0e-15
Match length
                   88
% identity
                   51
NCBI Description (AC009525) 60S ribosomal protein L22 [Arabidopsis
                   thaliana]
```



Seq. ID uC-osroM202007b08b1

Method BLASTX
NCBI GI g6056419
BLAST score 250
E value 3.0e-21
Match length 143
% identity 43

NCBI Description (AC009525) 60S ribosomal protein L22 [Arabidopsis

thaliana]

Seq. No. 416926

Seq. ID uC-osroM202007b09a1

Method BLASTX
NCBI GI g5902363
BLAST score 522
E value 4.0e-53
Match length 156
% identity 62

NCBI Description (AC009322) Putative coatomer protein complex, subunit beta

2 (beta prime) [Arabidopsis thaliana]

Seq. No. 416927

Seq. ID uC-osroM202007b10a1

Method BLASTX
NCBI GI g2832632
BLAST score 315
E value 4.0e-29
Match length 111
% identity 59

NCBI Description (AL021711) hypothetical protein [Arabidopsis thaliana]

Seq. No. 416928

Seq. ID uC-osroM202007b12a1

Method BLASTX
NCBI GI g3023271
BLAST score 611
E value 2.0e-63
Match length 115
% identity 99

NCBI Description GLUTATHIONE-DEPENDENT FORMALDEHYDE DEHYDROGENASE (FDH)

(FALDH) (GSH-FDH) >gi 1675394 (U77637) class III ADH enzyme

[Oryza sativa]

Seq. No. 416929

Seq. ID uC-osroM202007b12b1

Method BLASTN
NCBI GI g1675393
BLAST score 58
E value 2.0e-24
Match length 70
% identity 96

NCBI Description Oryza sativa class III ADH enzyme (AdhIII) gene, complete

cds

Seq. No. 416930

Seq. ID uC-osroM202007c01a1

Method BLASTX

Match length

95

```
NCBI GI
                  g1903021
BLAST score
                  152
E value
                  8.0e-10
Match length
                  34
% identity
                  85
NCBI Description (Y10216) hypothetical 3-isopropylmalate dehydrogenase
                  [Arabidopsis thaliana]
Seq. No.
                  416931
Seq. ID
                  uC-osroM202007c02a1
Method
                  BLASTX
NCBI GI
                  g283008
BLAST score
                  368
E value
                  4.0e-35
Match length
                  74
% identity
                  96
NCBI Description sucrose synthase (EC 2.4.1.13) - rice
                  >gi_20366 emb CAA46017 (X64770) sucrose synthase [Oryza
                  sativa]
Seq. No.
                  416932
Seq. ID
                  uC-osroM202007c04b1
Method
                  BLASTX
NCBI GI
                  q542157
BLAST score
                  388
E value
                  1.0e-37
Match length
                  91
% identity
                  84
NCBI Description ribosomal 5S RNA-binding protein - Rice
Seq. No.
                  416933
                  uC-osroM202007c05a1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g5679845
BLAST score
                  159
E value
                  1.0e-10
Match length
                  30
                  97
% identity
NCBI Description (AJ243961) 11332.9 [Oryza sativa]
Seq. No.
                  416934
Seq. ID
                  uC-osroM202007c05b1
Method
                  BLASTX
NCBI GI
                  g5852096
BLAST score
                  207
E value
                  2.0e-16
Match length
                  85
% identity
                  61
NCBI Description (AL117264) zwh19.1 [Oryza sativa]
Seq. No.
                  416935
Seq. ID
                  uC-osroM202007c07a1
Method
                  BLASTN
NCBI GI
                  g20367
BLAST score
                  79
E value
                  7.0e-37
```

```
% identity
                  Oryza sativa shoot GS1 mRNA for cytosolic glutamine
NCBI Description
                  synthetase (EC 6.3.1.2) (clone lambda-GS28)
Seq. No.
                  416936
                  uC-osroM202007c07b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g121349
BLAST score
                  795
E value
                  3.0e-85
                  157
Match length
                  95
% identity
                 GLUTAMINE SYNTHETASE SHOOT ISOZYME (GLUTAMATE--AMMONIA
NCBI Description
                  LIGASE) (CLONE LAMBDA-GS28) >gi 20368 emb_CAA32461
                  (X14245) cytosolic glutamine synthetase (AA 1-356) [Oryza
                  sativa]
                  416937
Seq. No.
                  uC-osroM202007c09b1
Seq. ID
                  BLASTX
Method
                  g3023713
NCBI GI
                  631
BLAST score
                  6.0e-66
E value
                  128
Match length
                  97
% identity
                  ENOLASE (2-PHOSPHOGLYCERATE DEHYDRATASE)
NCBI Description
                   (2-PHOSPHO-D-GLYCERATE HYDRO-LYASE) (OSE1) >gi_780372
                   (U09450) enolase [Oryza sativa]
                  416938
Seq. No.
Seq. ID
                  uC-osroM202007c10a1
Method
                  BLASTX
NCBI GI
                  g3915826
BLAST score
                  412
                  3.0e-40
E value
Match length
                  85
% identity
                  96
NCBI Description 60S RIBOSOMAL PROTEIN L5
                  416939
Seq. No.
Seq. ID
                  uC-osroM202007c10b1
Method
                  BLASTX
NCBI GI
                  q3915826
BLAST score
                  483
E value
                   4.0e-50
Match length
                  136
% identity
                  80
NCBI Description 60S RIBOSOMAL PROTEIN L5
                  416940
Seq. No.
Seq. ID
                  uC-osroM202007c11a1
Method
                  BLASTX
NCBI GI
                  g3522946
BLAST score
                  274
E value
                   4.0e-24
Match length
                  82
% identity
                  62
```



```
NCBI Description (AC004411) putative cytochrome P450 [Arabidopsis thaliana]
                  416941
Seq. No.
                  uC-osroM202007c11b1
Seq. ID
Method
                  BLASTX
                  g3522945
NCBI GI
BLAST score
                  280
                  9.0e-25
E value
Match length
                  135
% identity
                  41
NCBI Description (AC004411) putative cytochrome P450 [Arabidopsis thaliana]
Seq. No.
                  416942
                  uC-osroM202007d03a1
Seq. ID
Method
                  BLASTN
                  g20280
NCBI GI
BLAST score
                  328
E value
                  0.0e+00
Match length
                  344
                  99
% identity
NCBI Description Rice gene for phenylalanine ammonia-lyase (EC 4.3.1.5)
                  416943
Seq. No.
                  uC-osroM202007d05b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3169785
BLAST score
                  151
E value
                  5.0e-14
Match length
                  84
% identity
                  54
NCBI Description (AF026420) starch synthase [Chlamydomonas reinhardtii]
                  416944
Seq. No.
Seq. ID
                  uC-osroM202007d06b1
Method
                  BLASTX
NCBI GI
                  q2388580
BLAST score
                  288
E value
                  9.0e-26
Match length
                  84
% identity
                  60
NCBI Description
                  (AC000098) Similar to Sequence 10 from patent 5477002
                   (gb 1253956). [Arabidopsis thaliana]
                   416945
Seq. No.
Seq. ID
                  uC-osroM202007d08a1
Method
                  BLASTX
NCBI GI
                  q4887620
BLAST score
                  285
E value
                  2.0e-25
```

Match length 54 % identity 94

NCBI Description (AB007629) homeobox gene [Oryza sativa]

416946 Seq. No.

Seq. ID uC-osroM202007d09a1

Method BLASTX NCBI GI g4102839

% identity

95 NCBI Description 40S RIBOSOMAL PROTEIN S19

```
BLAST score
                  195
                  8.0e-15
E value
                  52
Match length
                  69
% identity
NCBI Description (AF016713) LeOPT1 [Lycopersicon esculentum]
                  416947
Seq. No.
                  uC-osroM202007d09b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4102839
BLAST score
                  220
E value
                  1.0e-17
                  77
Match length
                  56
% identity
NCBI Description (AF016713) LeOPT1 [Lycopersicon esculentum]
                  416948
Seq. No.
                  uC-osroM202007d12b1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g2443456
BLAST score
                  35
E value
                  6.0e-10
Match length
                  94
                  85
% identity
NCBI Description Oryza sativa ethylene responsive element binding protein
                  (Os-EREBP1) mRNA, complete cds
                  416949
Seq. No.
                  uC-osroM202007e01a1
Seq. ID
Method
                  BLASTN
NCBI GI
                  q508575
BLAST score
                  302
E value
                  1.0e-169
Match length
                  323
% identity
                  98
NCBI Description Oryza sativa beta-tubulin mRNA
Seq. No.
                  416950
                  uC-osroM202007e01b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1351202
BLAST score
                  227
E value
                  1.0e-18
Match length
                  93
                  54
% identity
NCBI Description TUBULIN BETA CHAIN > gi 312989 emb CAA42777 (X60216)
                  beta-tubulin [Glycine max]
Seq. No.
                  416951
Seq. ID
                  uC-osroM202007e02b1
Method
                  BLASTX
NCBI GI
                  g730456
BLAST score
                  443
E value
                  1.0e-52
Match length
                  112
```



Seq. No. 416952

Seq. ID uC-osroM202007e03b1

Method BLASTX
NCBI GI g485517
BLAST score 625
E value 3.0e-65
Match length 125
% identity 99

NCBI Description ADP, ATP carrier protein - rice

Seq. No. 416953

Seq. ID uC-osroM202007e04b1

Method BLASTX
NCBI GI g3341511
BLAST score 562
E value 4.0e-59
Match length 130
% identity 90

NCBI Description (AJ231134) cinnamoyl-CoA reductase [Saccharum officinarum]

Seq. No. 416954

Seq. ID uC-osroM202007e05a1

Method BLASTX
NCBI GI g2493123
BLAST score 325
E value 5.0e-30
Match length 69
% identity 91

NCBI Description VACUOLAR ATP SYNTHASE CATALYTIC SUBUNIT A (V-ATPASE 69 KD

SUBUNIT) >gi 1051258 (U36939) vacuolar ATPase catalytic

subunit [Hordeum vulgare]

Seq. No. 416955

Seq. ID uC-osroM202007e05b1

Method BLASTX
NCBI GI g401322
BLAST score 178
E value 6.0e-13
Match length 76
% identity 55

NCBI Description VACUOLAR ATP SYNTHASE CATALYTIC SUBUNIT A (V-ATPASE 69 KD

SUBUNIT) >gi 167313 (L03186) vacuolar H+-ATPase catalytic

subunit [Gossypium hirsutum]

Seq. No. 416956

Seq. ID uC-osroM202007e06a1

Method BLASTX
NCBI GI g585957
BLAST score 508
E value 2.0e-51
Match length 138
% identity 67

NCBI Description PROTEIN TRANSPORT PROTEIN SEC61 ALPHA SUBUNIT

>gi_346439_pir__A44170 membrane-bound ribosome-associated
translocating polypeptide Sec61p - dog >gi_164070 (M96629)

homologue to sec61 [Canis familiaris]

```
416957
Seq. No.
                   uC-osroM202007e06b1
Seq. ID
                   BLASTX
Method
                   q585958
NCBI GI
BLAST score
                   357
                   5.0e-34
E value
                   119
Match length
                   58
% identity
                  PROTEIN TRANSPORT PROTEIN SEC61 ALPHA SUBUNIT
NCBI Description
                   >gi 1076193_pir__S51499 sec61 protein - Pyrenomonas salina
                   >gi_495263_emb_CAA54828_ (X77805) sec61 protein
[Pyrenomonas salina] >gi_1097096_prf__2113247A sec61 gene
                   [Pyrenomonas salina]
                   416958
Seq. No.
                   uC-osroM202007e07a1
Seq. ID
Method
                   BLASTX
                   q730456
NCBI GI
                   169
BLAST score
                   8.0e-12
E value
Match length
                   44
                   80
% identity
NCBI Description 40S RIBOSOMAL PROTEIN S19
                   416959
Seq. No.
Seq. ID
                   uC-osroM202007e07b1
                   BLASTX
Method
                   g730456
NCBI GI
                   654
BLAST score
                   1.0e-68
E value
Match length
                   133
                   92
% identity
NCBI Description 40S RIBOSOMAL PROTEIN S19
                   416960
Seq. No.
Seq. ID
                   uC-osroM202007e09a1
                   BLASTX
Method
                   q4097942
NCBI GI
BLAST score
                   435
                   6.0e-43
E value
Match length
                   83
% identity
NCBI Description (U72252) beta-1,3-glucanase precursor [Oryza sativa]
                   416961
Seq. No.
Seq. ID
                   uC-osroM202007e09b1
Method
                   BLASTX
NCBI GI
                   q485517
BLAST score
                   494
E value
                   6.0e-50
Match length
                   116
% identity
                   83
NCBI Description ADP, ATP carrier protein - rice
```

54534

416962

uC-osroM202007e12a1

Seq. No.

Seq. ID



Method BLASTX
NCBI GI g3914899
BLAST score 312
E value 1.0e-28
Match length 66
% identity 91

NCBI Description 40S RIBOSOMAL PROTEIN S4 >gi_2331301 (AF013487) ribosomal

protein S4 type I [Zea mays]

Seq. No. 416963

Seq. ID uC-osroM202007e12b1

Method BLASTX
NCBI GI g3914899
BLAST score 516
E value 1.0e-71
Match length 160
% identity 91

NCBI Description 40S RIBOSOMAL PROTEIN S4 >gi 2331301 (AF013487) ribosomal

protein S4 type I [Zea mays]

Seq. No. 416964

Seq. ID uC-osroM202007f01b1

Method BLASTN
NCBI GI g5006848
BLAST score 40
E value 6.0e-13
Match length 100
% identity 85

NCBI Description Oryza sativa homeodomain leucine zipper protein (hox2)

mRNA, partial cds

Seq. No. 416965

Seq. ID uC-osroM202007f02a1

Method BLASTN
NCBI GI g6006355
BLAST score 140
E value 6.0e-73
Match length 216
% identity 91

NCBI Description Oryza sativa genomic DNA, chromosome 6, clone:P0493C11

Seq. No. 416966

Seq. ID uC-osroM202007f03b1

Method BLASTX
NCBI GI g2589164
BLAST score 347
E value 1.0e-32
Match length 125
% identity 54

NCBI Description (D88452) aldehyde oxidase-2 [Zea mays]

Seq. No. 416967

Seq. ID uC-osroM202007f04b1

Method BLASTX
NCBI GI g2498040
BLAST score 186
E value 8.0e-14

Match length 81 49 % identity NCBI Description DNA-BINDING PROTEIN SMUBP-2 (IMMUNOGLOBULIN MU BINDING PROTEIN 2) (INSULIN II GENE ENHANCER-BINDING PROTEIN) (RIPE3B-BINDING COMPLEX 3B2 P110 SUBUNIT) (RIP-1) >gi 290919 (L15625) insulin II gene enhancer-binding protein [Mesocricetus auratus] 416968 Seq. No. Seq. ID uC-osroM202007f06b1 Method BLASTX g3687237 NCBI GI BLAST score 253 E value 1.0e-21 71 Match length 63 % identity (AC005169) putative Cys3His zinc-finger protein NCBI Description [Arabidopsis thaliana] 416969 Seq. No. Seq. ID uC-osroM202007f07a1 Method BLASTN NCBI GI g5006848 BLAST score 410 E value 0.0e + 00Match length 465 % identity 97 NCBI Description Oryza sativa homeodomain leucine zipper protein (hox2) mRNA, partial cds Seq. No. 416970 uC-osroM202007f07b1 Seq. ID Method BLASTN NCBI GI g5006848 BLAST score 115 E value 9.0e-58 Match length 115 100 % identity NCBI Description Oryza sativa homeodomain leucine zipper protein (hox2) mRNA, partial cds Seq. No. 416971 uC-osroM202007f09a1 Seq. ID Method BLASTN NCBI GI g20378 BLAST score 328 E value 0.0e+00373 Match length 97 % identity NCBI Description Oryza sativa mRNA for alpha 1 tubulin

Seq. No. 416972

Seq. ID uC-osroM202007f09b1

Method BLASTX
NCBI GI g2589162
BLAST score 340
E value 7.0e-32

```
Match length
                   145
% identity
                   50
NCBI Description
                  (D88451) aldehyde oxidase [Zea mays]
Seq. No.
                   416973
                   uC-osroM202007g01a1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3023817
BLAST score
                   426
                   1.0e-45
E value
Match length
                   144
% identity
                   70
NCBI Description
                  GLUCOSE-6-PHOSPHATE 1-DEHYDROGENASE, CHOLOROPLAST ISOFORM
                   PRECURSOR (G6PD) >gi 1480344 emb CAA67782 (X99405)
                   glucose-6-phosphate dehydrogenase [Nicotiana tabacum]
Seq. No.
                   416974
Seq. ID
                   uC-osroM202007g03b1
Method
                   BLASTX
NCBI GI
                   q4803836
BLAST score
                   669
                   2.0e-70
E value
Match length
                   163
% identity
                   80
NCBI Description
                  (AB026987) a dynamin-like protein ADL3 [Arabidopsis
                  thaliana]
Seq. No.
                   416975
Seq. ID
                   uC-osroM202007g05b1
Method
                  BLASTX
                  g2244749
NCBI GI
BLAST score
                   427
E value
                   4.0e-42
Match length
                   120
% identity
                   69
NCBI Description (Z97335) hydroxymethyltransferase [Arabidopsis thaliana]
Seq. No.
                  416976
Seq. ID
                  uC-osroM202007g07b1
                  BLASTX
Method
NCBI GI
                  q4510376
BLAST score
                   288
E value
                  1.0e-25
Match length
                  94
                   57
% identity
NCBI Description (AC007017) unknown protein [Arabidopsis thaliana]
Seq. No.
                  416977
```

Seq. ID uC-osroM202007g08a1

Method BLASTX
NCBI GI g3927829
BLAST score 225
E value 2.0e-18
Match length 42
% identity 86

NCBI Description (AC005727) putative zinc finger protein [Arabidopsis

thaliana]



Seq. No. 416978

Seq. ID uC-osroM202007g10a1

Method BLASTX
NCBI GI g5354158
BLAST score 202
E value 1.0e-15
Match length 58
% identity 55

NCBI Description (AF149841) digalactosyldiacylglycerol synthase [Arabidopsis

thaliana] >gi_5354160_gb_AAD42379.1_AF149842_1 (AF149842) digalactosyldiacylglycerol synthase [Arabidopsis thaliana]

>gi_6041825_gb_AAF02140.1_AC009918 12 (AC009918)

digalactosyldiacylglycerol synthase [Arabidopsis thaliana]

Seq. No. 416979

Seq. ID uC-osroM202007g10b1

Method BLASTX
NCBI GI g5354158
BLAST score 386
E value 2.0e-37
Match length 96
% identity 76

NCBI Description (AF149841) digalactosyldiacylglycerol synthase [Arabidopsis

thaliana] >gi_5354160_gb_AAD42379.1_AF149842_1 (AF149842) digalactosyldiacylglycerol synthase [Arabidopsis thaliana]

>gi_6041825_gb_AAF02140.1_AC009918 12 (AC009918)

digalactosyldiacylglycerol synthase [Arabidopsis thaliana]

Seq. No. 416980

Seq. ID uC-osroM202007g11b1

Method BLASTX
NCBI GI g2435519
BLAST score 357
E value 9.0e-34
Match length 108
% identity 65

NCBI Description (AF024504) similar to mouse MEM3 (GB:U47024 and S.

cerevisiae vacuolar sorting protein 35 (SW; P34110)

[Arabidopsis thaliana]

Seq. No. 416981

Seq. ID uC-osroM202007g12a1

Method BLASTX
NCBI GI g4646206
BLAST score 293
E value 2.0e-26
Match length 67
% identity 76

NCBI Description (AC007230) Contains similarity to gb D13630 KIAA0005 gene

from Homo sapiens. ESTs gb_T45345, gb_T21086, gb_R90360, gb T20468, gb_T45191 and gb_AI100459 come from this gene.

[Arabidopsis thaliana]

Seq. No. 416982

Seq. ID uC-osroM202007g12b1

Method BLASTX



NCBI GI g4646206 BLAST score 285 E value 2.0e-25 Match length 67 % identity 75

NCBI Description (AC007230) Contains similarity to gb_D13630 KIAA0005 gene

from Homo sapiens. ESTs gb_T45345, gb_T21086, gb_R90360, gb_T20468, gb_T45191 and gb_AI100459 come from this gene.

[Arabidopsis thaliana]

Seq. No. 416983

Seq. ID uC-osroM202007h01a1

Method BLASTN
NCBI GI g20280
BLAST score 335
E value 0.0e+00
Match length 351
% identity 99

NCBI Description Rice gene for phenylalanine ammonia-lyase (EC 4.3.1.5)

Seq. No. 416984

Seq. ID uC-osroM202007h01b1

Method BLASTX
NCBI GI g129591
BLAST score 188
E value 3.0e-14
Match length 89
% identity 51

NCBI Description PHENYLALANINE AMMONIA-LYASE >gi_295824_emb_CAA34226_

(X16099) phenylalanine ammonia-lyase [Oryza sativa]

Seq. No. 416985

Seq. ID uC-osroM202007h02a1

Method BLASTN
NCBI GI g5852077
BLAST score 122
E value 5.0e-62
Match length 207
% identity 93

NCBI Description Oryza sativa indica(GLA4) genomic DNA, chromosome 4, BAC

clone: b6015

Seq. No. 416986

Seq. ID uC-osroM202007h03a1

Method BLASTN
NCBI GI g20280
BLAST score 276
E value 1.0e-154
Match length 344
% identity 95

NCBI Description Rice gene for phenylalanine ammonia-lyase (EC 4.3.1.5)

Seq. No. 416987

Seq. ID uC-osroM202007h03b1

Method BLASTX NCBI GI g129591 BLAST score 362



E value 2.0e-34 Match length 94 77

NCBI Description PHENYLALANINE AMMONIA-LYASE >gi_295824_emb_CAA34226_ (X16099) phenylalanine ammonia-lyase [Oryza sativa]

Seq. No. 416988

Seq. ID uC-osroM202007h05b1

Method BLASTX
NCBI GI g4519673
BLAST score 478
E value 6.0e-48
Match length 112
% identity 73

NCBI Description (AB017694) WREBP-2 [Nicotiana tabacum]

Seq. No. 416989

Seq. ID uC-osroM202007h06a1

Method BLASTX
NCBI GI g5915839
BLAST score 405
E value 2.0e-39
Match length 122
% identity 57

NCBI Description CYTOCHROME P450 71D10 >gi_2739000_gb_AAB94588_ (AF022459)

CYP71D10p [Glycine max]

Seq. No. 416990

Seq. ID uC-osroM202007h06b1

Method BLASTX
NCBI GI g5915838
BLAST score 267
E value 3.0e-23
Match length 125
% identity 43

NCBI Description CYTOCHROME P450 71D9 (P450 CP3) >gi 3334661 emb CAA71514

(Y10490) putative cytochrome P450 [Glycine max]

Seq. No. 416991

Seq. ID uC-osroM202007h08b1

Method BLASTX
NCBI GI g1747296
BLAST score 223
E value 2.0e-29
Match length 111
% identity 68

NCBI Description (D45384) vacuolar H+-pyrophosphatase [Oryza sativa]

>gi 3298476 dbj BAA31524 (AB012766) ovp2 [Oryza sativa]

Seq. No. 416992

Seq. ID uC-osroM202007h09b1

Method BLASTX
NCBI GI g5051780
BLAST score 366
E value 6.0e-35
Match length 123
% identity 54

Seq. ID



```
NCBI Description (AL078637) putative protein [Arabidopsis thaliana]
                  416993
Seq. No.
                  uC-osroM202007h10b1
Seq. ID
                  BLASTX
Method
                  g4455199
NCBI GI
                  413
BLAST score
                  2.0e-40
E value
                  143
Match length
                   62
% identity
                  (AL035440) putative protein [Arabidopsis thaliana]
NCBI Description
                   416994
Seq. No.
                  uC-osroM202007h12a1
Seq. ID
Method
                  BLASTN
                  g6016845
NCBI GI
                  213
BLAST score
                   1.0e-116
E value
                  293
Match length
                   93
% identity
NCBI Description Oryza sativa genomic DNA, chromosome 1, clone:P0711E10
                   416995
Seq. No.
                  uC-osroM202008a02a1
Seq. ID
                  BLASTX
Method
                   g6006853
NCBI GI
                   370
BLAST score
E value
                   3.0e - 35
                   108
Match length
                   66
% identity
NCBI Description (AC009540) unknown protein [Arabidopsis thaliana]
                   416996
Seq. No.
                   uC-osroM202008a04b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   q118390
BLAST score
                   179
                   9.0e-23
E value
Match length
                   82
                   73
% identity
NCBI Description PYRUVATE DECARBOXYLASE ISOZYME 1 (PDC)
                   >gi_2144526_pir__DCZMP pyruvate decarboxylase (EC 4.1.1.1)
                   - maize >gi_22395_emb_CAA42120_ (X59546) pyruvate
                   decarboxylase [Zea mays]
                   416997
Seq. No.
Seq. ID
                   uC-osroM202008a05a1
Method
                   BLASTX
NCBI GI
                   q3746581
BLAST score
                   250
E value
                   2.0e-21
Match length
                   50
% identity
NCBI Description (AF062403) glutathione S-transferase II [Oryza sativa]
Seq. No.
                   416998
```

uC-osroM202008a05b1



```
BLASTX
Method
NCBI GI
                  g3746581
                  332
BLAST score
E value
                  5.0e-31
Match length
                  61
                  98
% identity
NCBI Description
                 (AF062403) glutathione S-transferase II [Oryza sativa]
                  416999
Seq. No.
                  uC-osroM202008a06b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4926827
                  214
BLAST score
E value
                  3.0e-17
                  62
Match length
% identity
                  71
NCBI Description (AC004135) T17H7.12 [Arabidopsis thaliana]
                  417000
Seq. No.
                  uC-osroM202008a09a1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1076866
BLAST score
                  454
E value
                  4.0e-45
Match length
                  118
                  64
% identity
NCBI Description C-14 sterol reductase - fission yeast (Schizosaccharomyces
                  pombe) >gi_703464 (L36039) C-14 sterol reductase
                  [Schizosaccharomyces pombe] >gi_3133112_emb_CAA19037
                   (AL023554) sterol c-14 reductase. [Schizosaccharomyces
                  pombe]
                  417001
Seq. No.
Seq. ID
                  uC-osroM202008b01a1
Method
                  BLASTX
NCBI GI
                  g2129948
BLAST score
                  273
E value
                   6.0e-24
Match length
                  58
                  93
% identity
NCBI Description inorganic pyrophosphatase (EC 3.6.1.1) (clone TVP31) -
                  common tobacco
Seq. No.
                   417002
                  uC-osroM202008b01b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1747296
BLAST score
                  349
E value
                  1.0e-43
```

Match length 102 % identity 92

NCBI Description (D45384) vacuolar H+-pyrophosphatase [Oryza sativa] >qi 3298476 dbj BAA31524 (AB012766) ovp2 [Oryza sativa]

417003 Seq. No.

Seq. ID uC-osroM202008b02a1

BLASTX Method



NCBI GI g4982479 BLAST score 238 E value 2.0e-28 Match length 110 % identity 60

NCBI Description (AF069441) predicted protein of unknown function

[Arabidopsis thaliana]

Seq. No. 417004

Seq. ID uC-osroM202008b02b1

Method BLASTX
NCBI GI g3157932
BLAST score 244
E value 2.0e-35
Match length 114
% identity 74

NCBI Description (AC002131) Similar to hypothetical protein HYP1 gb_Z97338

from A. thaliana. [Arabidopsis thaliana]

Seq. No. 417005

Seq. ID uC-osroM202008b03a1

Method BLASTX
NCBI GI g4033424
BLAST score 380
E value 2.0e-36
Match length 75
% identity 97

NCBI Description SOLUBLE INORGANIC PYROPHOSPHATASE (PYROPHOSPHATE

PHOSPHO-HYDROLASE) (PPASE) >gi_2668746 (AF034947) inorganic

pyrophosphatase [Zea mays]

Seq. No. 417006

Seq. ID uC-osroM202008b03b1

Method BLASTX
NCBI GI 94033424
BLAST score 315
E value 6.0e-32
Match length 82
% identity 91

NCBI Description SOLUBLE INORGANIC PYROPHOSPHATASE (PYROPHOSPHATE

PHOSPHO-HYDROLASE) (PPASE) >gi_2668746 (AF034947) inorganic

pyrophosphatase [Zea mays]

Seq. No. 417007

Seq. ID uC-osroM202008b04a1

Method BLASTX
NCBI GI g135462
BLAST score 271
E value 9.0e-24
Match length 59
% identity 88

NCBI Description TUBULIN BETA-2 CHAIN >gi 170062 (M21297) S-beta-1 tubulin

[Glycine max]

Seq. No. 417008

Seq. ID uC-osroM202008b04b1

Method BLASTX



NCBI GI g135485 BLAST score 308 E value 3.0e-47 Match length 112 % identity 75

NCBI Description TUBULIN BETA CHAIN >gi_627031_pir__A54515 tubulin beta

chain - Leishmania mexicana amazonensis >gi 159416 (M23441)

beta tubulin [Leishmania mexicana]

Seq. No. 417009

Seq. ID uC-osroM202008b05b1

Method BLASTX
NCBI GI g2244805
BLAST score 152
E value 6.0e-10
Match length 70
% identity 44

NCBI Description (Z97336) hypothetical protein [Arabidopsis thaliana]

Seq. No. 417010

Seq. ID uC-osroM202008b09b1

Method BLASTX
NCBI GI g1657948
BLAST score 301
E value 2.0e-27
Match length 71
% identity 86

NCBI Description (U73466) MipC [Mesembryanthemum crystallinum]

Seq. No. 417011

Seq. ID uC-osroM202008b10b1

Method BLASTX
NCBI GI g4512684
BLAST score 285
E value 1.0e-31
Match length 92
% identity 79

NCBI Description (AC006931) unknown protein [Arabidopsis thaliana]

>gi 4559324 gb AAD22986.1 AC007087 5 (AC007087) unknown

protein [Arabidopsis thaliana]

Seq. No. 417012

Seq. ID uC-osroM202008c02a1

Method BLASTX
NCBI GI g3786005
BLAST score 235
E value 2.0e-19
Match length 52
% identity 81

NCBI Description (AC005499) putative phosphoethanolamine cytidylyltransferase [Arabidopsis thaliana]

Seq. No. 417013

Seq. ID uC-osroM202008c04b1

Method BLASTX
NCBI GI g1495251
BLAST score 270

```
Match length
                  113
                  74
% identity
                  (Z70314) heat-shock protein [Arabidopsis thaliana]
NCBI Description
                  417014
Seq. No.
                  uC-osroM202008c05a1
Seq. ID
                  BLASTN
Method
NCBI GI
                  g4730885
BLAST score
                  286
                  1.0e-160
E value
Match length
                  416
                   91
% identity
                  Oryza sativa mRNA for alanine aminotransferase, complete
NCBI Description
                  417015
Seq. No.
                  uC-osroM202008c05b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4730884
BLAST score
                  368
                  1.0e-48
E value
                  114
Match length
                   91
% identity
                  (AB007404) alanine aminotransferase [Oryza sativa]
NCBI Description
                  >gi_4730886_dbj_BAA77261.1_ (AB007405) alanine
                  aminotransferase [Oryza sativa]
                   417016
Seq. No.
                   uC-osroM202008c06b1
Seq. ID
Method
                   BLASTX
                   g5453379
NCBI GI
                   241
BLAST score
                   2.0e-20
E value
                   73
Match length
% identity
                   63
NCBI Description
                   (AF155124) bacterial-induced peroxidase precursor
                   [Gossypium hirsutum]
Seq. No.
                   417017
Seq. ID
                   uC-osroM202008c07b1
Method
                   BLASTX
NCBI GI
                   g4760700
BLAST score
                   247
E value
                   4.0e-21
Match length
                   71
% identity
                  (AB024437) peroxidase 1 [Scutellaria baicalensis]
NCBI Description
                   417018
Seq. No.
                   uC-osroM202008c08a1
Seq. ID
Method
                  BLASTX
NCBI GI
                   g4581156
BLAST score
                   397
E value
                   1.0e-38
Match length
                   87
                   89
% identity
                                       54545
```

5.0e-39

E value



NCBI Description (AC006919) putative pyruvate kinase [Arabidopsis thaliana] 417019 Seq. No. uC-osroM202008c08b1 Seq. ID Method BLASTX g4581156 NCBI GI BLAST score 262 8.0e-26 E value Match length 109 % identity 68 NCBI Description (AC006919) putative pyruvate kinase [Arabidopsis thaliana] Seq. No. 417020 uC-osroM202008c11b1 Seq. ID Method BLASTX g6056375 NCBI GI BLAST score 195 E value 5.0e-15 70 Match length 54 % identity NCBI Description (AC009894) Similar to serine/threonine kinases [Arabidopsis thaliana] 417021 Seq. No. Seq. ID uC-osroM202008c12a1 Method BLASTX g3763933 NCBI GI BLAST score 204 E value 8.0e-16 Match length 67 % identity 57 NCBI Description (AC004450) unknown protein [Arabidopsis thaliana] 417022 Seq. No. uC-osroM202008d03b1 Seq. ID Method BLASTX NCBI GI g1825687 BLAST score 145 E value 4.0e-09 Match length 71 % identity 38 NCBI Description (U88179) similar to human prostrate-specific membrane antigen (PSM) (SP:Q04609) [Caenorhabditis elegans]

417023 Seq. No.

Seq. ID uC-osroM202008d05b1

Method BLASTX NCBI GI g6049841 BLAST score 272 E value 6.0e-37 Match length 112 % identity 71

NCBI Description (AF190728) asparagine synthetase [Helianthus annuus]

Seq. No. 417024

Seq. ID uC-osroM202008d08b1

Method BLASTX NCBI GI g3341697 BLAST score 147 2.0e-09 E value 37 Match length 70 % identity (AC003672) hypothetical protein [Arabidopsis thaliana] NCBI Description 417025 Seq. No. uC-osroM202008d09a1 Seq. ID BLASTX Method NCBI GI g1136122 518 BLAST score 1.0e-52 E value Match length 101 98 % identity NCBI Description (X91807) alfa-tubulin [Oryza sativa] Seq. No. 417026 uC-osroM202008d09b1 Seq. ID BLASTX Method NCBI GI g1136122 BLAST score 367 1.0e-42 E value 92 Match length 95 % identity NCBI Description (X91807) alfa-tubulin [Oryza sativa] Seq. No. 417027 uC-osroM202008d10a1 Seq. ID Method BLASTX NCBI GI g3176686 BLAST score 144 E value 7.0e-09 Match length 40 70 % identity NCBI Description (AC003671) Similar to high affinity potassium transporter, HAK1 protein gb_U22945 from Schwanniomyces occidentalis. [Arabidopsis thaliana] 417028 Seq. No. uC-osroM202008d11b1 Seq. ID Method BLASTX NCBI GI q5734723 BLAST score 147 E value 2.0e-09 Match length 72 % identity 40 NCBI Description (AC007259) receptor-like protein kinase [Arabidopsis thaliana]

Seq. No. 417029

Seq. ID uC-osroM202008e01a1

Method BLASTX
NCBI GI g1518540
BLAST score 777
E value 5.0e-83
Match length 166

% identity

```
(U53418) UDP-glucose dehydrogenase [Glycine max]
NCBI Description
                  417030
Seq. No.
                  uC-osroM202008e01b1
Seq. ID
Method
                  BLASTX
                  g1518540
NCBI GI
BLAST score
                  368
                  2.0e-35
E value
                  76
Match length
% identity
                   87
                 (U53418) UDP-glucose dehydrogenase [Glycine max]
NCBI Description
                  417031
Seq. No.
                  uC-osroM202008e02b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q401140
BLAST score
                   361
                  2.0e-34
E value
Match length
                  73
                   100
% identity
                  SUCROSE SYNTHASE 2 (SUCROSE-UDP GLUCOSYLTRANSFERASE 2)
NCBI Description
                  >gi_20095_emb_CAA41774_ (X59046) sucrose-UDP
                   glucosyltransferase (isoenzyme 2) [Oryza sativa]
                   >gi 1587662 prf 2207194A sucrose synthase:ISOTYPE=2 [Oryza
                   sativa]
                   417032
Seq. No.
                  uC-osroM202008e04a1
Seq. ID
                  BLASTX
Method
NCBI GI
                   g3851005
BLAST score
                   215
                   4.0e-17
E value
Match length
                   60
                   72
% identity
NCBI Description
                  (AF069911) pyruvate dehydrogenase E1 alpha subunit [Zea
                   mays]
                   417033
Seq. No.
                   uC-osroM202008e04b1
Seq. ID
                   BLASTX
Method
NCBI GI
                   g3851005
BLAST score
                   337
E value
                   4.0e-32
Match length
                   84
% identity
                  (AF069911) pyruvate dehydrogenase E1 alpha subunit [Zea
NCBI Description
                   mays]
                   417034
Seq. No.
                   uC-osroM202008e05b1
Seq. ID
Method
                   BLASTN
NCBI GI
                   g5106766
BLAST score
                   35
E value
                   4.0e-10
                   59
Match length
% identity
                   90
```

54548



NCBI Description Arabidopsis thaliana BAC F17I23

Seq. No. 417035

Seq. ID uC-osroM202008e06b1

Method BLASTX
NCBI GI g5453379
BLAST score 238
E value 4.0e-20
Match length 75
% identity 63

NCBI Description (AF155124) bacterial-induced peroxidase precursor

[Gossypium hirsutum]

Seq. No. 417036

Seq. ID uC-osroM202008e08a1

Method BLASTN
NCBI GI g6069643
BLAST score 34
E value 2.0e-09

E value 2.0 Match length 54 % identity 91

NCBI Description Oryza sativa genomic DNA, chromosome 6, clone:P0514G12

Seq. No. 417037

Seq. ID uC-osroM202008e08b1

Method BLASTX
NCBI GI g2459424
BLAST score 178
E value 5.0e-13
Match length 64
% identity 59

NCBI Description (AC002332) unknown protein [Arabidopsis thaliana]

Seq. No. 417038

Seq. ID uC-osroM202008e09a1

Method BLASTN
NCBI GI g2624327
BLAST score 271
E value 1.0e-151
Match length 387
% identity 94

NCBI Description Oryza sativa mRNA for glycine rich RNA-binding protein 2

(OsGRP2)

Seq. No. 417039

Seq. ID uC-osroM202008e09b1

Method BLASTN
NCBI GI g2624327
BLAST score 182
E value 6.0e-98
Match length 285
% identity 92

NCBI Description Oryza sativa mRNA for glycine rich RNA-binding protein 2

(OsGRP2)

Seq. No. 417040

Seq. ID uC-osroM202008e10a1



Method BLASTX
NCBI GI g3879734
BLAST score 186
E value 1.0e-13
Match length 155
% identity 31

NCBI Description (Z93388) predicted using Genefinder; cDNA EST EMBL:D70912 comes from this gene; cDNA EST EMBL:D73452 comes from this gene; cDNA EST EMBL:D71574 comes from this gene; cDNA EST

EMBL:D74229 comes from this gene; cDNA EST EMBL:D7

Seq. No. 417041

Seq. ID uC-osroM202008e10b1

Method BLASTN
NCBI GI g6002791
BLAST score 144
E value 3.0e-75
Match length 237
% identity 91

NCBI Description Oryza sativa predicted protein gene, complete cds

Seq. No. 417042

Seq. ID uC-osroM202008e12a1

Method BLASTX
NCBI GI g1129134
BLAST score 344
E value 3.0e-32

Match length 77 % identity 81

NCBI Description (X94105) old yellow enzyme NADPH dehydrogenase [Chenopodium

rubrum]

Seq. No. 417043

Seq. ID uC-osroM202008e12b1

Method BLASTX
NCBI GI g1854443
BLAST score 293
E value 2.0e-26
Match length 70
% identity 77

NCBI Description (D83970) CPRD8 protein [Vigna unguiculata]

Seq. No. 417044

Seq. ID uC-osroM202008f02a1

Method BLASTX
NCBI GI g1871192
BLAST score 253
E value 2.0e-21
Match length 133
% identity 44

NCBI Description (U90439) Cys3His zinc finger protein isolog [Arabidopsis

thaliana]

Seq. No. 417045

Seq. ID uC-osroM202008f07a1

Method BLASTX NCBI GI g3128168



BLAST score 157
E value 2.0e-10
Match length 56
% identity 48

NCBI Description (AC004521) putative carboxyl-terminal peptidase

[Arabidopsis thaliana]

Seq. No. 417046

Seq. ID uC-osroM202008f08a1

Method BLASTX
NCBI GI g1370603
BLAST score 455
E value 3.0e-45
Match length 94
% identity 94

NCBI Description (X98245) annexin p35 [Zea mays]

Seq. No. 417047

Seq. ID uC-osroM202008f08b1

Method BLASTX
NCBI GI g1370603
BLAST score 200
E value 1.0e-25
Match length 102
% identity 62

NCBI Description (X98245) annexin p35 [Zea mays]

Seq. No. 417048

Seq. ID uC-osroM202008f10b1

Method BLASTN
NCBI GI g2443456
BLAST score 94
E value 2.0e-45
Match length 126

% identity 94

NCBI Description Oryza sativa ethylene responsive element binding protein

(Os-EREBP1) mRNA, complete cds

Seq. No. 417049

Seq. ID uC-osroM202008f11b1

Method BLASTX
NCBI GI g4150965
BLAST score 302
E value 6.0e-42
Match length 108
% identity 81

NCBI Description (AJ011096) glutamate dehydrogenase [Asparagus officinalis]

Seq. No. 417050

Seq. ID uC-osroM202008f12b1

Method BLASTN
NCBI GI g2443456
BLAST score 37
E value 3.0e-11
Match length 37
% identity 100

NCBI Description Oryza sativa ethylene responsive element binding protein

E value

Match length



(Os-EREBP1) mRNA, complete cds

Seq. No. 417051 Seq. ID uC-osroM202008g01b1 BLASTN Method NCBI GI q2224914 BLAST score 71 E value 1.0e-31 123 Match length 89 % identity NCBI Description Oryza sativa beta-expansin mRNA, complete cds 417052 Seq. No. uC-osroM202008g03b1 Seq. ID Method BLASTX g1657621 NCBI GI BLAST score 172 E value 2.0e-12 51 Match length 65 % identity NCBI Description (U72505) G6p [Arabidopsis thaliana] >gi 3068711 (AF049236) putative acyl-coA dehydrogenase [Arabidopsis thaliana] >gi_5478795_dbj_BAA82478.1_ (AB017643) Short-chain acyl CoA oxidase [Arabidopsis thaliana] Seq. No. 417053 Seq. ID uC-osroM202008g04a1 Method BLASTX NCBI GI q3550549 BLAST score 245 1.0e-20 E value Match length 48 98 % identity NCBI Description (AJ004965) cytosolic pyruvate orthophosphate dikinase [Oryza sativa subsp. indica] Seq. No. 417054 uC-osroM202008g04b1 Seq. ID Method BLASTX g3550549 NCBI GI BLAST score 200 E value 2.0e-47 Match length 112 % identity (AJ004965) cytosolic pyruvate orthophosphate dikinase NCBI Description [Oryza sativa subsp. indica] Seq. No. 417055 Seq. ID uC-osroM202008g06b1 Method BLASTX NCBI GI q3421123 BLAST score 231

% identity 66
NCBI Description (AF043538) 20S proteasome beta subunit PBG1 [Arabidopsis thaliana]

3.0e-19

64

Seq. ID

```
Seq. No.
                  417056
Seq. ID
                  uC-osroM202008g07b1
Method
                  BLASTX
NCBI GI
                  a5059025
BLAST score
                  333
E value
                  3.0e-31
Match length
                  73
                  93
% identity
NCBI Description
                  (AF110382) 3-hydroxy-3-methylglutaryl-coenzyme A reductase
                  [Oryza sativa]
Seq. No.
                  417057
                  uC-osroM202008g10a1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3046815
BLAST score
                  280
E value
                  7.0e-25
                  137
Match length
                  44
% identity
NCBI Description
                  (AL021687) cytochrome P450 [Arabidopsis thaliana]
                  417058
Seq. No.
                  uC-osroM202008g11a1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g439879
BLAST score
                  147
                  3.0e-09
E value
Match length
                  37
                  70
% identity
NCBI Description
                  (L15194) [Golden delicious apple fruit expressed mRNA,
                  complete cds.], gene product [Malus domestica]
                  417059
Seq. No.
                  uC-osroM202008h01b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3482967
BLAST score
                  167
E value
                  1.0e-11
Match length
                  34
% identity
                  91
NCBI Description
                  (AL031369) Protein phosphatase 2C-like protein [Arabidopsis
                  thaliana] >gi_4559345_gb_AAD23006.1_AC006585_1 (AC006585)
                  protein phosphatase 2C [Arabidopsis thaliana]
Seq. No.
                  417060
Seq. ID
                  uC-osroM202008h06a1
Method
                  BLASTX
NCBI GI
                  g4325369
BLAST score
                  460
E value
                  4.0e-47
Match length
                  120
                  73
% identity
                 (AF128396) T3H13.3 gene product [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  417061
```

uC-osroM202008h06b1

Match length

119

```
Method
                  BLASTX
NCBI GI
                  q3759184
                  179
BLAST score
                  4.0e-13
E value
Match length
                  68
                  46
% identity
NCBI Description (AB018441) phi-1 [Nicotiana tabacum]
                  417062
Seq. No.
                  uC-osroM202008h08b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g5360721
BLAST score
                  230
                  4.0e-19
E value
                  86
Match length
% identity
                  52
NCBI Description (AB023385) acid phosphatase [Lupinus albus]
                  417063
Seq. No.
                  uC-osroM202008h09b1
Seq. ID
Method
                  BLASTN
                  g218162
NCBI GI
                  108
BLAST score
                  9.0e-54
E value
Match length
                  117
% identity
                  98
NCBI Description Rice mRNA for ferredoxin-NADP+ reductase, complete cds
                  417064
Seq. No.
                  uC-osroM202008h12a1
Seq. ID
Method
                  BLASTX
                  g129591
NCBI GI
BLAST score
                  277
E value
                  2.0e-24
Match length
                  56
                  89
% identity
NCBI Description PHENYLALANINE AMMONIA-LYASE >gi 295824 emb CAA34226
                  (X16099) phenylalanine ammonia-lyase [Oryza sativa]
                  417065
Seq. No.
Seq. ID
                  uC-osroM202008h12b1
Method
                  BLASTX
NCBI GI
                  g129591
BLAST score
                  261
E value
                   1.0e-29
Match length
                  94
% identity
                  76
NCBI Description PHENYLALANINE AMMONIA-LYASE > gi 295824 emb CAA34226
                   (X16099) phenylalanine ammonia-lyase [Oryza sativa]
                   417066
Seq. No.
                  uC-osroM202010a03a1
Seq. ID
                  BLASTN
Method
NCBI GI
                  g5679685
BLAST score
                  75
E value
                   5.0e - 34
```

54554



% identity NCBI Description Oryza sativa RPA gene for protein phosphatase 2A A subunit, exons 1-12 417067 Seq. No. uC-osroM202010a08a1 Seq. ID Method BLASTN NCBI GI g5679685 BLAST score 293 1.0e-164 E value 301 Match length % identity 99 NCBI Description Oryza sativa RPA gene for protein phosphatase 2A A subunit, exons 1-12417068 Seq. No. uC-osroM202010a10a1 Seq. ID Method BLASTN NCBI GI q5732700 BLAST score 41 E value 1.0e-13 Match length 77 % identity 88 NCBI Description Secale cereale thioredoxin-like protein (Trx) mRNA, complete cds Seq. No. 417069 Seq. ID uC-osroM202010a10b1 Method BLASTX g1086147 NCBI GI BLAST score 386 E value 1.0e-37 Match length 130 67 % identity NCBI Description protein S2 - Phalaris coerulescens Seq. No. 417070 uC-osroM202010a11b1 Seq. ID Method BLASTX q1750376 NCBI GI BLAST score 158 E value 1.0e-10 Match length 33 % identity (U80808) ubiquitin activating enzyme [Arabidopsis thaliana] NCBI Description >gi 3150409 (AC004165) ubiquitin activating enzyme (UBA1) [Arabidopsis thaliana] Seq. No. 417071 uC-osroM202010a12b1 Seq. ID Method BLASTX NCBI GI q4506221 BLAST score 313

Method BLASTX
NCBI GI 94506221
BLAST score 313
E value 1.0e-28
Match length 132
% identity 49

NCBI Description proteasome (prosome, macropain) 26S subunit, non-ATPase, 12

>gi_1945611_dbj_BAA19749_ (AB003103) 26S proteasome subunit p55 [Homo sapiens]

Seq. No. 417072

Seq. ID uC-osroM202010b02a1

Method BLASTN
NCBI GI g2655290
BLAST score 112
E value 5.0e-56
Match length 132
% identity 96

NCBI Description Oryza sativa germin-like protein 4 (GER4) mRNA, complete

cds

Seq. No. 417073

Seq. ID uC-osroM202010b06a1

Method BLASTX
NCBI GI g730362
BLAST score 143
E value 7.0e-09
Match length 62

% identity 44

NCBI Description PHOSPHOENOLPYRUVATE CARBOXYKINASE [ATP]

Seq. No. 417074

Seq. ID uC-osroM202010b08a1

Method BLASTX
NCBI GI g1843440
BLAST score 169
E value 4.0e-12
Match length 95
% identity 38

NCBI Description (Z70521) unknown [Cucumis melo]

Seq. No. 417075

Seq. ID uC-osroM202010b12a1

Method BLASTX
NCBI GI g5702186
BLAST score 250
E value 3.0e-21
Match length 62
% identity 81

NCBI Description (AF106085) 4-coumarate: CoA ligase 2 [Arabidopsis thaliana]

>gi_5702188_gb_AAD47193.1_AF106086_1 (AF106086)
4-coumarate:CoA ligase 2 [Arabidopsis thaliana]

Seq. No. 417076

Seq. ID uC-osroM202010b12b1

Method BLASTX
NCBI GI g893294
BLAST score 262
E value 9.0e-23
Match length 116
% identity 46

NCBI Description (L43362) 4-coumarate:CoA ligase isoform 2 [Oryza sativa]

Seq. No. 417077

```
uC-osroM202010c02a1
Seq. ID
Method
                  BLASTN
                  g3641660
NCBI GI
BLAST score
                  143
                  7.0e-75
E value
Match length
                  151
                  99
% identity
NCBI Description Oryza sativa Nrt2 mRNA for high affinity nitrate
                  transporter, complete cds
                  417078
Seq. No.
                  uC-osroM202010c03a1
Seq. ID
                  BLASTX
Method
                  q4678924
NCBI GI
                  465
BLAST score
                  2.0e-46
E value
Match length
                  132
% identity
                  73
                 (AL049711) putative protein [Arabidopsis thaliana]
NCBI Description
                  417079
Seq. No.
                  uC-osroM202010c05b1
Seq. ID
Method
                  BLASTX
                  g4455330
NCBI GI
                  159
BLAST score
                  9.0e-11
E value
Match length
                  57
% identity
                  44
                 (AL035525) putative protein [Arabidopsis thaliana]
NCBI Description
                  417080
Seq. No.
                  uC-osroM202010c06b1
Seq. ID
                  BLASTN
Method
                  g6006355
NCBI GI
                  228
BLAST score
                  1.0e-125
E value
Match length
                  332
% identity
                  92
NCBI Description Oryza sativa genomic DNA, chromosome 6, clone:P0493C11
                  417081
Seq. No.
Seq. ID
                  uC-osroM202010c11a1
Method
                  BLASTX
NCBI GI
                  g4689474
                  398
BLAST score
                  1.0e-38
E value
Match length
                  99
% identity
                  74
NCBI Description (AC007213) unknown protein [Arabidopsis thaliana]
                  417082
Seq. No.
                  uC-osroM202010c11b1
Seq. ID
```

Method BLASTX
NCBI GI g4586246
BLAST score 332
E value 8.0e-31
Match length 84



```
% identity
NCBI Description
                  (AL049640) putative protein [Arabidopsis thaliana]
                   417083
Seq. No.
Seq. ID
                   uC-osroM202010c12a1
Method
                   BLASTX
                  g4586246
NCBI GI
BLAST score
                   469
                   6.0e-47
E value
Match length
                   111
                   75
% identity
                  (AL049640) putative protein [Arabidopsis thaliana]
NCBI Description
                   417084
Seq. No.
Seq. ID
                  uC-osroM202010c12b1
Method
                  BLASTX
                  g4689474
NCBI GI
BLAST score
                   319
E value
                   3.0e-29
Match length
                  79
% identity
                   70
NCBI Description (AC007213) unknown protein [Arabidopsis thaliana]
                   417085
Seq. No.
Seq. ID
                  uC-osroM202010d01a1
Method
                  BLASTX
                  g4867803
NCBI GI
BLAST score
                   231
E value
                   4.0e-19
Match length
                   71
% identity
NCBI Description (AJ133000) phospholipase D2 [Craterostigma plantagineum]
                   417086
Seq. No.
Seq. ID
                  uC-osroM202010d01b1
Method
                  BLASTX
NCBI GI
                   q3914365
BLAST score
                   231
E value
                   3.0e-19
Match length
                   84
% identity
                   60
NCBI Description
                  PHOSPHOLIPASE D 2 PRECURSOR (PLD 2) (CHOLINE PHOSPHATASE 2)
                   (PHOSPHATIDYLCHOLINE-HYDROLYZING PHOSPHOLIPASE D 2)
                  >gi_1902901_dbj_BAA19466_ (AB001919) phospholipase D [Oryza
                   sativa]
Seq. No.
                   417087
Seq. ID
                  uC-osroM202010d02a1
Method
                  BLASTX
NCBI GI
                  g1136122
BLAST score
                  242
E value
                  2.0e-20
                  54
Match length
                  87
% identity
```

Seq. No. 417088

NCBI Description

(X91807) alfa-tubulin [Oryza sativa]

```
uC-osroM202010d02b1
Seq. ID
Method
                  BLASTX
                  q267069
NCBI GI
BLAST score
                  330
                  8.0e-32
E value
                  75
Match length
                  83
% identity
                  TUBULIN ALPHA-2/ALPHA-4 CHAIN >gi_320183_pir__JQ1594
NCBI Description
                  tubulin alpha chain - Arabidopsis thaliana >gi_166914
                  (M84696) apha-2 tubulin [Arabidopsis thaliana] >gi 166916
                   (M84697) alpha-4 tubulin [Arabidopsis thaliana]
Seq. No.
                  417089
                  uC-osroM202010d03a1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q6016736
BLAST score
                  159
                  1.0e-10
E value
Match length
                  45
                  60
% identity
                 (AC009325) unknown protein [Arabidopsis thaliana]
NCBI Description
                  417090
Seq. No.
                  uC-osroM202010d04a1
Seq. ID
Method
                  BLASTN
NCBI GI
                  q169819
                  100
BLAST score
                  4.0e-49
E value
                  195
Match length
                  89
% identity
NCBI Description
                  Rice gene encoding three ribosomal RNA's: the 17S, 3' end;
                  5.8S, complete; 25S, 5' end
                  417091
Seq. No.
                  uC-osroM202010d05b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q5596996
BLAST score
                  154
E value
                  6.0e-10
Match length
                  83
                  43
% identity
NCBI Description
                  (Y14600) putative protein serine /threonine kinase [Sorghum
                  bicolor]
                   417092
Seq. No.
Seq. ID
                  uC-osroM202010d06b1
Method
                  BLASTX
NCBI GI
                  g4240305
                  242
BLAST score
                  3.0e-20
E value
                  166
Match length
% identity
                  36
```

Seq. No. 417093

Seq. ID uC-osroM202010d07a1

Method BLASTX

NCBI Description (AB020715) KIAA0908 protein [Homo sapiens]

% identity

35

```
q1346804
NCBI GI
                  633
BLAST score
                  3.0e-66
E value
                  133
Match length
% identity
                  85
                 PROFILIN 2 >gi 1008443 emb CAA61944 (X89826) profilin
NCBI Description
                  [Triticum aestīvum]
                  417094
Seq. No.
                  uC-osroM202010d08a1
Seq. ID
                  {\tt BLASTX}
Method
                  g3024363
NCBI GI
                  390
BLAST score
                  9.0e-38
E value
                  95
Match length
                  77
% identity
NCBI Description PHENYLALANINE AMMONIA-LYASE >gi_1483610_emb_CAA68036
                   (X99705) phenylalanine ammonia-lyase [Triticum aestivum]
                  417095
Seq. No.
                  uC-osroM202010d08b1
Seq. ID
                  BLASTX
Method
                  g478740
NCBI GI
                   315
BLAST score
                   5.0e-29
E value
Match length
                   68
                   93
% identity
NCBI Description phenylalanine ammonia-lyase (EC 4.1.3.5) - rice
                   417096
Seq. No.
                   uC-osroM202010d09a1
Seq. ID
Method
                  BLASTX
                   g4115377
NCBI GI
BLAST score
                   226
                   2.0e-18
E value
Match length
                   51
% identity
NCBI Description (AC005967) unknown protein [Arabidopsis thaliana]
                   417097
Seq. No.
                   uC-osroM202010d09b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   q4115377
                   224
BLAST score
                   7.0e-19
E value
                   57
Match length
% identity
                   75
NCBI Description (AC005967) unknown protein [Arabidopsis thaliana]
                   417098
Seq. No.
                   uC-osroM202010d10b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   q629669
BLAST score
                   147
E value
                   3.0e-09
Match length
                   103
```

54560



NCBI Description hypothetical protein - tomato

Seq. No. 417099

Seq. ID uC-osroM202010e08a1

Method BLASTX
NCBI GI g2129578
BLAST score 165
E value 2.0e-11
Match length 38
% identity 82

NCBI Description dTDP-glucose 4-6-dehydratases homolog - Arabidopsis thaliana >gi_928932_emb_CAA89205_ (Z49239) homolog of dTDP-glucose 4-6-dehydratases [Arabidopsis thaliana]

>gi_1585435_prf__2124427B diamide resistance gene

[Arabidopsis thaliana]

Seq. No. 417100

Seq. ID uC-osroM202010e11a1

Method BLASTX
NCBI GI g3913426
BLAST score 246
E value 7.0e-21
Match length 46
% identity 98

NCBI Description S=ADENOSYLMETHIONINE DECARBOXYLASE PROENZYME (ADOMETDC)

(SAMDC) >gi_1532048_emb_CAA69074_ (Y07766)

S-adenosylmethionine decarboxylase [Oryza sativa]

Seq. No. 417101

Seq. ID uC-osroM202010e11b1

Method BLASTX
NCBI GI g2129921
BLAST score 171
E value 5.0e-12
Match length 51
% identity 65

NCBI Description hypothetical protein 1 - Madagascar periwinkle >gi_758694

(U12573) putative [Catharanthus roseus]

Seq. No. 417102

Seq. ID uC-osroM202010e12a1

Method BLASTN
NCBI GI g1532047
BLAST score 142
E value 7.0e-74
Match length 273
% identity 95

NCBI Description O.sativa mRNA for S-adenosylmethionine decarboxylase

Seq. No. 417103

Seq. ID uC-osroM202010f01b1

Method BLASTN
NCBI GI g6006355
BLAST score 124
E value 2.0e-63
Match length 152
% identity 95

54561

```
NCBI Description Oryza sativa genomic DNA, chromosome 6, clone:P0493C11
                  417104
Seq. No.
                  uC-osroM202010f05a1
Seq. ID
                  BLASTX
Method
NCBI GI
                  g4336205
BLAST score
                  187
E value
                  5.0e-14
                  41
Match length
% identity
                  85
NCBI Description (AF077372) cytochrome b5 reductase [Zea mays]
Seq. No.
                  417105
Seq. ID
                  uC-osroM202010f05b1
Method
                  BLASTX
NCBI GI
                  q4336205
BLAST score
                  287
E value
                  7.0e-40
Match length
                  117
                  75
% identity
NCBI Description (AF077372) cytochrome b5 reductase [Zea mays]
                  417106
                  uC-osroM202010f06b1
                  BLASTX
```

Seq. No. Seq. ID Method NCBI GI q5734761

BLAST score 233 E value 3.0e-19 Match length 143 % identity 41

NCBI Description (AC007651) Similar to disease resistance proteins

[Arabidopsis thaliana]

Seq. No. 417107

Seq. ID uC-osroM202010f08a1

Method BLASTX g626598 NCBI GI BLAST score 272 7.0e-24E value Match length 138 % identity 45

NCBI Description hypothetical protein YHR016c - yeast (Saccharomyces

cerevisiae) >gi 500710 (U10400) Ysc84p [Saccharomyces

cerevisiae]

Seq. No. 417108

Seq. ID uC-osroM202010f10b1

Method BLASTX NCBI GI g5230785 BLAST score 223 E value 5.0e-18 Match length 65 % identity 66

NCBI Description (AF107024) histone H1 WH1B.1 [Triticum aestivum]

Seq. No. 417109

Seq. ID uC-osroM202010f11b1

Match length

100

```
Method
                  BLASTX
NCBI GI
                  g5353567
BLAST score
                  146
                  5.0e-09
E value
Match length
                  63
% identity
                  48
                  (AF130997) D-alanine:D-lactate ligase [Enterococcus
NCBI Description
                  faecium]
                  417110
Seq. No.
Seq. ID
                  uC-osroM202010f12b1
Method
                  BLASTX
NCBI GI
                  g3548810
BLAST score
                  320
E value
                  2.0e-29
Match length
                  158
% identity
                  47
NCBI Description (AC005313) putative chloroplast nucleoid DNA binding
                  protein [Arabidopsis thaliana]
Seq. No.
                  417111
Seq. ID
                  uC-osroM202010g02a1
Method
                  BLASTN
NCBI GI
                  g20280
BLAST score
                  37
E value
                  2.0e-11
Match length
                  49
% identity
                  94
NCBI Description Rice gene for phenylalanine ammonia-lyase (EC 4.3.1.5)
Seq. No.
                  417112
Seq. ID
                  uC-osroM202010g03b1
Method
                  BLASTN
                  g394735
NCBI GI
BLAST score
                  143
E value
                  8.0e-75
Match length
                  159
% identity
NCBI Description Rice lip19 mRNA for basic/leucine zipper protein
                   417113
Seq. No.
Seq. ID
                  uC-osroM202010q06a1
Method
                  BLASTN
NCBI GI
                  q3868753
BLAST score
                  123
E value
                  8.0e-63
Match length
                  170
% identity
NCBI Description Oryza sativa CatB gene for catalase, complete cds
Seq. No.
                  417114
Seq. ID
                  uC-osroM202010q06b1
Method
                  BLASTX
NCBI GI
                  g3868754
BLAST score
                  400
E value
                  5.0e-39
```

54563

% identity NCBI Description (D64013) catalase [Oryza sativa] Seq. No. 417115 Seq. ID uC-osroM202010g07a1 Method BLASTN NCBI GI g3763844 BLAST score 63 E value 5.0e-27 Match length 206 84 % identity NCBI Description Oryza sativa OsENOD93a gene for early nodulin, complete cds Seq. No. 417116 uC-osroM202010q07b1 Seq. ID Method BLASTX NCBI GI g3763845 BLAST score 188 E value 2.0e-14 Match length 47 87 % identity NCBI Description (AB018375) early nodulin [Oryza sativa] >gi_3763847_dbj BAA33814 (AB018376) early nodulin [Oryza satīva] >gi_5803255 dbj BAA83565.1 (AP000399) ESTs C98096(C0688), C98097(C0688) correspond to a region of the predicted gene; similar to OsENOD93a gene for early nodulin (AB018375) [Oryza sativa] Seq. No. 417117 uC-osroM202010g08a1 Seq. ID Method BLASTN NCBI GI g394735 BLAST score 370 E value 0.0e+00Match length 382 % identity 99 NCBI Description Rice lip19 mRNA for basic/leucine zipper protein Seq. No. 417118 Seq. ID uC-osroM202010g08b1 Method BLASTX NCBI GI q129591 BLAST score 239 E value 1.0e-20 Match length 49 % identity NCBI Description PHENYLALANINE AMMONIA-LYASE >gi_295824_emb_CAA34226_ (X16099) phenylalanine ammonia-Tyase [Oryza sativa] Seq. No. 417119 Seq. ID uC-osroM202010g09a1 Method BLASTN

Method BLASTN
NCBI GI g6006355
BLAST score 295
E value 1.0e-165
Match length 346
% identity 96

```
NCBI Description Oryza sativa genomic DNA, chromosome 6, clone:P0493C11
Seq. No.
                  417120
                  uC-osroM202010g10a1
Seq. ID
Method
                  BLASTX
                  q4539004
NCBI GI
BLAST score
                  166
                  1.0e-11
E value
Match length
                  44
                  70
% identity
                  (AL049481) putative protein kinase [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  417121
                  uC-osroM202010g10b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3482933
BLAST score
                  536
                  7.0e-55
E value
Match length
                  137
                  70
% identity
                  (AC003970) Similar to cdc2 protein kinases [Arabidopsis
NCBI Description
                  thaliana]
                  417122
Seq. No.
                  uC-osroM202010g11a1
Seq. ID
Method
                  BLASTX
                  q3915082
NCBI GI
BLAST score
                  246
E value
                  7.0e-21
                  46
Match length
                  100
% identity
                  TUBULIN ALPHA CHAIN >gi_1220545 (M97956) alpha tubulin
NCBI Description
                   [Trypanosoma cruzi] >gi_1220548 (M96849) alpha tubulin
                   [Trypanosoma cruzi]
                   417123
Seq. No.
                   uC-osroM202010g11b1
Seq. ID
Method
                  BLASTX
                   g1136120
NCBI GI
                   543
BLAST score
                   1.0e-55
E value
                   102
Match length
                   98
% identity
NCBI Description (X91806) alpha-tubulin [Oryza sativa]
                   417124
Seq. No.
                   uC-osroM202010g12a1
Seq. ID
Method
                   BLASTN
                   g287400
NCBI GI
BLAST score
                   346
                   0.0e + 00
E value
```

% identity NCBI Description Rice mRNA for peroxidase, complete cds

417125 Seq. No.

Match length

uC-osroM202010g12b1 Seq. ID

397

96



```
BLASTN
Method
                  g287400
NCBI GI
                  126
BLAST score
                  2.0e-64
E value
                  271
Match length
                  87
% identity
NCBI Description Rice mRNA for peroxidase, complete cds
                  417126
Seq. No.
                  uC-osroM202010h03a1
Seq. ID
                  BLASTN
Method
                  g2429287
NCBI GI
                  228
BLAST score
                  1.0e-125
E value
Match length
                  256
                  97
% identity
NCBI Description Oryza sativa peroxidase (POX8.1) mRNA, complete cds
                  417127
Seq. No.
                  uC-osroM202010h03b1
Seq. ID
                  BLASTX
Method
NCBI GI
                  g2429288
BLAST score
                  202
                   4.0e-16
E value
                  40
Match length
                   95
% identity
NCBI Description
                 (AF014468) peroxidase [Oryza sativa]
                   417128
Seq. No.
                  uC-osroM202010h05a1
Seq. ID
                  BLASTX
Method
                  g2853039
NCBI GI
                  157
BLAST score
                   1.0e-10
E value
                   38
Match length
                   74
% identity
NCBI Description (X94289) phosphoinositide-specific phospholipase C [Solanum
                   tuberosum]
                   417129
Seq. No.
                   uC-osroM202010h06a1
Seq. ID
                   BLASTN
Method
NCBI GI
                   g529093
                   162
```

BLAST score 5.0e-86 E value Match length 186 97 % identity

NCBI Description Rice mRNA for proteasome C2 subunit, complete cds

Seq. No. 417130

Seq. ID uC-osroM202010h06b1

Method BLASTN NCBI GI a529093 49 BLAST score 6.0e-19 E value Match length 73 92 % identity

```
NCBI Description Rice mRNA for proteasome C2 subunit, complete cds
Seq. No.
                  417131
                  uC-osroM202010h07a1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3935181
BLAST score
                  340
                  6.0e-32
E value
                  90
Match length
                  69
% identity
                 (AC004557) F17L21.24 [Arabidopsis thaliana]
NCBI Description
                  417132
Seq. No.
                  uC-osroM202010h09b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g407938
BLAST score
                  153
E value
                  4.0e-10
                  59
Match length
% identity
                  46
NCBI Description
                 (U02494) epoxide hydrolase [Solanum tuberosum]
Seq. No.
                  417133
                  uC-osroM202011a01b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g5834807
BLAST score
                  149
E value
                  2.0e-09
Match length
                  48
                  62
% identity
NCBI Description (AL117212) hypothetical protein [Schizosaccharomyces pombe]
Seq. No.
                  417134
                  uC-osroM202011a04a1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g303841
BLAST score
                  277
E value
                  1.0e-154
                  296
Match length
                  99
% identity
NCBI Description Rice mRNA for beta-tubulin, complete cds
Seq. No.
                  417135
                  uC-osroM202011a04b1
Seq. ID
Method
                  BLASTX
                  g586078
NCBI GI
BLAST score
                  686
E value
                  2.0e-72
Match length
                  130
% identity
                  98
                  TUBULIN BETA CHAIN >gi 1076736 pir JC2518 beta-tubulin
NCBI Description
```

Seq. No. 417136

Seq. ID uC-osroM202011a05a1

Method BLASTN

beta-tubulin [Oryza sativa]

pTUB22 - rice >gi_303842_dbj_BAA02505_ (D13224)

```
NCBI GI
                  g2773153
BLAST score
                  157
                  5.0e-83
E value
                  233
Match length
                  92
% identity
                  Oryza sativa abscisic acid- and stress-inducible protein
NCBI Description
                  (Asr1) mRNA, complete cds
                  417137
Seq. No.
Seq. ID
                  uC-osroM202011a05b1
Method
                  BLASTN
NCBI GI
                  g2773153
BLAST score
                  446
                  0.0e + 00
E value
                  469
Match length
                  99
% identity
NCBI Description Oryza sativa abscisic acid- and stress-inducible protein
                  (Asr1) mRNA, complete cds
                  417138
Seq. No.
Seq. ID
                  uC-osroM202011a07a1
Method
                  BLASTN
NCBI GI
                  g1778820
BLAST score
                  211
E value
                  1.0e-115
                  382
Match length
% identity
                  95
                  Oryza sativa S-adenosyl-L-methionine synthetase (pOS-SAMS2)
NCBI Description
                  mRNA, complete cds
                  417139
Seq. No.
                  uC-osroM202011a07b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3024122
                  575
BLAST score
E value
                  2.0e-59
Match length
                  112
                  98
% identity
NCBI Description
                  S-ADENOSYLMETHIONINE SYNTHETASE 2 (METHIONINE
                  ADENOSYLTRANSFERASE 2) (ADOMET SYNTHETASE 2) >gi 1778821
                  (U82833) S-adenosyl-L-methionine synthetase [Oryza sativa]
Seq. No.
                  417140
Seq. ID
                  uC-osroM202011a08b1
Method
                  BLASTX
NCBI GI
                  g5326825
BLAST score
                  157
E value
                  3.0e-10
Match length
                  87
% identity
                  (AF044953) NADH: ubiquinone oxidoreductase PGIV subunit
NCBI Description
                   [Homo sapiens]
```

Seq. No. 417141

Seq. ID uC-osroM202011a09b1

Method BLASTX NCBI GI g4827060

E value

2.0e-14

```
BLAST score
                  267
                  3.0e-23
E value
                  128
Match length
                  45
% identity
                  xylulokinase (H. influenzae) homolog
NCBI Description
                  >gi 3298502 dbj BAA31527_ (AB015046) xylulokinase [Homo
                  sapiens]
                   417142
Seq. No.
                  uC-osroM202011a11b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3093294
                  563
BLAST score
E value
                  1.0e-58
                  174
Match length
% identity
                  63
                  (Y12782) putative villin [Arabidopsis thaliana]
NCBI Description
                  >gi 5730126 emb CAB52460.1 (AL109796) putative villin
                   [Arabidopsis thaliana]
                   417143
Seq. No.
                  uC-osroM202011b01a1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1632831
                  184
BLAST score
                  1.0e-13
E value
Match length
                  38
% identity
                  95
NCBI Description (Z49698) orf [Ricinus communis]
Seq. No.
                   417144
Seq. ID
                  uC-osroM202011b02a1
Method
                  BLASTX
                  g2078350
NCBI GI
BLAST score
                   463
E value
                   3.0e-46
Match length
                  118
% identity
                   71
NCBI Description (U95923) transaldolase [Solanum tuberosum]
                   417145
Seq. No.
Seq. ID
                  uC-osroM202011b07a1
Method
                  BLASTX
NCBI GI
                  g2160185
BLAST score
                  260
E value
                   2.0e-22
Match length
                   63
% identity
                   75
NCBI Description (AC000132) Similar to S. pombe ISP4 (gb D83992).
                   [Arabidopsis thaliana]
Seq. No.
                   417146
                  uC-osroM202011b07b1
Seq. ID
Method
                  BLASTX
NCBI GI
                   g2160185
BLAST score
                  189
```

54569



Match length 48 % identity 73

NCBI Description (AC000132) Similar to S. pombe ISP4 (gb_D83992).

[Arabidopsis thaliana]

Seq. No. 417147

Seq. ID uC-osroM202011b11b1

Method BLASTX
NCBI GI g4914439
BLAST score 147
E value 3.0e-09
Match length 64
% identity 42

NCBI Description (AL050351) receptor protein kinase-like protein

[Arabidopsis thaliana]

Seq. No. 417148

Seq. ID uC-osroM202011c01a1

Method BLASTN
NCBI GI g2662340
BLAST score 344
E value 0.0e+00
Match length 348
% identity 100

NCBI Description Oryza sativa mRNA for EF-1 alpha, complete cds

Seq. No. 417149

Seq. ID uC-osroM202011c01b1

Method BLASTX
NCBI GI g5257275
BLAST score 597
E value 5.0e-62
Match length 119
% identity 98

NCBI Description (AP000364) ESTs AU030740(E60171), AU030739(E60171)

correspond to a region of the predicted gene.; Similar to Populus tremuloides caffeoyl-CoA 3-0-methyltransferase.

(U27116) [Oryza sativa]

Seq. No. 417150

Seq. ID uC-osroM202011c02b1

Method BLASTX
NCBI GI g4467153
BLAST score 467
E value 1.0e-46
Match length 135
% identity 65

NCBI Description (AL035540) putative thaumatin-like protein [Arabidopsis

thaliana]

Seq. No. 417151

Seq. ID uC-osroM202011c05b1

Method BLASTX
NCBI GI g1184774
BLAST score 383
E value 5.0e-37
Match length 86



% identity 83

NCBI Description (U45856) cytosolic glyceroldehyde-3-phosphate dehydrogenase

GAPC3 [Zea mays]

Seq. No. 417152

Seq. ID uC-osroM202011c07b1

Method BLASTX
NCBI GI g2688824
BLAST score 148
E value 3.0e-09
Match length 113
% identity 36

NCBI Description (U93273) putative auxin-repressed protein [Prunus

armeniaca]

Seq. No. 417153

Seq. ID uC-osroM202011c08b1

Method BLASTX
NCBI GI 94760700
BLAST score 245
E value 1.0e-20
Match length 78
% identity 60

NCBI Description (AB024437) peroxidase 1 [Scutellaria baicalensis]

Seq. No. 417154

Seq. ID uC-osroM202011c11b1

Method BLASTX
NCBI GI g3790100
BLAST score 425
E value 8.0e-42
Match length 111
% identity 76

NCBI Description (AF095520) pyrophosphate-dependent phosphofructokinase beta

subunit [Citrus X paradisi]

Seq. No. 417155

Seq. ID uC-osroM202011d01b1

Method BLASTX
NCBI GI g3421413
BLAST score 226
E value 2.0e-18
Match length 54
% identity 85

NCBI Description (AF081922) protein phosphatase 2A 55 kDa B regulatory

subunit [Oryza sativa] >gi_3421415 (AF081923) protein
phosphatase 2A 55 kDa B regulatory subunit [Oryza sativa]

Seq. No. 417156

Seq. ID uC-osroM202011d02a1

Method BLASTX
NCBI GI g1076421
BLAST score 198
E value 3.0e-15
Match length 52
% identity 79

NCBI Description transcription factor TGA3 - Arabidopsis thaliana >gi 304113



(L10209) transcription factor [Arabidopsis thaliana]

Seq. No. 417157

Seq. ID uC-osroM202011d04a1

Method BLASTX
NCBI GI g1519249
BLAST score 293
E value 3.0e-26
Match length 61
% identity 97

NCBI Description (U65956) GF14-b protein [Oryza sativa]

Seq. No. 417158

Seq. ID uC-osroM202011d05b1

Method BLASTN
NCBI GI g1815625
BLAST score 280
E value 1.0e-156
Match length 368
% identity 94

NCBI Description Oryza sativa metallothionein-like type 1 (OsMT-1) mRNA,

complete cds

Seq. No. 417159

Seq. ID uC-osroM202011d07a1

Method BLASTX
NCBI GI g4406756
BLAST score 475
E value 1.0e-47
Match length 114
% identity 78

NCBI Description (AC006836) putative integral membrane protein A3

[Arabidopsis thaliana]

Seq. No. 417160

Seq. ID uC-osroM202011d07b1

Method BLASTX
NCBI GI g4335747
BLAST score 144
E value 8.0e-09
Match length 38
% identity 79

NCBI Description (AC006284) putative A3 protein [Vigna unguiculata] (integral membrane protein) [Arabidopsis thaliana]

Seq. No. 417161

Seq. ID uC-osroM202011d11a1

Method BLASTX
NCBI GI g1170937
BLAST score 152
E value 6.0e-10
Match length 27
% identity 96

NCBI Description S-ADENOSYLMETHIONINE SYNTHETASE 1 (METHIONINE ADENOSYLTRANSFERASE 1) (ADOMET SYNTHETASE 1)

>gi_450549_emb_CAA81481_ (Z26867) S-adenosyl methionine

synthetase [Oryza sativa]

```
Seq. No.
                  417162
Seq. ID
                  uC-osroM202011d11b1
Method
                  BLASTX
NCBI GI
                  q1170937
BLAST score
                  620
                  1.0e-64
E value
Match length
                  121
                  98
% identity
                  S-ADENOSYLMETHIONINE SYNTHETASE 1 (METHIONINE
NCBI Description
                  ADENOSYLTRANSFERASE 1) (ADOMET SYNTHETASE 1)
                  >gi 450549 emb CAA81481 (Z26867) S-adenosyl methionine
                  synthetase [Oryza sativa]
Seq. No.
                  417163
Seq. ID
                  uC-osroM202011d12a1
Method
                  BLASTN
NCBI GI
                  g20280
BLAST score
                  267
                  1.0e-148
E value
Match length
                  291
                  98
% identity
NCBI Description Rice gene for phenylalanine ammonia-lyase (EC 4.3.1.5)
Seq. No.
                  417164
Seq. ID
                  uC-osroM202011d12b1
Method
                  BLASTX
NCBI GI
                  g82496
BLAST score
                  531
                  3.0e-54
E value
Match length
                  126
                  83
% identity
NCBI Description phenylalanine ammonia-lyase (EC 4.3.1.5) - rice
Seq. No.
                  417165
                  uC-osroM202011e01b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2494175
BLAST score
                  316
E value
                  4.0e-29
Match length
                  85
                  67
% identity
NCBI Description GLUTAMATE DECARBOXYLASE 2 (GAD 2) >gi 1184960 (U46665)
                  glutamate decarboxylase 2 [Arabidopsis thaliana]
                  >gi 1236619 (U49937) glutamate decarboxylase [Arabidopsis
                  thaliana]
Seq. No.
                  417166
Seq. ID
                  uC-osroM202011e02b1
Method
                  BLASTX
NCBI GI
                  q1488297
BLAST score
                  274
                  4.0e-24
E value
Match length
                  91
% identity
                  57
NCBI Description (U63530) osRAD23 [Oryza sativa]
```



```
Seq. No.
                  417167
Seq. ID
                  uC-osroM202011e05a1
Method
                  BLASTX
NCBI GI
                  q3548808
BLAST score
                  327
E value
                  3.0e-30
Match length
                  124
% identity
                  49
NCBI Description (AC005313) unknown protein [Arabidopsis thaliana]
Seq. No.
                  417168
Seq. ID
                  uC-osroM202011e05b1
Method
                  BLASTX
NCBI GI
                  q3548808
BLAST score
                  201
E value
                  6.0e-22
Match length
                  92
                  58
% identity
NCBI Description (AC005313) unknown protein [Arabidopsis thaliana]
Seq. No.
                  417169
Seq. ID
                  uC-osroM202011e06a1
Method
                  BLASTX
NCBI GI
                  g4220535
BLAST score
                  232
E value
                  3.0e-19
Match length
                  51
                  82
% identity
NCBI Description
                 (AL035356) clathrin coat assembly like protein [Arabidopsis
                  thaliana]
                  417170
Seq. No.
                  uC-osroM202011e06b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4220535
BLAST score
                  603
                  1.0e-62
E value
Match length
                  173
% identity
                  72
                 (AL035356) clathrin coat assembly like protein [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  417171
                  uC-osroM202011e07a1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g118011
BLAST score
                  177
E value
                  9.0e-13
Match length
                  35
% identity
                  97
NCBI Description CYTOCHROME C >gi_625189_pir__CCRZ cytochrome c - rice
                  >gi_169786 (M63704) cytochrome c [Oryza sativa]
                  >gi_218249_dbj_BAA02159_ (D12634) 'cytochrome C' [Oryza
                  sativa]
```

Seq. No. 417172

Seq. ID uC-osroM202011e07b1



Method BLASTX
NCBI GI g118011
BLAST score 562
E value 8.0e-58
Match length 105
% identity 98

NCBI Description CYTOCHROME C >gi_625189_pir__CCRZ cytochrome c - rice

>gi_169786 (M63704) cytochrome c [Oryza sativa]

>gi_218249_dbj_BAA02159_ (D12634) 'cytochrome C' [Oryza

sativa]

Seq. No. 417173

Seq. ID uC-osroM202011e09a1

Method BLASTX
NCBI GI g3386621
BLAST score 220
E value 1.0e-17

E value 1.0 Match length 60 % identity 70

NCBI Description (AC004665) unknown protein [Arabidopsis thaliana]

Seq. No. 417174

Seq. ID uC-osroM202011e09b1

Method BLASTX
NCBI GI g3386621
BLAST score 525
E value 2.0e-53
Match length 125
% identity 81

NCBI Description (AC004665) unknown protein [Arabidopsis thaliana]

Seq. No. 417175

Seq. ID uC-osroM202011e12b1

Method BLASTX
NCBI GI 94262174
BLAST score 355
E value 2.0e-33
Match length 116
% identity 60

NCBI Description (AC005508) 9058 [Arabidopsis thaliana]

Seq. No. 417176

Seq. ID uC-osroM202011f01b1

Method BLASTX
NCBI GI g2623304
BLAST score 210
E value 1.0e-16
Match length 80
% identity 54

NCBI Description (AC002409) similar to Medicago nodulin N21 [Arabidopsis

thaliana]

Seq. No. 417177

Seq. ID uC-osroM202011f04b1

Method BLASTX
NCBI GI g3522956
BLAST score 572



E value 6.0e-59
Match length 179
% identity 56

NCBI Description (AC004411) putative pectinacetylesterase precursor

[Arabidopsis thaliana]

Seq. No. 417178

Seq. ID uC-osroM202011f06a1

Method BLASTX
NCBI GI g2827755
BLAST score 242
E value 2.0e-20
Match length 52
% identity 90

NCBI Description INORGANIC PYROPHOSPHATASE, VACUOLAR (PYROPHOSPHATE

PHOSPHOHYDROLASE) (PPASE) >gi 951323 (U31467)

pyrophosphatase [Vigna radiata]

Seq. No. 417179

Seq. ID uC-osroM202011f06b1

Method BLASTX
NCBI GI g728938
BLAST score 807
E value 2.0e-86
Match length 170
% identity 93

NCBI Description PYROPHOSPHATE-ENERGIZED VACUOLAR MEMBRANE PROTON PUMP

(PYROPHOSPHATE-ENERGIZED INORGANIC PYROPHOSPHATASE)

(H+-PPASE) >gi_322841_pir__JC1466 inorganic pyrophosphatase

(EC 3.6.1.1) - barley

Seq. No. 417180

Seq. ID uC-osroM202011f07b1

Method BLASTX
NCBI GI g1657621
BLAST score 284
E value 2.0e-25
Match length 73
% identity 71

NCBI Description (U72505) G6p [Arabidopsis thaliana] >gi_3068711 (AF049236)

putative acyl-coA dehydrogenase [Arabidopsis thaliana]

>gi 5478795 dbj BAA82478.1 (AB017643) Short-chain acyl CoA

oxidase [Arabidopsis thaliana]

Seq. No. 417181

Seq. ID uC-osroM202011f10b1

Method BLASTX
NCBI GI g4584525
BLAST score 674
E value 6.0e-71
Match length 161
% identity 78

NCBI Description (AL049607) protein phosphatase 2C-like protein [Arabidopsis

thaliana]

Seq. No. 417182

Seq. ID uC-osroM202011f12b1

Method BLASTX
NCBI GI g2462748
BLAST score 161
E value 1.0e-14
Match length 64

NCBI Description (AC002292) putative Clathrin Coat Assembly protein

[Arabidopsis thaliana]

Seq. No. 417183

% identity

Seq. ID uC-osroM202011g02b1

72

Method BLASTX
NCBI GI g1084461
BLAST score 344
E value 2.0e-32
Match length 113
% identity 62

NCBI Description RCc3 protein - rice >gi 786132 (L27208) RCc3 [Oryza sativa]

Seq. No. 417184

Seq. ID uC-osroM202011g03a1

Method BLASTN
NCBI GI g2331130
BLAST score 103
E value 1.0e-50
Match length 227
% identity 87

NCBI Description Oryza sativa glycine-rich protein (OSGRP1) mRNA, complete

cds

Seq. No. 417185

Seq. ID uC-osroM202011g03b1

Method BLASTX
NCBI GI g2293480
BLAST score 217
E value 5.0e-18
Match length 48
% identity 88

NCBI Description (AF011331) glycine-rich protein [Oryza sativa]

Seq. No. 417186

Seq. ID uC-osroM202011g04b1

Method BLASTX
NCBI GI g1350742
BLAST score 313
E value 1.0e-28
Match length 102
% identity 58

NCBI Description PROBABLE 60S RIBOSOMAL PROTEIN L35A >gi_1086831 (U41264)

coded for by C. elegans cDNA yk64g10.5; coded for by C. elegans cDNA yk51f3.5; coded for by C. elegans cDNA

yk115e7.3; coded for by C. elegans cDNA yk99d1.3; coded for by C. elegans cDNA yk99d1.5; coded for by C. elegans cDNA

yk64g1

Seq. No. 417187

Seq. ID uC-osroM202011g05b1



Method BLASTX
NCBI GI g1350742
BLAST score 310
E value 4.0e-28
Match length 102
% identity 58

NCBI Description PROBABLE 60S RIBOSOMAL PROTEIN L35A >gi_1086831 (U41264) coded for by C. elegans cDNA yk64g10.5; coded for by C. elegans cDNA

yk115e7.3; coded for by C. elegans cDNA yk99d1.3; coded for by C. elegans cDNA yk99d1.5; coded for by C. elegans cDNA

yk64g1

Seq. No. 417188

Seq. ID uC-osroM202011g07b1

Method BLASTX
NCBI GI g3641837
BLAST score 426
E value 5.0e-42
Match length 106
% identity 79

NCBI Description (AL023094) Nonclathrin coat protein gamma-like protein

[Arabidopsis thaliana]

Seq. No. 417189

Seq. ID uC-osroM202011g11a1

Method BLASTX
NCBI GI g5926740
BLAST score 169
E value 8.0e-12
Match length 34
% identity 97

NCBI Description (AB025310) asparaginyl endopeptidase [Oryza sativa]

Seq. No. 417190

Seq. ID uC-osroM202011g11b1

Method BLASTX
NCBI GI g5926740
BLAST score 883
E value 2.0e-95
Match length 165
% identity 99

NCBI Description (AB025310) asparaginyl endopeptidase [Oryza sativa]

Seq. No. 417191

Seq. ID uC-osroM202011h01b1

Method BLASTX
NCBI GI 94455359
BLAST score 327
E value 1.0e-30
Match length 97
% identity 64

NCBI Description (AL035524) putative protein [Arabidopsis thaliana]

Seq. No. 417192

Seq. ID uC-osroM202011h02a1

Method BLASTX



NCBI GI g2281705 BLAST score 425 E value 8.0e-42 Match length 79 % identity 100

NCBI Description (AF013979) ethylene responsive factor [Oryza sativa]

Seq. No. 417193

Seq. ID uC-osroM202011h02b1

Method BLASTX
NCBI GI g2281705
BLAST score 442
E value 7.0e-44
Match length 114
% identity 75

NCBI Description (AF013979) ethylene responsive factor [Oryza sativa]

Seq. No. 417194

Seq. ID uC-osroM202011h07b1

Method BLASTX
NCBI GI g5915841
BLAST score 200
E value 8.0e-16
Match length 79
% identity 52

NCBI Description CYTOCHROME P450 71E1 >gi_2766452 (AF029858) cytochrome P450

CYP71E1 [Sorghum bicolor]

Seq. No. 417195

Seq. ID uC-osroM202011h09a1

Method BLASTX
NCBI GI g548770
BLAST score 331
E value 7.0e-31
Match length 79
% identity 86

NCBI Description 60S RIBOSOMAL PROTEIN L3 >gi_481228_pir__S38359 ribosomal

protein L3 - rice >gi_303853_dbj_BAA02155_ (D12630)

ribosomal protein L3 [Oryza sativa]

Seq. No. 417196

Seq. ID uC-osroM202011h10a1

Method BLASTN
NCBI GI g20191
BLAST score 397
E value 0.0e+00
Match length 401
% identity 100

NCBI Description O.sativa mRNA for catalase

Seq. No. 417197

Seq. ID uC-osroM202011h10b1

Method BLASTX
NCBI GI g2130069
BLAST score 672
E value 1.0e-70
Match length 131

E value Match length

% identity

```
% identity
                   95
NCBI Description
                  catalase (EC 1.11.1.6) catA - rice
                  >gi 1261858 dbj BAA06232 (D29966) catalase [Oryza sativa]
                   417198
Seq. No.
                  uC-osroM202011h11a1
Seq. ID
Method
                  BLASTX
                  g2062172
NCBI GI
BLAST score
                  164
                  2.0e-11
E value
Match length
                  112
% identity
                  38
                 (AC001645) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  417199
Seq. ID
                  uC-osroM202011h12b1
Method
                  BLASTX
NCBI GI
                  q4454307
BLAST score
                  347
                  9.0e-33
E value
                  80
Match length
                  78
% identity
NCBI Description
                 (AJ132763) cyclophilin [Pseudotsuga menziesii]
                  417200
Seq. No.
                  uC-osroM202012d11a1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g5545339
BLAST score
                  204
                  5.0e-16
E value
                  99
Match length
                  45
% identity
NCBI Description (AB030083) lectin-like protein kinase [Populus nigra]
                  417201
Seq. No.
                  uC-osroM202012e04a1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g5679838
BLAST score
                  309
E value
                  3.0e-28
Match length
                  133
% identity
                  44
NCBI Description
                  (AJ243961) has similarity to Arabidopsis thaliana
                  gi 3068705 [Oryza sativa]
                  417202
Seq. No.
                  uC-osroM202012e06a1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2129698
                  320
BLAST score
```

NCBI Description protein kinase ATN1 (EC 2.7.1.-) - Arabidopsis thaliana >gi_1054633_emb_CAA63387_ (X92728) protein kinase

[Arabidopsis thaliana]

1.0e-29

99

62



Seq. No. 417203

Seq. ID uC-osroM202012e10a1

Method BLASTN
NCBI GI g287400
BLAST score 328
E value 0.0e+00
Match length 359
% identity 97

NCBI Description Rice mRNA for peroxidase, complete cds

Seq. No. 417204

Seq. ID uC-osroM202012f05a1

Method BLASTX
NCBI GI g1706325
BLAST score 394
E value 4.0e-38
Match length 87
% identity 83

NCBI Description PYRUVATE DECARBOXYLASE ISOZYME 1 (PDC) >gi 476286 (U07339)

pyruvate decarboxylase 1 [Oryza sativa] >gi_1098559

(U26660) pyruvate decarboxylase [Oryza sativa]

Seq. No. 417205

Seq. ID uC-osroM202012f11a1

Method BLASTX
NCBI GI g729305
BLAST score 283
E value 3.0e-25
Match length 62
% identity 87

NCBI Description PYRUVATE DECARBOXYLASE ISOZYME 3 (PDC)

>gi_22765_emb_CAA79819_ (Z21722) pyruvate decarboxylase
[Zea mays] >gi_217972_dbj_BAA03354_ (D14457) Pyruvate

Decarboxylase [Zea mays]

Seq. No. 417206

Seq. ID uC-osroM202012g01b1

Method BLASTX
NCBI GI g2623307
BLAST score 167
E value 8.0e-12
Match length 105
% identity 41

NCBI Description (AC002409) putative ubiquitin protease [Arabidopsis

thaliana]

Seq. No. 417207

Seq. ID uC-osroM202012g03b1

Method BLASTX
NCBI GI 94559333
BLAST score 194
E value 6.0e-24
Match length 126
% identity 48

NCBI Description (AC007087) unknown protein [Arabidopsis thaliana]

Seq. No. 417208

NCBI GI

BLAST score

```
uC-osroM202012g04a1
Seq. ID
                  BLASTX
Method
NCBI GI
                  q4063821
BLAST score
                   509
                  1.0e-51
E value
                  106
Match length
% identity
                  94
                  (AB015204) plastidic ATP sulfurylase [Oryza sativa]
NCBI Description
                   417209
Seq. No.
                  uC-osroM202012g05a1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2696221
BLAST score
                   334
                  5.0e-31
E value
                  111
Match length
                   59
% identity
NCBI Description (D55708) chitinase [Oryza sativa]
                   417210
Seq. No.
                  uC-osroM202012q08b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2224915
                  235
BLAST score
                  1,0e-19
E value
Match length
                   63
% identity
                   60
NCBI Description (U95968) beta-expansin [Oryza sativa]
                   417211
Seq. No.
                  uC-osroM202012g10a1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g6015059
                   469
BLAST score
                   6.0e-47
E value
Match length
                   91
                   100
% identity
NCBI Description ELONGATION FACTOR 1-ALPHA (EF-1-ALPHA) >gi 2996096
                   (AF030517) translation elongation factor-1 alpha; EF-1
                   alpha [Oryza sativa]
                   417212
Seq. No.
Seq. ID
                   uC-osroM202012q12a1
Method
                  BLASTX
                  g3912917
NCBI GI
BLAST score
                   224
E value
                   3.0e-18
Match length
                   87
                   62
% identity
                  (AF001308) putative NAK-like ser/thr protein kinase
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                   417213
Seq. ID
                   uC-osroM202012h03b1
Method
                   BLASTX
```

54582

g2625154

379

E value 2.0e-48
Match length 156
% identity 69

NCBI Description (AF032877) alpha-tubulin [Chloromonas sp. ANT3]

Seq. No. 417214

Seq. ID uC-osroM202012h07a1

Method BLASTN
NCBI GI g968995
BLAST score 153
E value 1.0e-80
Match length 241
% identity 91

NCBI Description Oryza sativa clone glyceraldehyde-3-phosphate dehydrogenase

(Gpc) mRNA, complete cds

Seq. No. 417215

Seq. ID uC-osroM202012h07b1

Method BLASTX
NCBI GI g3023816
BLAST score 589
E value 3.0e-64
Match length 129
% identity 95

NCBI Description GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC

>gi 968996 (U31676) glyceraldehyde-3-phosphate

dehydrogenase [Oryza sativa]

Seq. No. 417216

Seq. ID uC-osroM202012h09b1

Method BLASTX
NCBI GI g2623307
BLAST score 623
E value 5.0e-65
Match length 151
% identity 78

NCBI Description (AC002409) putative ubiquitin protease [Arabidopsis

thaliana]

Seq. No. 417217

Seq. ID uC-osroM202012h10a1

Method BLASTN
NCBI GI 9487291
BLAST score 48
E value 5.0e-18
Match length 56
% identity 96

NCBI Description Rice mRNA EN171, partial sequence

Seq. No. 417218

Seq. ID uC-osroM202012h12a1

Method BLASTN
NCBI GI g5803242
BLAST score 402
E value 0.0e+00
Match length 402
% identity 100

54583



```
NCBI Description Oryza sativa genomic DNA, chromosome 6, clone:P0535G04
                  417219
Seq. No.
                  uC-osroM202013a01b1
Seq. ID
                  BLASTX
Method
NCBI GI
                  q4006914
BLAST score
                  315
                  2.0e-32
E value
                  106
Match length
                  68
% identity
NCBI Description
                  (Z99708) serine C-palmitoyltransferase like protein
                   [Arabidopsis thaliana]
                  417220
Seq. No.
                  uC-osroM202013a02b1
Seq. ID
Method
                  BLASTX
                  q3337356
NCBI GI
BLAST score
                  599
                  3.0e-62
E value
Match length
                  126
                  93
% identity
                  (AC004481) putative protein transport protein SEC61 alpha
NCBI Description
                  subunit [Arabidopsis thaliana]
                   417221
Seq. No.
                  uC-osroM202013a07b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4572679
BLAST score
                  282
                  4.0e-25
E value
                  109
Match length
                  55
% identity
                  (AC006954) RSZp22 splicing factor; contains RNA recognition
NCBI Description
                  motif [Arabidopsis thaliana]
                   417222
Seq. No.
Seq. ID
                  uC-osroM202013a08b1
Method
                  BLASTN
NCBI GI
                   q22322
                   215
BLAST score
E value
                  1.0e-117
Match length
                   375
                   90
% identity
NCBI Description Z.mays mRNA for H2B histone (clone cH2B214)
                   417223
Seq. No.
Seq. ID
                  uC-osroM202013a09b1
Method
                  BLASTX
NCBI GI
                   q2213624
```

Method BLASTX
NCBI GI g2213624
BLAST score 176
E value 2.0e-12
Match length 174
% identity 27

NCBI Description (AC000103) F21J9.16 [Arabidopsis thaliana]

Seq. No. 417224

Seq. ID uC-osroM202013a11b1



Method BLASTX NCBI GI g3281853 BLAST score 284 E value 3.0e-25 Match length 61 85 % identity NCBI Description (AL031004) putative protein [Arabidopsis thaliana] Seq. No. 417225 uC-osroM202013b01b1 Seq. ID Method BLASTX NCBI GI g567893 BLAST score 253 E value 7.0e-22 Match length 96 56 % identity NCBI Description (L37382) beta-galactosidase-complementation protein [Cloning vector] 417226 Seq. No. uC-osroM202013b04b1 Seq. ID BLASTX g2191172

Method NCBI GI BLAST score 168 E value 1.0e-11 Match length 122 % identity 37

NCBI Description (AF007270) contains similarity to GATA-type zinc fingers

(PS:PS00344) [Arabidopsis thaliana]

417227 Seq. No.

Seq. ID uC-osroM202013b05b1

Method BLASTX NCBI GI g2827559 BLAST score 165 3.0e-11 E value Match length 126 % identity 29

(AL021635) predicted protein [Arabidopsis thaliana] NCBI Description

>gi_3292808_emb_CAA19798.1_ (AL031018) putative protein

[Arabidopsis thaliana]

Seq. No. 417228

uC-osroM202013b06b1 Seq. ID

Method BLASTX g6049841 NCBI GI BLAST score 630 E value 9.0e-66 Match length 165 % identity 70

(AF190728) asparagine synthetase [Helianthus annuus] NCBI Description

Seq. No. 417229

Seq. ID uC-osroM202013b10b1

Method BLASTX NCBI GI g4469009 BLAST score 447

E value 2.0e-44
Match length 105
% identity 81
NCBI Description (AL0356

NCBI Description (AL035602) putative protein [Arabidopsis thaliana]

Seq. No. 417230

Seq. ID uC-osroM202013b12b1

Method BLASTX
NCBI GI g543867
BLAST score 476
E value 1.0e-47
Match length 154
% identity 66

NCBI Description ATP SYNTHASE GAMMA CHAIN, MITOCHONDRIAL PRECURSOR

>gi_1076684_pir__A47493 H+-transporting ATP synthase (EC

3.6.1.34) gamma chain precursor - sweet potato

>gi 303626 dbj BAA03526 (D14699) F1-ATPase gammma subunit

[Ipomoea batatas]

Seq. No. 417231

Seq. ID uC-osroM202013c02b1

Method BLASTX
NCBI GI g542200
BLAST score 333
E value 5.0e-31
Match length 116
% identity 59

NCBI Description hypothetical protein - garden asparagus

>gi 452714 emb CAA54526 (X77320) unknown [Asparagus

officinalis]

Seq. No. 417232

Seq. ID uC-osroM202013c03b1

Method BLASTX
NCBI GI g1931641
BLAST score 331
E value 1.0e-30
Match length 156
% identity 49

NCBI Description (U95973) unknown protein [Arabidopsis thaliana]

Seq. No. 417233

Seq. ID uC-osroM202013c04b1

Method BLASTX
NCBI GI g2239229
BLAST score 589
E value 5.0e-61
Match length 152
% identity 70

NCBI Description (Z97210) conserved hypothetical protein

[Schizosaccharomyces pombe]

Seq. No. 417234

Seq. ID uC-osroM202013c05b1

Method BLASTX NCBI GI g3687235 BLAST score 400

E value 8.0e-39 Match length 103 % identity 79 NCBI Description (AC005169) putative copia-like transposable element [Arabidopsis thaliana] 417235 Seq. No. uC-osroM202013c06b1 Seq. ID Method BLASTX NCBI GI g3687235 510 BLAST score 1.0e-51 E value 128 Match length % identity 81 (AC005169) putative copia-like transposable element NCBI Description [Arabidopsis thaliana] 417236 Seq. No. uC-osroM202013c07b1 Seq. ID Method BLASTX NCBI GI g1136122 BLAST score 727 E value 4.0e-77 Match length 149 % identity 93 NCBI Description (X91807) alfa-tubulin [Oryza sativa] Seq. No. 417237 Seq. ID uC-osroM202013c08b1 Method BLASTX NCBI GI q2493123 BLAST score 531 E value 4.0e-54 Match length 107 % identity 93 NCBI Description VACUOLAR ATP SYNTHASE CATALYTIC SUBUNIT A (V-ATPASE 69 KD SUBUNIT) >gi_1051258 (U36939) vacuolar ATPase catalytic subunit [Hordeum vulgare] 417238 Seq. No. Seq. ID uC-osroM202013c10b1 Method BLASTX NCBI GI q4104220 BLAST score 313 E value 1.0e-28 Match length 124

% identity 57

NCBI Description (AF033538) caffeic acid O-methyltransferase; LPOMT1 [Lolium

perenne]

417239 Seq. No.

Seq. ID uC-osroM202013c12b1

Method BLASTX NCBI GI g3334142 BLAST score 666 E value 5.0e-70Match length 170

% identity 76 NCBI Description CENTROMERE/MICROTUBULE BINDING PROTEIN CBF5 (CENTROMERE-BINDING FACTOR 5) (NUCLEOLAR PROTEIN CBF5) >gi 2737892 (U59150) nucleolar protein AfCbf5p [Sartorya fumigata] Seq. No. 417240 uC-osroM202013d01b1 Seq. ID Method BLASTX NCBI GI g1814403 BLAST score 631 E value 6.0e-66 Match length 132 % identity 88 NCBI Description (U84889) methionine synthase [Mesembryanthemum crystallinum] 417241 Seq. No. uC-osroM202013d02b1 Seq. ID Method BLASTX NCBI GI g3831463 BLAST score 390 E value 1.0e-37 Match length 131 % identity 58 NCBI Description (AC005700) unknown protein [Arabidopsis thaliana] Seq. No. 417242 uC-osroM202013d04b1 Seq. ID Method BLASTX NCBI GI g4099408 BLAST score 684 4.0e-72 E value Match length 147 88 % identity NCBI Description (U86763) delta-type tonoplast intrinsic protein [Triticum aestivum] 417243 Seq. No. Seq. ID uC-osroM202013d06b1 Method BLASTX NCBI GI q129591 BLAST score 822 E value 2.0e-88 Match length 160 99 % identity

NCBI Description PHENYLALANINE AMMONIA-LYASE >gi_295824_emb_CAA34226_ (X16099) phenylalanine ammonia-lyase [Oryza sativa]

Seq. No. 417244

Seq. ID uC-osroM202013d07b1

Method BLASTX
NCBI GI g2244831
BLAST score 166
E value 3.0e-20
Match length 85
% identity 71

```
NCBI Description (Z97337) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  417245
                  uC-osroM202013d08b1
Seq. ID
                  BLASTX
Method
                  g1076809
NCBI GI
                  709
BLAST score
                  9.0e-78
E value
                  170
Match length
                  88
% identity
                  H+-transporting ATPase (EC 3.6.1.35) - maize
NCBI Description
                   >gi_758355_emb_CAA59800_ (X85805) H(+)-transporting ATPase
                   [Zea mays]
                   417246
Seq. No.
                  uC-osroM202013d10b1
Seq. ID
                  BLASTX
Method
NCBI GI
                  q82512
                  643
BLAST score
                  2.0e-67
E value
                  129
Match length
% identity
                   44
                  ubiquitin precursor - rice (fragment)
NCBI Description
                  >gi 218189 dbj BAA02241 (D12776) poly-ubiquitin [Oryza
                   sativa]
Seq. No.
                   417247
Seq. ID
                  uC-osroM202013e01b1
                  BLASTX
Method
                  g4559330
NCBI GI
                   298
BLAST score
                   7.0e-27
E value
                  159
Match length
                   42
% identity
NCBI Description (AC007087) unknown protein [Arabidopsis thaliana]
                   417248
Seq. No.
                  uC-osroM202013e03b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2245138
BLAST score
                   205
E value
                   4.0e-16
                   77
Match length
% identity
NCBI Description (Z97344) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   417249
Seq. ID
                   uC-osroM202013e04b1
Method
                   BLASTX
NCBI GI
                   g3851005
BLAST score
                   655
                   1.0e-68
E value
Match length
                   151
% identity
                  (AF069911) pyruvate dehydrogenase E1 alpha subunit [Zea
NCBI Description
```

54589

mays]

```
Seq. No.
                  417250
                  uC-osroM202013e05b1
Seq. ID
Method
                  BLASTX
                  g417154
NCBI GI
BLAST score
                  571
                  8.0e-59
E value
Match length
                  173
% identity
                  66
                  HEAT SHOCK PROTEIN 82 >gi 100685 pir S25541 heat shock
NCBI Description
                  protein 82 - rice (strain Taichung Native One)
                  >gi 20256 emb CAA77978_ (Z11920) heat shock protein 82
                  (HSP82) [Oryza sativa]
                  417251
Seq. No.
Seq. ID
                  uC-osroM202013e06b1
Method
                  BLASTX
                  q417154
NCBI GI
BLAST score
                  666
                  6.0e-70
E value
Match length
                  181
% identity
                  72
                 HEAT SHOCK PROTEIN 82 >gi_100685_pir__S25541 heat shock
NCBI Description
                  protein 82 - rice (strain Taichung Native One)
                  >gi 20256 emb CAA77978 (Z11920) heat shock protein 82
                  (HSP82) [Oryza sativa]
                  417252
Seq. No.
Seq. ID
                  uC-osroM202013e10b1
Method
                  BLASTX
                  g5430753
NCBI GI
BLAST score
                  166
                  2.0e-11
E value
Match length
                  127
% identity
                  33
NCBI Description (AC007504) Unknown Protein [Arabidopsis thaliana]
                  417253
Seq. No.
                  uC-osroM202013e12b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2130072
BLAST score
                  515
                  2.0e-52
E value
Match length
                  118
% identity
                  86
                  ferredoxin--nitrite reductase (EC 1.7.7.1) - rice
NCBI Description
                  >gi_809514_dbj_BAA09122_ (D50556) ferredoxin-nitrite
                  reductase [Oryza sativa]
Seq. No.
                  417254
                  uC-osroM202013f02b1
Seq. ID
```

BLASTX Method NCBI GI q4586107 BLAST score 375 6.0e-36 E value Match length 135 % identity

NCBI Description (AL049638) putative disease resistance protein [Arabidopsis



thaliana]

Seq. No. 417255

Seq. ID uC-osroM202013f12b1

Method BLASTN
NCBI GI g2662342
BLAST score 245
E value 1.0e-135
Match length 245
% identity 100

NCBI Description Oryza sativa mRNA for EF-1 alpha, complete cds

Seq. No. 417256

Seq. ID uC-osroM202013g02b1

Method BLASTX
NCBI GI g5545339
BLAST score 464
E value 2.0e-46
Match length 131
% identity 66

NCBI Description (AB030083) lectin-like protein kinase [Populus nigra]

Seq. No. 417257

Seq. ID uC-osroM202013g04b1

Method BLASTX
NCBI GI g122106
BLAST score 410
E value 4.0e-40
Match length 82
% identity 100

NCBI Description HISTONE H4 >gi_70771_pir__HSZM4 histone H4 - maize

>gi_81642_pir__S06904 histone H4 - Arabidopsis thaliana

>gi 2119028 pir S60475 histone H4 - garden pea

>gi_21795_emb_CAA24924_ (X00043) histone H4 [Triticum
aestivum] >gi_166740 (M17132) histone H4 [Arabidopsis
thaliana] >gi_166742 (M17133) histone H4 [Arabidopsis

thaliana] >gi_168499 (M36659) histone H4 (H4C13) [Zea mays]

>gi_168501 (M13370) histone H4 [Zea mays] >gi_168503

 $(M1\overline{3}377)$ histone H4 [Zea mays] $>gi_498898$ (U1 $\overline{0}042$) histone

H4 homolog [Pisum sativum] >gi_1806285_emb_CAB01914_(Z79638) histone H4 homologue [Sesbania rostrata]

>gi_3927823 (AC005727) histone H4 [Arabidopsis thaliana]
>gi_4580385_gb_AAD24364.1_AC007184_4 (AC007184) histone H4

[Arabidopsis thaliana] >gi_6009915_dbj_BAA85120.1_ (AB018245) histone H4-like protein [Solanum melongena] >gi_225838_prf__1314298A histone H4 [Arabidopsis thaliana]

Seq. No. 417258

Seq. ID uC-osroM202013g06b1

Method BLASTX
NCBI GI g3176690
BLAST score 277
E value 3.0e-24
Match length 197
% identity 37

NCBI Description (AC003671) Similar to ubiquitin ligase gb D63905 from S.

cerevisiae. EST gb R65295 comes from this gene.

[Arabidopsis thaliana]

Seq. No. 417259 uC-osroM202013q07b1 Seq. ID Method BLASTX NCBI GI q4406781 BLAST score 330 1.0e-30 E value Match length 136 60 % identity NCBI Description

(AC006532) putative Na+/H+ antiporter [Arabidopsis

thaliana]

417260 Seq. No.

Seq. ID uC-osroM202013g09b1

Method BLASTX NCBI GI g3719211 BLAST score 260 E value 2.0e-22 Match length 106 % identity 51

NCBI Description (U97021) UIP2 [Arabidopsis thaliana]

Seq. No. 417261

uC-osroM202013g10b1 Seq. ID

Method BLASTX NCBI GI g4220518 BLAST score 176 E value 1.0e-12 91 Match length 40 % identity

NCBI Description (AL035356) hypothetical protein [Arabidopsis thaliana]

Seq. No. 417262

uC-osroM202013g11b1 Seq. ID

Method BLASTX NCBI GI g5051777 BLAST score 265 E value 6.0e-23 141 Match length 45 % identity

NCBI Description (AL078637) putative protein [Arabidopsis thaliana]

417263 Seq. No.

uC-osroM202013g12b1 Seq. ID

BLASTX Method NCBI GI g2246625 BLAST score 698 E value 9.0e-74Match length 172 83 % identity

NCBI Description (AF004947) protein kinase [Oryza sativa]

417264 Seq. No.

Seq. ID uC-osroM202013h01a1

Method BLASTX NCBI GI g5545339

```
BLAST score
                  352
                   2.0e-33
E value
Match length
                  101
                  66
% identity
NCBI Description (AB030083) lectin-like protein kinase [Populus nigra]
                  417265
Seq. No.
                  uC-osroM202013h01b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g5545339
BLAST score
                  323
E value
                  3.0e-30
Match length
                  92
% identity
                  64
NCBI Description (AB030083) lectin-like protein kinase [Populus nigra]
                  417266
Seq. No.
                  uC-osroM202013h04b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g99733
BLAST score
                  513
E value
                  4.0e-52
                  153
Match length
                  66
% identity
NCBI Description
                  hypothetical protein H1flk - Arabidopsis thaliana
                   (fragment) >gi_16482_emb_CAA44318_ (X62461) H1flk
                   [Arabidopsis thaliana]
                  417267
Seq. No.
                  uC-osroM202013h06b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1084461
BLAST score
                  475
E value
                  1.0e-47
                  133
Match length
% identity
                  71
NCBI Description RCc3 protein - rice >gi_786132 (L27208) RCc3 [Oryza sativa]
                   417268
Seq. No.
Seq. ID
                  uC-osroM202013h07a1
Method
                  BLASTN
NCBI GI
                  q968995
BLAST score
                  165
E value
                  1.0e-87
Match length
                  308
% identity
NCBI Description Oryza sativa clone glyceraldehyde-3-phosphate dehydrogenase
                   (Gpc) mRNA, complete cds
Seq. No.
                  417269
```

Seq. ID uC-osroM202013h07b1

Method BLASTX
NCBI GI g3023816
BLAST score 434
E value 4.0e-43
Match length 84
% identity 99

NCBI Description GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC >gi 968996 (U31676) glyceraldehyde-3-phosphate dehydrogenase [Oryza sativa] 417270 Seq. No. Seq. ID uC-osroM202013h10b1 Method BLASTX NCBI GI g3360291 BLAST score 289 7.0e-26 E value Match length 116 % identity 54 NCBI Description (AF023165) leucine-rich repeat transmembrane protein kinase 2 [Zea mays] Seq. No. 417271 Seq. ID uC-osroM202013h11b1 Method BLASTX NCBI GI q3043694 BLAST score 175 2.0e-12 E value Match length 42 71 % identity NCBI Description (AB011157) KIAA0585 protein [Homo sapiens] Seq. No. 417272 Seq. ID uC-osroM202013h12b1 Method BLASTX NCBI GI q1169384 BLAST score 505 4.0e-51 E value Match length 125 78 % identity NCBI Description DNAJ PROTEIN HOMOLOG ANJ1 >gi 543510 pir JQ2142 chaperone ANJ1 protein - Atriplex nummularia Seq. No. 417273 Seq. ID uC-osroM202014a01b1 Method BLASTX NCBI GI a3914431 BLAST score 309 E value 3.0e-28 Match length 87 74 % identity NCBI Description PROTEASOME COMPONENT C8 (MACROPAIN SUBUNIT C8) (MULTICATALYTIC ENDOPEPTIDASE COMPLEX SUBUNIT C8) >gi_2285802_dbj_BAA21651_ (D78173) 26S proteasome alpha subunit [Spinacia oleracea]

Seq. No. 417274

Seq. ID uC-osroM202014a04b1

Method BLASTX
NCBI GI g3294467
BLAST score 252
E value 3.0e-22
Match length 52
% identity 92

Seq. No.

Seq. ID

417280

uC-osroM202014b08b1

```
NCBI Description (U89341) phosphoglucomutase 1 [Zea mays]
                   417275
Seq. No.
                  uC-osroM202014a05b1
Seq. ID
Method
                  BLASTN
                  g4468795
NCBI GI
BLAST score
                  33
                  4.0e-09
E value
                  61
Match length
                  89
% identity
NCBI Description Zea mays mRNA for glutathione transferase GST6
Seq. No.
                   417276
                  uC-osroM202014a06b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4468796
BLAST score
                  218
                  1.0e-20
E value
Match length
                  83
% identity
                  66
NCBI Description (AJ010439) GST6 protein [Zea mays]
Seq. No.
                  417277
Seq. ID
                  uC-osroM202014a09b1
Method
                  BLASTX
NCBI GI
                  g417745
BLAST score
                  741
E value
                  9.0e-79
Match length
                  156
% identity
                  88
NCBI Description ADENOSYLHOMOCYSTEINASE (S-ADENOSYL-L-HOMOCYSTEINE
                  HYDROLASE) (ADOHCYASE) >gi_170773 (L11872)
                  S-adenosyl-L-homocysteine hydrolase [Triticum aestivum]
                  417278
Seq. No.
Seq. ID
                  uC-osroM202014a11b1
Method
                  BLASTX
NCBI GI
                  g3549667
BLAST score
                  389
E value
                  7.0e - 38
Match length
                  99
% identity
                  75
NCBI Description (AL031394) Arabidopsis dynamin-like protein ADL2
                   [Arabidopsis thaliana]
                  417279
Seq. No.
Seq. ID
                  uC-osroM202014b07b1
Method
                  BLASTX
NCBI GI
                  g2194132
BLAST score
                  524
E value
                  2.0e-53
Match length
                  159
% identity
                  67
NCBI Description (AC002062) No definition line found [Arabidopsis thaliana]
```

54595

Method BLASTX NCBI GI q3915826 BLAST score 572 E value 6.0e-59 Match length 134 84 % identity NCBI Description 60S RIBOSOMAL PROTEIN L5 Seq. No. 417281 uC-osroM202014c01b1 Seq. ID Method BLASTX NCBI GI g3258575 BLAST score 522 E value 3.0e-53 Match length 145 % identity 70 NCBI Description (U89959) Hypothetical protein [Arabidopsis thaliana] Seq. No. 417282 Seq. ID uC-osroM202014c03b1 Method BLASTX NCBI GI g2944088 BLAST score 498 E value 2.0e-50 Match length 128 % identity 76 NCBI Description (AF050102) glutathione s-transferase [Oryza sativa] 417283 Seq. No. Seq. ID uC-osroM202014c04b1 Method BLASTX NCBI GI q3618312 BLAST score 422 E value 2.0e-41 Match length 89 % identity NCBI Description (AB001884) zinc finger protein [Oryza sativa]

Seq. No. 417284

Seq. ID uC-osroM202014c05b1

Method BLASTN
NCBI GI g451192
BLAST score 85
E value 8.0e-40
Match length 129
% identity 91

NCBI Description Triticum aestivum (wali7) mRNA, 3' end, partial cds

Seq. No. 417285

Seq. ID uC-osroM202014c06b1

Method BLASTX
NCBI GI g2944088
BLAST score 595
E value 9.0e-62
Match length 144
% identity 81

NCBI Description (AF050102) glutathione s-transferase [Oryza sativa]

E value

7.0e-58

```
417286
Seq. No.
Seq. ID
                   uC-osroM202014c08b1
Method
                   BLASTX
NCBI GI
                   q2576361
BLAST score
                   418
                   5.0e-41
E value
Match length
                   116
                   66
% identity
NCBI Description
                  (U39782) lysine and histidine specific transporter
                   [Arabidopsis thaliana]
Seq. No.
                   417287
Seq. ID
                   uC-osroM202014c11b1
Method
                   BLASTX
NCBI GI
                   q5051781
BLAST score
                   509
                   1.0e-51
E value
Match length
                   136
% identity
                   68
NCBI Description
                  (AL078637) transport inhibitor response-like protein
                   [Arabidopsis thaliana]
                   417288
Seq. No.
Seq. ID
                   uC-osroM202014d02b1
Method
                   BLASTX
NCBI GI
                   g136636
                   467
BLAST score
E value
                   1.0e-46
Match length
                   93
% identity
                   91
NCBI Description
                   UBIQUITIN-CONJUGATING ENZYME E2-17 KD 1 (UBIQUITIN-PROTEIN
                   LIGASE 1) (UBIQUITIN CARRIER PROTEIN 1)
                   >gi_1076424_pir__S43781 ubiquitin-conjugating enzyme UBC1 -
                   Arabidopsis thaliana >gi_442594_pdb_1AAK_ Ubiquitin
                   Conjugating Enzyme (E.C.\overline{6}.3.2.1\overline{9}) >\overline{g}i 29\overline{8}1894 pdb 2AAK
                   Ubiquitin Conjugating Enzyme From Arabidopsis Thaliana
                   >gi_166924 (M62721) ubiquitin carrier protein [Arabidopsis
                   thaliana] >gi_431260 (L19351) ubiquitin conjugating enzyme
                   [Arabidopsis thaliana]
Seq. No.
                   417289
Seq. ID
                   uC-osroM202014d03b1
Method
                   BLASTX
NCBI GI
                   g1531674
BLAST score
                   584
E value
                   1.0e-60
Match length
                   116
% identity
NCBI Description (U68462) actin [Striga asiatica]
Seq. No.
                   417290
Seq. ID
                   uC-osroM202014d07b1
Method
                   BLASTX
NCBI GI
                   g82496
BLAST score
                   562
```

```
131
Match length
% identity
NCBI Description phenylalanine ammonia-lyase (EC 4.3.1.5) - rice
                  417291
Seq. No.
                  uC-osroM202014d08b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3885884
BLAST score
                  728
E value
                  3.0e-77
                  149
Match length
                  93
% identity
                 (AF093630) 60S ribosomal protein L21 [Oryza sativa]
NCBI Description
                  417292
Seq. No.
Seq. ID
                  uC-osroM202014d10b1
Method
                  BLASTX
NCBI GI
                  q4982478
BLAST score
                  632
E value
                  4.0e-66
Match length
                  140
% identity
                  81
                  (AF069441) putative leucyl tRNA synthetase [Arabidopsis
NCBI Description
                  thaliana]
                  417293
Seq. No.
Seq. ID
                  uC-osroM202014d11b1
Method
                  BLASTX
NCBI GI
                  q4063743
BLAST score
                  147
                  3.0e-09
E value
Match length
                  64
                  48
% identity
NCBI Description (AC005851) hypothetical protein [Arabidopsis thaliana]
                  417294
Seq. No.
Seq. ID
                  uC-osroM202014e01b1
Method
                  BLASTX
NCBI GI
                  q1304215
BLAST score
                  480
E value
                  3.0e-48
Match length
                  117
% identity
                  86
                  (D84392) precursor of rice 22 kDa protein of photosystem II
NCBI Description
                   (PSII-S) [Oryza sativa]
Seq. No.
                  417295
Seq. ID
                  uC-osroM202014e02b1
Method
                  BLASTX
NCBI GI
                  q4587549
BLAST score
                  149
E value
                  2.0e-09
Match length
                  37
                  70
% identity
                  (AC006577) Similar to gb U55861 RNA binding protein
NCBI Description
                  nucleolysin (TIAR) from Mus musculus and contains several
                  PF_00076 RNA recognition motif domains. ESTs gb_T21032 and
```

Match length

% identity

115

[Oryza sativa]

97

gb T44127 come from this gene. [Arabidopsis t Seq. No. 417296 Seq. ID uC-osroM202014e03b1 Method BLASTX NCBI GI g5007084 BLAST score 693 E value 4.0e-73 Match length 137 % identity 96 NCBI Description (AF155333) NADP-specific isocitrate dehydrogenase [Oryza sativa] 417297 Seq. No. uC-osroM202014e06b1 Seq. ID Method BLASTX g1169797 NCBI GI BLAST score 330 1.0e-30 E value Match length 62 100 % identity NCBI Description GLUCOSE-6-PHOSPHATE ISOMERASE, CYTOSOLIC A (GPI-A) (PHOSPHOGLUCOSE ISOMERASE A) (PGI-A) (PHOSPHOHEXOSE ISOMERASE A) (PHI-A) >gi_639684_dbj_BAA08148_ (D45217) phosphoglucose isomerase (Pgi-a) [Oryza sativa] 417298 Seq. No. uC-osroM202014e07b1 Seq. ID Method BLASTX NCBI GI g1542941 BLAST score 362 E value 2.0e-34 109 Match length % identity 72 NCBI Description (X78116) Acetoacetyl-coenzyme A thiolase [Raphanus sativus] Seq. No. 417299 uC-osroM202014e08b1 Seq. ID Method BLASTX NCBI GI q3242717 BLAST score 289 E value 6.0e-26 Match length 70 % identity NCBI Description (AC003040) putative APG protein [Arabidopsis thaliana] Seq. No. 417300 uC-osroM202014e10b1 Seq. ID Method BLASTX NCBI GI g130187 BLAST score 557 E value 3.0e-57

phy18) - rice >gi 20288 emb CAA32375 (X14172) phytochrome

NCBI Description PHYTOCHROME A >gi 82499 pir S03728 phytochrome (clone

Seq. No. uC-osroM202014f02b1 Seq. ID

417301

Method BLASTN g4097947 NCBI GI BLAST score 43 2.0e-15 E value Match length 63 92 % identity

NCBI Description Oryza sativa beta-1,3-glucanase precursor (Gns9) gene,

complete cds

Seq. No. 417302

uC-osroM202014f03b1 Seq. ID

BLASTX Method NCBI GI g462234 BLAST score 250 7.0e-24E value 92 Match length 71 % identity

HISTONE H2A >gi 419741 pir S30155 histone H2A - Norway NCBI Description

spruce >gi 297871 emb CAA48030 (X67819) histone H2A [Picea

abies]

417303 Seq. No.

uC-osroM202014f06b1 Seq. ID

Method BLASTX NCBI GI g401140 BLAST score 671 9.0e-71 E value 130 Match length % identity 98

SUCROSE SYNTHASE 2 (SUCROSE-UDP GLUCOSYLTRANSFERASE 2) NCBI Description

>gi_20095_emb_CAA41774 (X59046) sucrose-UDP glucosyltransferase (isoenzyme 2) [Oryza sativa]

>gi_1587662_prf__2207194A sucrose synthase:ISOTYPE=2 [Oryza

sativa]

417304 Seq. No.

Seq. ID uC-osroM202014f08b1

Method BLASTX NCBI GI q121332 BLAST score 729 9.0e-85 E value Match length 153 % identity

GLUTAMINE SYNTHETASE ROOT ISOZYME (GLUTAMATE--AMMONIA NCBI Description

LIGASE) (CLONE LAMBDA-GS8) >gi_68590_pir__AJRZQB

glutamate--ammonia ligase (EC 6.3.1.2) beta, cytosolic rice >gi_20358_emb_CAA32460_ (X14244) cytosolic glutamine

syntethase (AA 1-357) [Oryza sativa]

Seq. No. 417305

Seq. ID uC-osroM202014f09b1

Method BLASTX NCBI GI g5295980 BLAST score 672

```
E value
                  1.0e-70
                  140
Match length
% identity
                  94
NCBI Description (AB003323) MADS box-like protein [Oryza sativa]
                  417306
Seq. No.
                  uC-osroM202014g01b1
Seq. ID
Method
                  BLASTX
                  g530088
NCBI GI
                  509
BLAST score
                  1.0e-51
E value
Match length
                  107
% identity
                  85
NCBI Description (U12735) aminoalcoholphosphotransferase [Glycine max]
Seq. No.
                  417307
                  uC-osroM202014g02b1
Seq. ID
Method
                  BLASTN
NCBI GI
                  q4097945
BLAST score
                  57
E value
                  1.0e-23
Match length
                  69
% identity
                  96
NCBI Description Oryza sativa beta-1,3-glucanase precursor (Gns8) gene,
                  partial cds
                  417308
Seq. No.
Seq. ID
                  uC-osroM202014g04b1
Method
                  BLASTN
NCBI GI
                  q1808687
                  47
BLAST score
                  3.0e-17
E value
Match length
                  67
                  93
% identity
NCBI Description S.stapfianus pSD.13 mRNA
                  417309
Seq. No.
Seq. ID
                  uC-osroM202014g05b1
Method
                  BLASTX
NCBI GI
                  q4850396
BLAST score
                  235
                  1.0e-19
E value
Match length
                  95
% identity
                  46
NCBI Description (AC007357) F3F19.15 [Arabidopsis thaliana]
                  417310
Seq. No.
Seq. ID
                  uC-osroM202014g07b1
Method
                  BLASTX
NCBI GI
                  g5821406
```

Method BLASTX
NCBI GI g5821406
BLAST score 323
E value 6.0e-30
Match length 129
% identity 47

NCBI Description (AB025531) 24 kDa vacuolar protein VP24 [Ipomoea batatas]

Seq. No. 417311

uC-osroM202014g08b1 Seq. ID BLASTX Method NCBI GI g2829913 313 BLAST score 1.0e-28 E value 85 Match length 74 % identity (AC002291) putative carboxyphosphonoenolpyruvate mutase NCBI Description [Arabidopsis thaliana] Seq. No. 417312 uC-osroM202014g09b1 Seq. ID BLASTX Method NCBI GI g3868758 BLAST score 217 1.0e-17 E value 42 Match length 88 % identity NCBI Description (D89802) elongation factor 1B gamma [Oryza sativa] 417313 Seq. No. uC-osroM202014g11b1 Seq. ID BLASTX Method g602292 NCBI GI 209 BLAST score 2.0e-16 E value Match length 76 % identity 51 NCBI Description (U17987) RCH2 protein [Brassica napus] Seq. No. 417314 uC-osroM202014h01b1 Seq. ID Method BLASTN g4097945 NCBI GI BLAST score 423 E value 0.0e + 00Match length 431 % identity 100 NCBI Description Oryza sativa beta-1,3-glucanase precursor (Gns8) gene, partial cds Seq. No. 417315 uC-osroM202014h02b1 Seq. ID Method BLASTX NCBI GI q2789660 BLAST score 604 E value 1.0e-62 Match length 175

% identity

NCBI Description (AF040102) p105 [Arabidopsis thaliana]

Seq. No. 417316

uC-osroM202014h03b1 Seq. ID

Method BLASTX NCBI GI g3913804 BLAST score 201 E value 1.0e-15



```
Match length
                  70
% identity
                  63
NCBI Description
                  HISTONE H2B.3 >gi 577825 emb CAA49584 (X69960) H2B histone
                  [Zea mays]
                  417317
Seq. No.
Seq. ID
                  uC-osroM202014h04b1
Method
                  BLASTX
NCBI GI
                  q1402918
BLAST score
                  272
                  7.0e-24
E value
Match length
                  74
% identity
                  72
                  (X98320) peroxidase [Arabidopsis thaliana]
NCBI Description
                  >gi_1429215_emb_CAA67310_ (X98774) peroxidase ATP6a
                  [Arabidopsis thaliana]
                  417318
Seq. No.
Seq. ID
                  uC-osroM202014h08b1
                  BLASTX
Method
NCBI GI
                  q4666287
BLAST score
                  746
                  2.0e-79
E value
Match length
                  170
                  88
% identity
NCBI Description
                  (D85764) cytosolic monodehydroascorbate reductase [Oryza
                  sativa]
Seq. No.
                   417319
                  uC-osroM202014h09b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q5565981
BLAST score
                   442
E value
                  7.0e-44
                  118
Match length
% identity
                  78
NCBI Description
                  (AF152600) unknown [Zea mays]
Seq. No.
                   417320
```

uC-osroM202014h10b1 Seq. ID

Method BLASTX g4538961 NCBI GI 514 BLAST score E value 3.0e-52 137 Match length 69 % identity

(AL049488) isoleucine-tRNA ligase-like protein [Arabidopsis NCBI Description

thaliana]

417321 Seq. No.

uC-osroM202014h11b1 Seq. ID

Method BLASTX NCBI GI q1688233 BLAST score 264 E value 7.0e-23 Match length 108 % identity 56

Seq. No.

```
NCBI Description (U77655) DNA binding protein homolog [Solanum tuberosum]
Seq. No.
                   417322
Seq. ID
                  uC-osroM202014h12b1
Method
                  BLASTX
NCBI GI
                  q4581156
BLAST score
                  233
                  3.0e-19
E value
                  50
Match length
% identity
                  88
NCBI Description (AC006919) putative pyruvate kinase [Arabidopsis thaliana]
                   417323
Seq. No.
                  uC-osroM202016a01b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3355632
BLAST score
                  366
E value
                  6.0e-35
Match length
                  89
                  76
% identity
NCBI Description
                  (AJ006957) stearoyl-acyl carrier protein desaturase [Linum
                  usitatissimum]
Seq. No.
                  417324
                  uC-osroM202016a02b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2914710
BLAST score
                  337
E value
                  2.0e-31
Match length
                  74
                  78
% identity
NCBI Description (AC003974) putative beta-D-galactosidase [Arabidopsis
                  thaliana]
Seq. No.
                  417325
                  uC-osroM202016a04b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q5830787
BLAST score
                  216
E value
                  3.0e-17
Match length
                  129
% identity
                  39
NCBI Description
                  (AL117188) ankyrin repeat-containing protein 2 [Arabidopsis
                  thaliana]
Seq. No.
                  417326
Seq. ID
                  uC-osroM202016a05a1
Method
                  BLASTX
NCBI GI
                  g100865
BLAST score
                  795
                  4.0e-85
E value
Match length
                  170
% identity
NCBI Description chaperonin hsp60 precursor - maize >gi_22242_emb_CAA77645
                  (Z11546) chaperonin hsp60 [Zea mays]
```



Seq. ID uC-osroM202016a05b1

Method BLASTX
NCBI GI g2493646
BLAST score 668
E value 3.0e-70
Match length 146
% identity 95

NCBI Description MITOCHONDRIAL CHAPERONIN HSP60-2 PRECURSOR >gi_309559

(L21008) chaperonin 60 [Zea mays] >gi 309561 (L21006)

mitochondrial chaperonin 60 [Zea mays]

Seq. No. 417328

Seq. ID uC-osroM202016a08b1

Method BLASTX
NCBI GI g2493123
BLAST score 550
E value 2.0e-56
Match length 114
% identity 91

NCBI Description VACUOLAR ATP SYNTHASE CATALYTIC SUBUNIT A (V-ATPASE 69 KD

SUBUNIT) >gi 1051258 (U36939) vacuolar ATPase catalytic

subunit [Hordeum vulgare]

Seq. No. 417329

Seq. ID uC-osroM202016a10a1

Method BLASTX
NCBI GI g5922624
BLAST score 681
E value 6.0e-72
Match length 144
% identity 97

NCBI Description (AP000492) ESTs C97742(C62458), AU078102(C62458) correspond

to a region of the predicted gene.; similar to syntaxin

related protein AtVam3p (U88045) [Oryza sativa] >gi_6016857_dbj_BAA85200.1_ (AP000570) ESTs

C97742(C62458), $\overline{A}U078102(C62458)$ correspond to a region of the predicted gene.; Similar to syntaxin related protein

AtVam3p (U88045) [Oryza sativa]

Seq. No. 417330

Seq. ID uC-osroM202016a10b1

Method BLASTN
NCBI GI g6016845
BLAST score 406
E value 0.0e+00
Match length 414
% identity 100

NCBI Description Oryza sativa genomic DNA, chromosome 1, clone:P0711E10

Seq. No. 417331

Seq. ID uC-osroM202016a12b1

Method BLASTX
NCBI GI g4467145
BLAST score 288
E value 8.0e-26
Match length 98
% identity 56



NCBI Description (AL035540) farnesylated protein (ATFP6) [Arabidopsis thaliana]

Seq. No. 417332

Seq. ID uC-osroM202016b01a1

Method BLASTN
NCBI GI g218144
BLAST score 263
E value 1.0e-146
Match length 310
% identity 96

NCBI Description Rice mRNA for ATP/ADP translocator, complete cds

Seq. No. 417333

Seq. ID uC-osroM202016b01b1

Method BLASTX
NCBI GI g485517
BLAST score 532
E value 2.0e-55
Match length 127
% identity 89

NCBI Description ADP, ATP carrier protein - rice

Seq. No. 417334

Seq. ID uC-osroM202016b02a1

Method BLASTX
NCBI GI g1477428
BLAST score 293
E value 2.0e-26
Match length 58
% identity 97

NCBI Description (X99623) alpha-tubulin 1 [Hordeum vulgare]

Seq. No. 417335

Seq. ID uC-osroM202016b02b1

Method BLASTX
NCBI GI g135399
BLAST score 800
E value 1.0e-85
Match length 169
% identity 91

NCBI Description TUBULIN ALPHA-1 CHAIN >gi 100716 pir S20758 tubulin

alpha-1 chain - rice >gi \(\bar{2}\)0379 \(emb \) \(\bar{CAA}\)77988 \((Z11931) \) alpha 1 tubulin [Oryza sativa] \(>\)gi \(\bar{1}\)136124 \(emb \) CAA62918 \((X91808) \)

alfa-tubulin [Oryza sativa]

Seq. No. 417336

Seq. ID uC-osroM202016b06b1

Method BLASTX
NCBI GI g2668744
BLAST score 792
E value 1.0e-84
Match length 148
% identity 98

NCBI Description (AF034946) ubiquitin conjugating enzyme [Zea mays]

Seq. No. 417337

```
Seq. ID
                  uC-osroM202016b09b1
Method
                  BLASTX
NCBI GI
                   g2708624
BLAST score
                   396
E value
                   2.0e-41
Match length
                   127
% identity
                   66
                  (AF036618) acetyl-CoA synthetase [Arabidopsis thaliana]
NCBI Description
                   417338
Seq. No.
                  uC-osroM202016b10a1
Seq. ID
Method
                  BLASTX
NCBI GI
                   q480450
BLAST score
                   509
E value
                   1.0e-51
Match length
                   108
                   91
% identity
NCBI Description
                  ketol-acid reductoisomerase (EC 1.1.1.86) - Arabidopsis
                   thaliana >gi 402552 emb CAA49506 (X69880) ketol-acid
                   reductoisomerase [Arabidopsis thaliana]
                   417339
Seq. No.
Seq. ID
                   uC-osroM202016b10b1
Method
                   BLASTX
NCBI GI
                   g266346
BLAST score
                   369
E value
                   4.0e-35
Match length
                  147
% identity
                   44
NCBI Description
                  KETOL-ACID REDUCTOISOMERASE PRECURSOR (ACETOHYDROXY-ACID
                  REDUCTOISOMERASE) (ALPHA-KETO-BETA-HYDROXYLACIL
                  REDUCTOISOMERASE) >gi 81509 pir S17180 ketol-acid
                  reductoisomerase (EC \overline{1.1.1.86}) precursor - spinach
                  >gi_21234_emb_CAA40356_ (X57073) ketol-acid
                   reductoisomerase [Spinacia oleracea]
Seq. No.
                   417340
Seq. ID
                  uC-osroM202016b12a1
Method
                  BLASTX
NCBI GI
                  q478409
BLAST score
                   226
E value
                   2.0e-18
Match length
                   67
% identity
                   64
NCBI Description
                  peroxidase (EC 1.11.1.7), cationic - adzuki bean
                  >gi_218328_dbj_BAA01950_ (D11337) peroxidase [Vigna
                  angularis]
Seq. No.
                   417341
Seq. ID
                  uC-osroM202016b12b1
Method
                  BLASTX
NCBI GI
                  q82410
BLAST score
                   301
E value
                  3.0e-27
Match length
                  84
% identity
NCBI Description peroxidase (EC 1.11.1.7) BP1 precursor - barley >gi_167081
```

(M73234) peroxidase BP 1 [Hordeum vulgare]

417342 Seq. No. uC-osroM202016c01b1 Seq. ID Method BLASTX q1203832 NCBI GI 344 BLAST score 3.0e - 32E value 82 Match length 80 % identity (U46003) beta-D-glucan exohydrolase, isoenzyme ExoII NCBI Description [Hordeum vulgare] >gi 1588407 prf__2208395A beta-D-glucan exohydrolase [Hordeum vulgare] 417343 Seq. No. uC-osroM202016c02b1 Seq. ID Method BLASTX NCBI GI q4235430 BLAST score 412 3.0e-40E value 142 Match length % identity (AF098458) latex-abundant protein [Hevea brasiliensis] NCBI Description Seq. No. 417344 Seq. ID uC-osroM202016c04b1 BLASTN Method g6002785 NCBI GI BLAST score 35 E value 6.0e-10 Match length 59 90 % identity NCBI Description Oryza sativa circumsporozoite protein precursor homolog gene, partial cds 417345 Seq. No. uC-osroM202016c05a1 Seq. ID BLASTX Method NCBI GI g129591 BLAST score 201 1.0e-15 E value Match length 41 85 % identity NCBI Description PHENYLALANINE AMMONIA-LYASE >gi_295824_emb_CAA34226_ (X16099) phenylalanine ammonia-Tyase [Oryza sativa] 417346 Seq. No. uC-osroM202016c05b1 Seq. ID BLASTX Method g82496 NCBI GI BLAST score 671 1.0e-70 E value 152 Match length % identity NCBI Description phenylalanine ammonia-lyase (EC 4.3.1.5) - rice

54608

417347

Seq. No.

```
uC-osroM202016c07a1
Seq. ID
                  BLASTX
Method
                  q3913426
NCBI GI
BLAST score
                  216
                  2.0e-17
E value
                  45
Match length
                  89
% identity
                  S-ADENOSYLMETHIONINE DECARBOXYLASE PROENZYME (ADOMETDC)
NCBI Description
                  (SAMDC) >qi 1532048 emb CAA69074 (Y07766)
                  S-adenosylmethionine decarboxylase [Oryza sativa]
                  417348
Seq. No.
Seq. ID
                  uC-osroM202016c07b1
                  BLASTX
Method
                  q2129921
NCBI GI
                  179
BLAST score
                  6.0e-13
E value
                  51
Match length
                  67
% identity
                  hypothetical protein 1 - Madagascar periwinkle >gi 758694
NCBI Description
                   (U12573) putative [Catharanthus roseus]
                  417349
Seq. No.
Seq. ID
                  uC-osroM202016c08a1
Method
                  BLASTX
                  q209603
NCBI GI
                  218
BLAST score
                  1.0e-17
E value
Match length
                  95
% identity
                   53
                 (M31426) ubiquitin/relaxin fusion protein [Artificial gene]
NCBI Description
Seq. No.
                   417350
                   uC-osroM202016c08b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g82734
BLAST score
                   684
                   4.0e-72
E value
Match length
                   137
% identity
                   30
                  ubiquitin precursor - maize (fragment)
NCBI Description
                   >qi 226763 prf 1604470A poly-ubiquitin [Zea mays]
                   417351
Seq. No.
                   uC-osroM202016c09b1
Seq. ID
                   BLASTX
Method
                   g3334756
NCBI GI
                   152
BLAST score
                   5.0e-10
E value
Match length
                   75
                   48
% identity
                  (Y16672) putative arginine/serine-rich splicing factor
NCBI Description
                   [Medicago sativa]
                   417352
Seq. No.
                   uC-osroM202016c10a1
Seq. ID
```

54609

BLASTX

Method

```
g2499488
NCBI GI
BLAST score
                   296
                   1.0e-26
E value
Match length
                  96
                   64
% identity
NCBI Description PYROPHOSPHATE--FRUCTOSE 6-PHOSPHATE 1-PHOSPHOTRANSFERASE
                  ALPHA SUBUNIT (PFP) (6-PHOSPHOFRUCTOKINASE (PYROPHOSPHATE))
                   (PYROPHOSPHATE-DEPENDENT 6-PHOSPHOFRUCTOSE-1-KINASE)
                   (PPI-PFK) >qi 483547 emb CAA83682 (Z32849)
                  pyrophosphate-dependent phosphofructokinase alpha subunit
                   [Ricinus communis]
Seq. No.
                   417353
                  uC-osroM202016c10b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3790102
BLAST score
                  476
E value
                  3.0e-49
Match length
                  162
% identity
                  61
NCBI Description
                  (AF095521) pyrophosphate-dependent phosphofructokinase
                  alpha subunit [Citrus X paradisi]
Seq. No.
                  417354
                  uC-osroM202016d01a1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1709563
BLAST score
                  191
E value
                  2.0e-35
Match length
                  116
                  78
% identity
NCBI Description PHENYLALANINE AMMONIA-LYASE >gi_2130081_pir__S66313
                  phenylalanine ammonia-lyase (EC 4.3.1.5) - rice
                  >gi_871494_emb_CAA61198 (X87946) phenylalanine
                  ammonia-lyase [Oryza sativa]
Seq. No.
                  417355
Seq. ID
                  uC-osroM202016d01b1
Method
                  BLASTX
NCBI GI
                  q1710841
BLAST score
                  607
E value
                   3.0e-63
Match length
                  121
% identity
                  95
NCBI Description
                  ADENOSYLHOMOCYSTEINASE (S-ADENOSYL-L-HOMOCYSTEINE
                  HYDROLASE) (ADOHCYASE) >gi_758247_emb_CAA56278_ (X79905)
                  S-adenosylhomocysteine hydrolase [Phalaenopsis sp.]
Seq. No.
                  417356
                  uC-osroM202016d02b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q82410
BLAST score
                  275
E value
                  5.0e-25
                  92
Match length
% identity
```

NCBI Description peroxidase (EC 1.11.1.7) BP1 precursor - barley >gi_167081

(M73234) peroxidase BP 1 [Hordeum vulgare]

Seq. No. 417357

Seq. ID uC-osroM202016d07a1

Method BLASTX
NCBI GI g1710401
BLAST score 199
E value 2.0e-15
Match length 50
% identity 78

NCBI Description RIBONUCLEOSIDE-DIPHOSPHATE REDUCTASE SMALL CHAIN

(RIBONUCLEOTIDE REDUCTASE) (R2 SUBUNIT)

>gi 1044912 emb CAA63194 (X92443) ribonucleotide reductase

R2 [Nicotiana tabacum]

Seq. No. 417358

Seq. ID uC-osroM202016d07b1

Method BLASTX
NCBI GI g1710401
BLAST score 476
E value 9.0e-48
Match length 119
% identity 76

NCBI Description RIBONUCLEOSIDE-DIPHOSPHATE REDUCTASE SMALL CHAIN

(RIBONUCLEOTIDE REDUCTASE) (R2 SUBUNIT)

>gi 1044912 emb CAA63194 (X92443) ribonucleotide reductase

R2 [Nicotiana tabacum]

Seq. No. 417359

Seq. ID uC-osroM202016d08b1

Method BLASTX
NCBI GI g4966344
BLAST score 232
E value 4.0e-19
Match length 87
% identity 53

NCBI Description (AC006341) ESTs gb_F15498, gb_H37515, gb_T41906, gb_T22448,

gb W43356 and gb T20739 come from this gene. [Arabidopsis

thaliana]

Seq. No. 417360

Seq. ID uC-osroM202016d09b1

Method BLASTX
NCBI GI g129960
BLAST score 318
E value 3.0e-29
Match length 130
% identity 49

NCBI Description 4-NITROPHENYLPHOSPHATASE (PNPPASE)

>gi_5924022_emb_CAB56540.1_ (X51611)

p-nitrophenylphosphatase [Saccharomyces cerevisiae]

Seq. No. 417361

Seq. ID uC-osroM202016d10a1

Method BLASTX NCBI GI g3023817 BLAST score 444



E value 5.0e-44
Match length 94
% identity 87

NCBI Description GLUCOSE-6-PHOSPHATE 1-DEHYDROGENASE, CHOLOROPLAST ISOFORM

PRECURSOR (G6PD) >gi_1480344_emb_CAA67782_ (X99405) glucose-6-phosphate dehydrogenase [Nicotiana tabacum]

Seq. No. 417362

Seq. ID uC-osroM202016d10b1

Method BLASTX
NCBI GI g3023817
BLAST score 371
E value 2.0e-35
Match length 108
% identity 71

NCBI Description GLUCOSE-6-PHOSPHATE 1-DEHYDROGENASE, CHOLOROPLAST ISOFORM

PRECURSOR (G6PD) >gi_1480344_emb_CAA67782_ (X99405) qlucose-6-phosphate dehydrogenase [Nicotiana tabacum]

Seq. No. 417363

Seq. ID uC-osroM202016d11a1

Method BLASTX
NCBI GI g4580389
BLAST score 223
E value 3.0e-18
Match length 65
% identity 63

NCBI Description (AC007171) unknown protein [Arabidopsis thaliana]

Seq. No. 417364

Seq. ID uC-osroM202016d11b1

Method BLASTX
NCBI GI g4580389
BLAST score 500
E value 2.0e-50
Match length 145
% identity 67

NCBI Description (AC007171) unknown protein [Arabidopsis thaliana]

Seq. No. 417365

Seq. ID uC-osroM202016d12a1

Method BLASTX
NCBI GI g5734619
BLAST score 260
E value 2.0e-22
Match length 60
% identity 78

NCBI Description (AP000391) Similar to Arabidopsis thaliana BAC F15P23

(AF128392) [Oryza sativa]

Seq. No. 417366

Seq. ID uC-osroM202016d12b1

Method BLASTX
NCBI GI g5734619
BLAST score 674
E value 6.0e-71
Match length 165

% identity 73

NCBI Description (AP000391) Similar to Arabidopsis thaliana BAC F15P23

(AF128392) [Oryza sativa]

Seq. No. 417367

Seq. ID uC-osroM202016e03a1

Method BLASTN
NCBI GI g20357
BLAST score 42
E value 3.0e-14
Match length 138
% identity 83

NCBI Description Oryza sativa root GS1 mRNA for cytosolic glutamine

synthetase (EC 6.3.1.2) (clone lambda-GS8)

Seq. No. 417368

Seq. ID uC-osroM202016e03b1

Method BLASTX
NCBI GI g121332
BLAST score 715
E value 8.0e-76
Match length 134
% identity 99

NCBI Description GLUTAMINE SYNTHETASE ROOT ISOZYME (GLUTAMATE--AMMONIA

LIGASE) (CLONE LAMBDA-GS8) >gi 68590 pir AJRZQB

glutamate--ammonia ligase (EC 6.3.1.2) beta, cytosolic - rice >gi_20358_emb_CAA32460_ (X14244) cytosolic glutamine

syntethase (AA 1-357) [Oryza sativa]

Seq. No. 417369

Seq. ID uC-osroM202016e04a1

Method BLASTX
NCBI GI g4587519
BLAST score 303
E value 2.0e-27
Match length 76
% identity 78

NCBI Description (AC007060) Strong similarity to F19I3.7 gi 3033380 putative

coatomer epsilon subunit from Arabidopsis Thaliana BAC gb_AC004238. ESTs gb_Z17908, gb_AA728673, gb_N96555, gb_H76335, gb_AA712463, gb_W43247, gb_T45611, g

Seq. No. 417370

Seq. ID uC-osroM202016e04b1

Method BLASTX
NCBI GI g3738319
BLAST score 378
E value 3.0e-36
Match length 93
% identity 71

NCBI Description (AC005170) hypothetical protein [Arabidopsis thaliana]

Seq. No. 417371

Seq. ID uC-osroM202016e06b1

Method BLASTN NCBI GI g3798727

BLAST score 35



```
E value 3.0e-10
Match length 71
% identity 87
NCBI Description Arabidon
```

NCBI Description Arabidopsis thaliana transgenic line A DNA, 5'-junction

region

Seq. No. 417372

Seq. ID uC-osroM202016e07a1

Method BLASTX
NCBI GI 94835757
BLAST score 153
E value 5.0e-10
Match length 33
% identity 85

NCBI Description (AC007202) EST gb_AA404917 comes from this gene.

[Arabidopsis thaliana]

Seq. No. 417373

Seq. ID uC-osroM202016e07b1

Method BLASTX
NCBI GI 94835757
BLAST score 169
E value 8.0e-12
Match length 80
% identity 51

NCBI Description (AC007202) EST gb_AA404917 comes from this gene.

[Arabidopsis thaliana]

Seq. No. 417374

Seq. ID uC-osroM202016e09a1

Method BLASTX
NCBI GI g1709563
BLAST score 652
E value 2.0e-68
Match length 132
% identity 96

NCBI Description PHENYLALANINE AMMONIA-LYASE >gi_2130081_pir__S66313

phenylalanine ammonia-lyase (EC 4.3.1.5) - rice >gi_871494_emb_CAA61198_ (X87946) phenylalanine

ammonia-lyase [Oryza sativa]

Seq. No. 417375

Seq. ID uC-osroM202016e09b1

Method BLASTX
NCBI GI g3024363
BLAST score 423
E value 1.0e-41
Match length 104
% identity 76

NCBI Description PHENYLALANINE AMMONIA-LYASE >gi_1483610_emb_CAA68036_ (X99705) phenylalanine ammonia-lyase [Triticum aestivum]

Seq. No. 417376

Seq. ID uC-osroM202016e11a1

Method BLASTX
NCBI GI g5263320
BLAST score 186

Seq. ID

Method

```
1.0e-13
E value
Match length
                  64
                  62
% identity
                  (AC007727) Similar to gb M87339 replication factor C,
NCBI Description
                  37-kDa subunit from Homo sapiens and is a member of
                  PF 00004 ATPases associated with various cellular
                  activities. [Arabidopsis thaliana]
                  417377
Seq. No.
                  uC-osroM202016e11b1
Seq. ID
                  BLASTX
Method
                  q5263320
NCBI GI
BLAST score
                  603
                  1.0e-62
E value
                  131
Match length
% identity
                   (AC007727) Similar to qb M87339 replication factor C,
NCBI Description
                  37-kDa subunit from Homo sapiens and is a member of
                  PF 00004 ATPases associated with various cellular
                  activities. [Arabidopsis thaliana]
                   417378
Seq. No.
                  uC-osroM202016f02a1
Seq. ID
Method
                  BLASTX
                   q6017123
NCBI GI
BLAST score
                   221
                   5.0e-18
E value
                   61
Match length
% identity
                   69
NCBI Description
                  (AC009895) unknown protein [Arabidopsis thaliana]
Seq. No.
                   417379
                   uC-osroM202016f02b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g6017123
BLAST score
                   346
                   4.0e-36
E value
Match length
                   128
% identity
                   67
                  (AC009895) unknown protein [Arabidopsis thaliana]
NCBI Description
                   417380
Seq. No.
                   uC-osroM202016f03a1
Seq. ID
                   BLASTX
Method
                   g4325345
NCBI GI
                   257
BLAST score
                   4.0e-22
E value
                   86
Match length
% identity
                   22
NCBI Description
                  (AF128393) similar to thioredoxin-like proteins (Pfam:
                   PF00085, Score=42.9, E=1.4e-11, N=1); contains similarity
                   to dihydroorotases (Pfam: PF00744, Score=154.9, E=1.4e-42,
                   N=1) [Arabidopsis thaliana]
                   417381
Seq. No.
```

uC-osroM202016f05a1

BLASTX



NCBI GI g3746060 BLAST score 156 E value 3.0e-10 Match length 36 % identity 83

NCBI Description (AC005311) unknown protein [Arabidopsis thaliana]

Seq. No. 417382

Seq. ID uC-osroM202016f06a1

Method BLASTN
NCBI GI g6063530
BLAST score 350
E value 0.0e+00
Match length 362
% identity 99

NCBI Description Oryza sativa genomic DNA, chromosome 3, clone:P0043E01

Seq. No. 417383

Seq. ID uC-osroM202016f06b1

Method BLASTN
NCBI GI g6063530
BLAST score 518
E value 0.0e+00
Match length 522
% identity 100

NCBI Description Oryza sativa genomic DNA, chromosome 3, clone:P0043E01

Seq. No. 417384

Seq. ID uC-osroM202016f07a1

Method BLASTX
NCBI GI g1354849
BLAST score 167
E value 1.0e-11
Match length 67
% identity 45

NCBI Description (U57350) epoxide hydrolase [Nicotiana tabacum]

Seq. No. 417385

Seq. ID uC-osroM202016f07b1

Method BLASTX
NCBI GI g1354849
BLAST score 265
E value 3.0e-23
Match length 78
% identity 60

NCBI Description (U57350) epoxide hydrolase [Nicotiana tabacum]

Seq. No. 417386

Seq. ID uC-osroM202016f08a1

Method BLASTN
NCBI GI g1777454
BLAST score 237
E value 1.0e-131
Match length 280
% identity 96

NCBI Description Oryza sativa pyruvate decarboxylase 2 (pdc2) gene, complete

cds

```
Seq. No.
                   417387
                   uC-osroM202016f08b1
Seq. ID
                   BLASTN
Method
                   q1777454
NCBI GI
BLAST score
                   179
                   6.0e-96
E value
                   396
Match length
                   97
% identity
                   Oryza sativa pyruvate decarboxylase 2 (pdc2) gene, complete
NCBI Description
                   417388
Seq. No.
                   uC-osroM202016f10b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g4506233
BLAST score
                   158
                   2.0e-10
E value
                   96
Match length
                   33
% identity
                   proteasome (prosome, macropain) 26S subunit, non-ATPase, 8
NCBI Description
                   >gi 1346766_sp_P48556_PSD8_HUMAN 26S PROTEASOME REGULATORY
                   SUBUNIT S14^-(P\overline{3}1) >gi^-1362\overline{7}41^-pir^-S56108 multicatalytic
                   endopeptidase complex (EC 3.4.99.46) regulatory chain 31 -
                   human >gi_1037164_dbj_BAA07237_ (D38047) 26S proteasome subunit p31 [Homo sapiens] >gi_3702282 (AC005789)
                   PP31 HUMAN [Homo sapiens]
                    417389
Seq. No.
                   uC-osroM202016f11a1
Seq. ID
                   BLASTX
Method
NCBI GI
                   g1136122
BLAST score
                   284
                   3.0e-25
E value
                   61
Match length
                    92
% identity
NCBI Description (X91807) alfa-tubulin [Oryza sativa]
                    417390
Seq. No.
                   uC-osroM202016f11b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   q1136122
                   816
BLAST score
E value
                    5.0e-93
Match length
                   173
% identity
NCBI Description (X91807) alfa-tubulin [Oryza sativa]
Seq. No.
                    417391
                   uC-osroM202016f12a1
Seq. ID
Method
                   BLASTX
NCBI GI
                   q4587519
BLAST score
                    468
E value
                    1.0e-46
Match length
                   110
% identity
NCBI Description (AC007060) Strong similarity to F19I3.7 gi 3033380 putative
```



coatomer epsilon subunit from Arabidopsis thaliana BAC gb_AC004238. ESTs gb_Z17908, gb_AA728673, gb_N96555, gb_H76335, gb_AA712463, gb_W43247, gb_T45611, g

Seq. No. 417392

Seq. ID uC-osroM202016f12b1

Method BLASTX
NCBI GI 94587519
BLAST score 496
E value 4.0e-50
Match length 134
% identity 72

NCBI Description (AC007060) Strong similarity to F19I3.7 gi_3033380 putative

coatomer epsilon subunit from Arabidopsis thaliana BAC gb_AC004238. ESTs gb_Z17908, gb_AA728673, gb_N96555,

gb_H76335, gb_AA712463, gb_W43247, gb_T45611, g

Seq. No. 417393

Seq. ID uC-osroM202016g01a1

Method BLASTN
NCBI GI g2894533
BLAST score 176
E value 2.0e-94
Match length 268
% identity 92

NCBI Description Oryza sativa mRNA for aquaporin, complete CDS

Seq. No. 417394

Seq. ID uC-osroM202016g02b1

Method BLASTX
NCBI GI g2708745
BLAST score 179
E value 5.0e-13
Match length 122
% identity 32

NCBI Description (AC003952) putative calcium-dependent ser/thr protein

kinase [Arabidopsis thaliana]

Seq. No. 417395

Seq. ID uC-osroM202016g03a1

Method BLASTX
NCBI GI g1168537
BLAST score 175
E value 9.0e-13
Match length 36
% identity 86

NCBI Description ASPARTIC PROTEINASE PRECURSOR >gi_82458_pir__JS0732

aspartic proteinase (EC 3.4.23.-) - rice

>gi_218143_dbj_BAA02242_ (D12777) aspartic proteinase

[Oryza sativa]

Seq. No. 417396

Seq. ID uC-osroM202016g03b1

Method BLASTX NCBI GI g1168537 BLAST score 507 E value 2.0e-51



```
Match length
                  118
% identity
                  85
                  ASPARTIC PROTEINASE PRECURSOR >gi_82458_pir__JS0732
NCBI Description
                  aspartic proteinase (EC 3.4.23.-) - rice
                  >gi 218143 dbj BAA02242 (D12777) aspartic proteinase
                  [Oryza sativa]
Seq. No.
                  417397
Seq. ID
                  uC-osroM202016g05b1
                  BLASTX
Method
                  g2244818
                  327
```

NCBI GI g2244818
BLAST score 327
E value 3.0e-30
Match length 99
% identity 61

NCBI Description (Z97336) hypothetical protein [Arabidopsis thaliana]

 Seq. No.
 417398

 Seq. ID
 uC-osroM202016g06b1

 Method
 BLASTX

 NCBI GI
 g1076748

 BLAST score
 235

BLAST score 235 E value 2.0e-19 Match length 86 % identity 52

NCBI Description major intrinsic protein - rice >gi_440869_dbj_BAA04257_

(D17443) major intrinsic protein [Oryza sativa]

Seq. No. 417399

Seq. ID uC-osroM202016g07a1

Method BLASTX
NCBI GI g2696804
BLAST score 195
E value 5.0e-15
Match length 40
% identity 93

NCBI Description (AB009665) water channel protein [Oryza sativa]

Seq. No. 417400

Seq. ID uC-osroM202016g07b1

Method BLASTX
NCBI GI g2894534
BLAST score 675
E value 4.0e-71
Match length 134
% identity 98

NCBI Description (AJ224327) aquaporin [Oryza sativa]

Seq. No. 417401

Seq. ID uC-osroM202016g08a1

Method BLASTX
NCBI GI g2065531
BLAST score 503
E value 6.0e-51
Match length 157
% identity 57

NCBI Description (U78526) endo-1,4-beta-glucanase [Lycopersicon esculentum]

Seq. No. 417402

Seq. ID uC-osroM202016g09a1

Method BLASTX
NCBI GI g1203832
BLAST score 658
E value 4.0e-69
Match length 149
% identity 84

NCBI Description (U46003) beta-D-glucan exohydrolase, isoenzyme ExoII

[Hordeum vulgare] >gi_1588407_prf__2208395A beta-D-glucan

exohydrolase [Hordeum vulgare]

Seq. No. 417403

Seq. ID uC-osroM202016g09b1

Method BLASTX
NCBI GI g1203832
BLAST score 183
E value 2.0e-13
Match length 64
% identity 62

NCBI Description (U46003) beta-D-glucan exohydrolase, isoenzyme ExoII

[Hordeum vulgare] >gi_1588407_prf__2208395A beta-D-glucan

exohydrolase [Hordeum vulgare]

Seq. No. 417404

Seq. ID uC-osroM202016h05b1

Method BLASTN
NCBI GI g6006355
BLAST score 442
E value 0.0e+00
Match length 453

% identity 100

NCBI Description Oryza sativa genomic DNA, chromosome 6, clone:P0493C11

Seq. No. 417405

Seq. ID uC-osroM202016h10b1

Method BLASTX
NCBI GI g5007080
BLAST score 637
E value 1.0e-66
Match length 166
% identity 71

NCBI Description (AF153689) poly(A)-binding protein [Oryza sativa]

Seq. No. 417406

Seq. ID uC-osroM202017a01b1

Method BLASTX
NCBI GI 94104060
BLAST score 417
E value 8.0e-41
Match length 162
% identity 54

NCBI Description (AF031231) S222 [Triticum aestivum]

Seq. No. 417407

Seq. ID uC-osroM202017a03a1



```
Method
                  BLASTX
NCBI GI
                  g6041822
BLAST score
                  250
                  1.0e-21
E value
Match length
                  68
                  74
% identity
NCBI Description
                  (AC009918) unknown protein [Arabidopsis thaliana]
                  417408
Seq. No.
                  uC-osroM202017a04a1
Seq. ID
Method
                  BLASTX
                  g6041822
                  268
```

NCBI GI BLAST score 1.0e-23 E value Match length 69 % identity 80

(AC009918) unknown protein [Arabidopsis thaliana] NCBI Description

417409 Seq. No.

uC-osroM202017a06a1 Seq. ID

Method BLASTX g4544438 NCBI GI BLAST score 157 7.0e-11E value 98 Match length 37 % identity

NCBI Description (AC006592) hypothetical protein [Arabidopsis thaliana]

Seq. No. 417410

uC-osroM202017a08b1 Seq. ID

Method BLASTX NCBI GI q4678310 BLAST score 216 E value 2.0e-17 86 Match length 44 % identity

NCBI Description (AL049655) putative protein [Arabidopsis thaliana]

417411 Seq. No.

uC-osroM202017a09a1 Seq. ID

Method BLASTX NCBI GI q1839188 BLAST score 210 E value 6.0e-17 Match length 50 % identity 82

NCBI Description (U86081) root hair defective 3 [Arabidopsis thaliana]

Seq. No. 417412

uC-osroM202017a11b1 Seq. ID

Method BLASTX NCBI GI q5902363 BLAST score 445 E value 3.0e-44Match length 145 % identity 63

NCBI Description (AC009322) Putative coatomer protein complex, subunit beta

Seq. No.

417418

```
2 (beta prime) [Arabidopsis thaliana]
Seq. No.
                   417413
Seq. ID
                   uC-osroM202017a12b1
Method
                   BLASTX
NCBI GI
                   q451193
BLAST score
                   271
                   1.0e-23
E value
Match length
                   86
% identity
                   65
NCBI Description
                   (L28008) wali7 [Triticum aestivum]
                   >gi_1090845_prf__2019486B wali7 gene [Triticum aestivum]
Seq. No.
                   417414
Seq. ID
                   uC-osroM202017b01b1
Method
                   BLASTX
NCBI GI
                   g3914015
BLAST score
                   291
                   5.0e-26
E value
                  134
Match length
% identity
                   50
NCBI Description
                  TRANSCRIPTION-REPAIR COUPLING FACTOR (TRCF)
                   >gi 1001661 dbj BAA10395 (D64002) transcription-repair
                   coupling factor [Synechocystis sp.]
Seq. No.
                   417415
Seq. ID
                   uC-osroM202017b02a1
Method
                  BLASTN
NCBI GI
                   g20280
BLAST score
                   269
E value
                   1.0e-150
Match length
                  269
                   100
% identity
NCBI Description Rice gene for phenylalanine ammonia-lyase (EC 4.3.1.5)
Seq. No.
                   417416
Seq. ID
                  uC-osroM202017b02b1
Method
                  BLASTX
NCBI GI
                  q82496
BLAST score
                   647
E value
                  1.0e-67
Match length
                  152
% identity
NCBI Description phenylalanine ammonia-lyase (EC 4.3.1.5) - rice
Seq. No.
                  417417
Seq. ID
                  uC-osroM202017b03b1
Method
                  BLASTX
NCBI GI
                  q4455364
BLAST score
                  220
E value
                  7.0e-18
Match length
                  83
% identity
                  53
                  (AL035524) senescence-associated protein-like [Arabidopsis
NCBI Description
                  thaliana]
```

```
uC-osroM202017b05a1
Seq. ID
                  BLASTN
Method
                  g3273242
NCBI GI
                  266
BLAST score
                  1.0e-148
E value
                  266
Match length
                  100
% identity
NCBI Description Oryza sativa mRNA for NLS receptor, complete cds
                  417419
Seq. No.
                  uC-osroM202017b05b1
Seq. ID
Method
                  BLASTX
                  g3273243
NCBI GI
BLAST score
                  371
E value
                  1.0e-35
Match length
                  94
                  83
% identity
NCBI Description
                  (AB004660) NLS receptor [Oryza sativa]
                  >qi 3273245 dbj BAA31166 (AB004814) NLS receptor [Oryza
                  sativa]
                  417420
Seq. No.
Seq. ID
                  uC-osroM202017b06b1
Method
                  BLASTX
NCBI GI
                  q2342735
BLAST score
                  389
                  1.0e-37
E value
Match length
                  133
% identity
                  64
                 (AC002341) unknown protein [Arabidopsis thaliana]
NCBI Description
                  417421
Seq. No.
                  uC-osroM202017b08b1
Seq. ID
                  BLASTX
Method
NCBI GI
                  g2493318
BLAST score
                  237
E value
                  1.0e-19
Match length
                  99
                  48
% identity
NCBI Description BLUE COPPER PROTEIN PRECURSOR >gi_562779 emb CAA80963
                   (Z25471) blue copper protein [Pisum sativum]
                  >gi 1098264 prf 2115352A blue Cu protein [Pisum sativum]
                   417422
Seq. No.
                  uC-osroM202017b09b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1814403
BLAST score
                  637
E value
                   1.0e-66
Match length
                  134
```

% identity

(U84889) methionine synthase [Mesembryanthemum NCBI Description

crystallinum]

Seq. No. 417423

uC-osroM202017b11b1 Seq. ID

Method BLASTX NCBI GI g5702231
BLAST score 243
E value 1.0e-20
Match length 117
% identity 47
NCBI Description (AF14538

ICBI Description (AF145386) hypersensitive reaction associated Ca2+-binding

protein [Phaseolus vulgaris]

Seq. No. 417424

Seq. ID uC-osroM202017b12b1

Method BLASTX
NCBI GI g1170606
BLAST score 374
E value 8.0e-36
Match length 83
% identity 90

NCBI Description ADENYLATE KINASE, CHLOROPLAST (ATP-AMP TRANSPHOSPHORYLASE)

>gi_629863_pir__S45634 adenylate kinase (EC 2.7.4.3),
chloroplast - maize >gi_3114421_pdb_1ZAK_A Chain A,
Adenylate Kinase From Maize In Complex With The Inhibitor

P1, P5-Bis(Adenosine-5'-)pentaphosphate (Ap5a)

>gi_3114422 pdb 1ZAK B Chain B, Adenylate Kinase From Maize

In Complex With The Inhibitor

P1, P5-Bis (Adenosine-5'-) pentaphosphate (Ap5a)

Seq. No. 417425

Seq. ID uC-osroM202017c02b1

Method BLASTX
NCBI GI g2827708
BLAST score 573
E value 4.0e-59
Match length 118
% identity 85

NCBI Description (AL021684) myb - related protein [Arabidopsis thaliana]

Seq. No. 417426

Seq. ID uC-osroM202017c03b1

Method BLASTX
NCBI GI g5478530
BLAST score 161
E value 9.0e-11
Match length 90
% identity 19

NCBI Description (AF130441) UVB-resistance protein UVR8 [Arabidopsis

thaliana]

Seq. No. 417427

Seq. ID uC-osroM202017c05a1

Method BLASTN
NCBI GI g3789949
BLAST score 235
E value 1.0e-129
Match length 259
% identity 98

NCBI Description Oryza sativa translation initiation factor (GOS2) mRNA,

complete cds

```
Seq. No.
                  417428
Seq. ID
                  uC-osroM202017c05b1
Method
                  BLASTX
NCBI GI
                  g462195
                  309
BLAST score
                  2.0e-33
E value
Match length
                  109
% identity
                  80
NCBI Description
                  PROTEIN TRANSLATION FACTOR SUI1 HOMOLOG (GOS2 PROTEIN)
                  >gi 100682 pir S21636 GOS2 protein - rice
                  >gi 20238 emb CAA36190 (X51910) GOS2 [Oryza sativa]
                  >gi 3789950 (AF094774) translation initiation factor [Oryza
                  sativa]
Seq. No.
                  417429
Seq. ID
                  uC-osroM202017c06b1
Method
                  BLASTX
NCBI GI
                  q5091622
BLAST score
                  251
E value
                  2.0e-21
Match length
                  126
% identity
                  37
NCBI Description
                 (AC007454) F23M19.10 [Arabidopsis thaliana]
Seq. No.
                  417430
Seq. ID
                  uC-osroM202017c08a1
Method
                  BLASTN
NCBI GI
                  g2224914
BLAST score
                  197
                  1.0e-107
E value
Match length
                  197
                  100
% identity
NCBI Description Oryza sativa beta-expansin mRNA, complete cds
                  417431
Seq. No.
                  uC-osroM202017c08b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2224915
BLAST score
                  812
E value
                  3.0e-87
Match length
                  145
                  99
% identity
NCBI Description (U95968) beta-expansin [Oryza sativa]
Seq. No.
                  417432
                  uC-osroM202017c09b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4097690
BLAST score
                  595
E value
                  1.0e-61
Match length
                  136
% identity
                  82
NCBI Description
                  (U66592) prohibitin 2 [Arabidopsis thaliana] >gi 4099801
                   (U89791) prohibitin-like protein [Arabidopsis thaliana]
```

Seq. No. 417433

>gi_4204301 (AC003027) prohibitin 2 [Arabidopsis thaliana]

BLAST score

```
uC-osroM202017c10b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1763063
BLAST score
                  244
E value
                  1.0e-20
Match length
                  155
                  42
% identity
NCBI Description (U68763) SCOF-1 [Glycine max]
Seq. No.
                  417434
                  uC-osroM202017c11a1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g435648
BLAST score
                  245
E value
                  1.0e-135
Match length
                  257
                  99
% identity
NCBI Description Rice mRNA for gamma-Tip, complete cds
                  417435
Seq. No.
Seq. ID
                  uC-osroM202017c11b1
Method
                  BLASTX
NCBI GI
                  g1729971
BLAST score
                  341
E value
                  4.0e-32
Match length
                  99
% identity
                  71
                  TONOPLAST INTRINSIC PROTEIN, GAMMA (GAMMA TIP)
NCBI Description
                   (AQUAPORIN-TIP) >gi_1076745_pir__S52004 gamma-Tip protein -
                  rice >gi_473997_dbj_BAA05017 (D25534) gamma-Tip [Oryza
                  sativa]
                  417436
Seq. No.
Seq. ID
                  uC-osroM202017c12b1
Method
                  BLASTN
NCBI GI
                  q575425
BLAST score
                  107
E value
                  6.0e-53
Match length
                  238
                  87
% identity
NCBI Description Z.mays mRNA for sugar-starvation induced protein
Seq. No.
                   417437
Seq. ID
                  uC-osroM202017d01b1
Method
                  BLASTX
NCBI GI
                  g4895183
BLAST score
                  408
E value
                  8.0e-40
Match length
                  156
% identity
                  56
NCBI Description (AC007661) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  417438
Seq. ID
                  uC-osroM202017d02a1
Method
                  BLASTN
NCBI GI
                  g450548
```



E value 1.0e-112 Match length 206 % identity 100

NCBI Description O.sativa (pRSAM-1) gene for S-adenosyl methionine

synthetase

Seq. No. 417439

Seq. ID uC-osroM202017d02b1

Method BLASTX
NCBI GI g1170937
BLAST score 558
E value 2.0e-57
Match length 107
% identity 100

NCBI Description S-ADENOSYLMETHIONINE SYNTHETASE 1 (METHIONINE

ADENOSYLTRANSFERASE 1) (ADOMET SYNTHETASE 1)

>gi_450549 emb CAA81481 (Z26867) S-adenosyl methionine

synthetase [Oryza sativa]

Seq. No. 417440

Seq. ID uC-osroM202017d03a1

Method BLASTN
NCBI GI g4158220
BLAST score 251
E value 1.0e-139

E value 1.0e-Match length 278 % identity 98

NCBI Description Oryza sativa mRNA for reversibly glycosylated polypeptide

Seq. No. 417441

Seq. ID uC-osroM202017d03b1

Method BLASTX
NCBI GI g3646373
BLAST score 604
E value 1.0e-70
Match length 138
% identity 95

NCBI Description (AJ011078) RGP1 protein [Oryza sativa]

Seq. No. 417442

Seq. ID uC-osroM202017d06b1

Method BLASTX
NCBI GI g2961346
BLAST score 314
E value 2.0e-33
Match length 86
% identity 76

NCBI Description (AL022140) pectinesterase like protein [Arabidopsis

thaliana]

Seq. No. 417443

Seq. ID uC-osroM202017d08b1

Method BLASTX
NCBI GI 94803927
BLAST score 348
E value 1.0e-32
Match length 137

Seq. No.

```
% identity
NCBI Description
                  (AC006264) signal sequence receptor, alpha subunit
                   (SSR-alpha) [Arabidopsis thaliana]
Seq. No.
                   417444
Seq. ID
                  uC-osroM202017d09a1
Method
                  BLASTX
NCBI GI
                  q4406812
BLAST score
                   202
E value
                   6.0e-16
Match length
                   69
                   58
% identity
NCBI Description
                  (AC006201) putative DNA binding protein [Arabidopsis
                  thaliana]
Seq. No.
                   417445
Seq. ID
                  uC-osroM202017d10b1
Method
                  BLASTX
NCBI GI
                  q5579444
BLAST score
                   187
E value
                   8.0e-14
Match length
                   69
% identity
                   54
NCBI Description (AF030091) cyclin ania-6a [Rattus norvegicus]
Seq. No.
                   417446
Seq. ID
                  uC-osroM202017d11b1
Method
                  BLASTX
NCBI GI
                  q3915254
BLAST score
                  147
                   4.0e-09
E value
Match length
                   44
                  73
% identity
NCBI Description VACUOLAR ATP SYNTHASE 16 KD PROTEOLIPID SUBUNIT (V-ATPASE
                  16 KD PROTEOLIPID SUBUNIT)
Seq. No.
                   417447
Seq. ID
                  uC-osroM202017d12a1
Method
                  BLASTN
NCBI GI
                  g20280
BLAST score
                   276
E value
                  1.0e-154
Match length
                  276
                   100
% identity
NCBI Description Rice gene for phenylalanine ammonia-lyase (EC 4.3.1.5)
Seq. No.
                   417448
Seq. ID
                  uC-osroM202017d12b1
Method
                  BLASTX
NCBI GI
                  q82496
BLAST score
                  555
E value
                   4.0e-57
Match length
                  131
% identity
```

54628

NCBI Description phenylalanine ammonia-lyase (EC 4.3.1.5) - rice

```
Seq. ID
                  uC-osroM202017e01a1
                  BLASTN
Method
NCBI GI
                  q435648
                  264
BLAST score
                  1.0e-147
E value
                  272
Match length
                  100
% identity
NCBI Description Rice mRNA for gamma-Tip, complete cds
Seq. No.
                  417450
Seq. ID
                  uC-osroM202017e01b1
Method
                  BLASTX
                  g1729971
NCBI GI
BLAST score
                  346
E value
                  1.0e-32
Match length
                  99
                  72
% identity
                 TONOPLAST INTRINSIC PROTEIN, GAMMA (GAMMA TIP)
NCBI Description
                  (AQUAPORIN-TIP) >gi_1076745_pir__S52004 gamma-Tip protein -
                  rice >gi 473997 dbj BAA05017 (D25534) gamma-Tip [Oryza
                  sativa]
                  417451
Seq. No.
                  uC-osroM202017e04b1
Seq. ID
                  BLASTX
Method
NCBI GI
                  g3850999
BLAST score
                  370
                  2.0e-35
E value
Match length
                  101
% identity
                  76
                  (AF069908) pyruvate dehydrogenase E1 beta subunit isoform 1
NCBI Description
                  [Zea mays]
                  417452
Seq. No.
                  uC-osroM202017e05a1
Seq. ID
                  BLASTX
Method
                  g5668813
NCBI GI
BLAST score
                  170
                   3.0e-12
E value
Match length
                  99
                   38
% identity
NCBI Description (AC007519) Similar to gb X77136 HSR203J protein from
                  Nicotiana tabacum and is a member of the PF_00135
                   Carboxylesterase family. ESTs gb_Z25688 and gb_F14025 come
                   from this gene. [Arabidopsis thaliana]
                   417453
Seq. No.
                  uC-osroM202017e06b1
Seq. ID
                  BLASTX
Method
NCBI GI
                  q1781336
BLAST score
                  447
                   2.0e-44
E value
Match length
                  144
% identity
NCBI Description (Y10469) peroxidase [Spinacia oleracea]
```

417454

Seq. No.

Method

BLASTX

Seq. ID uC-osroM202017e08b1 Method BLASTN q949979 NCBI GI BLAST score 49 E value 3.0e-18 Match length 97 88 % identity NCBI Description Z.mays Glossy2 locus DNA Seq. No. 417455 Seq. ID uC-osroM202017e11b1 Method BLASTX NCBI GI g2392895 501 BLAST score E value 1.0e-50 Match length 160 59 % identity NCBI Description (AF017056) brassinosteroid insensitive 1 [Arabidopsis thaliana] >gi_5042156 emb CAB44675.1 (AL078620) brassinosteroid insensitive 1 gene (BRI1) [Arabidopsis thaliana] Seq. No. 417456 Seq. ID uC-osroM202017f05b1 Method BLASTX NCBI GI q5080773 BLAST score 156 E value 3.0e-10 Match length 101 % identity 46 NCBI Description (AC007576) Hypothetical protein [Arabidopsis thaliana] Seq. No. 417457 Seq. ID uC-osroM202017f07b1 Method BLASTX NCBI GI q5302775 BLAST score 151 E value 1.0e-09 Match length 65 % identity 45 NCBI Description (Z97337) hypothetical protein [Arabidopsis thaliana] Seq. No. 417458 Seq. ID uC-osroM202017f09b1 Method BLASTX NCBI GI g3176690 BLAST score 274 E value 5.0e-24 Match length 123 % identity 52 NCBI Description (AC003671) Similar to ubiquitin ligase qb D63905 from S. cerevisiae. EST gb R65295 comes from this gene. [Arabidopsis thaliana] Seq. No. 417459 Seq. ID uC-osroM202017f12b1

E value

5.0e-28

```
NCBI GI
                  g2052383
                  622
BLAST score
E value
                  8.0e-65
                  138
Match length
% identity
                  80
                  (U66345) calreticulin [Arabidopsis thaliana]
NCBI Description
                  417460
Seq. No.
                  uC-osroM202017g02b1
Seq. ID
Method
                  BLASTX
                  q4680207
NCBI GI
BLAST score
                  205
                  3.0e-16
E value
                  97
Match length
% identity
                  45
NCBI Description
                  (AF114171) disease resistance protein RPM1 homolog [Sorghum
                  bicolor]
Seq. No.
                  417461
                  uC-osroM202017q03b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2129622
BLAST score
                  546
                  6.0e-56
E value
Match length
                  124
                  81
% identity
                  immunophilin FKBP15-1 - Arabidopsis thaliana >gi 1272406
NCBI Description
                   (U52046) immunophilin [Arabidopsis thaliana]
                  417462
Seq. No.
                  uC-osroM202017q04a1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g4886265
                  49
BLAST score
                  1.0e-18
E value
                  65
Match length
                  94
% identity
NCBI Description Arabidopsis thaliana DNA chromosome 3, BAC clone F2206
Seq. No.
                  417463
                  uC-osroM202017g04b1
Seq. ID
Method
                  BLASTX
                  g131773
NCBI GI
BLAST score
                  680
E value
                  1.0e-71
Match length
                  140
                  97
% identity
NCBI Description
                  40S RIBOSOMAL PROTEIN S14 (CLONE MCH2)
                  >gi_82724_pir__B30097 ribosomal protein S14 (clone MCH2) -
                  maize
                  417464
Seq. No.
Seq. ID
                  uC-osroM202017q05b1
Method
                  BLASTX
                  g401140
NCBI GI
BLAST score
                  308
```



```
Match length
                   65
                   94
% identity
NCBI Description
                  SUCROSE SYNTHASE 2 (SUCROSE-UDP GLUCOSYLTRANSFERASE 2)
                   >gi_20095_emb_CAA41774_ (X59046) sucrose-UDP
                   glucosyltransferase (isoenzyme 2) [Oryza sativa]
                   >gi 1587662 prf 2207194A sucrose synthase:ISOTYPE=2 [Oryza
                   sativa]
Seq. No.
                   417465
Seq. ID
                   uC-osroM202017g06b1
Method
                  BLASTX
NCBI GI
                  g534982
BLAST score
                   247
                   7.0e-21
E value
                  129
Match length
                   45
% identity
NCBI Description (X75898) phosphoglucomutase [Spinacia oleracea]
                   417466
Seq. No.
Seq. ID
                  uC-osroM202017q10a1
Method
                  BLASTX
NCBI GI
                  g400803
BLAST score
                  191
                  9.0e-15
E value
                  41
Match length
% identity
                  90
NCBI Description 2,3-BISPHOSPHOGLYCERATE-INDEPENDENT PHOSPHOGLYCERATE MUTASE
                   (PHOSPHOGLYCEROMUTASE) (BPG-INDEPENDENT PGAM) (PGAM-I)
                  >gi_283033 pir A42807 phosphoglycerate mutase (EC
                   5.4.2.1), 2, 3-bisphosphoglycerate-independent - maize
                   >gi 168588 (M80912) 2,3-bisphosphoglycerate-independent
                  phosphoglycerate mutase [Zea mays]
Seq. No.
                  417467
Seq. ID
                  uC-osroM202017g10b1
Method
                  BLASTX
NCBI GI
                  g551288
BLAST score
                  755
                  2.0e-80
E value
Match length
                  164
% identity
                  89
NCBI Description (Z33611) phosphoglycerate mutase [Zea mays]
Seq. No.
                  417468
Seq. ID
                  uC-osroM202017g11a1
Method
                  BLASTN
NCBI GI
                  g20094
BLAST score
                  280
E value
                  1.0e-156
                  280
Match length
% identity
                  100
                  O.sativa RSs2 gene for sucrose-UDP glucosyltransferase
NCBI Description
```

(isozyme 2)

Seq. No. 417469

Seq. ID uC-osroM202017g11b1

Method BLASTX



```
NCBI GI
                  g401140
BLAST score
                  620
                  1.0e-64
E value
Match length
                  124
% identity
                  100
NCBI Description
                  SUCROSE SYNTHASE 2 (SUCROSE-UDP GLUCOSYLTRANSFERASE 2)
                  >gi 20095 emb CAA41774 (X59046) sucrose-UDP
                  qlucosyltransferase (isoenzyme 2) [Oryza sativa]
                  >gi_1587662_prf__2207194A sucrose synthase:ISOTYPE=2 [Oryza
                  sativa]
Seq. No.
                  417470
                  uC-osroM202017h01b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2995990
BLAST score
                  272
E value
                  7.0e-24
Match length
                  125
% identity
                  46
                  (AF053746) dormancy-associated protein [Arabidopsis
NCBI Description
                  thaliana] >gi 2995992 (AF053747) dormancy-associated
                  protein [Arabidopsis thaliana]
Seq. No.
                  417471
                  uC-osroM202017h02b1
Seq. ID
                  BLASTX
Method
NCBI GI
                  g1619300
BLAST score
                  347
E value
                  5.0e-33
Match length
                  102
% identity
                  65
NCBI Description (X95269) LRR protein [Lycopersicon esculentum]
Seq. No.
                  417472
                  uC-osroM202017h04a1
Seq. ID
                  BLASTN
Method
                  g2801537
NCBI GI
BLAST score
                  204
E value
                  1.0e-111
                  273
Match length
% identity
                  93
NCBI Description Oryza sativa harpin induced gene 1 homolog (Hin1) mRNA,
                  complete cds
                   417473
Seq. No.
                  uC-osroM202017h04b1
Seq. ID
                  BLASTX
Method
NCBI GI
                  g2801538
BLAST score
                  459
E value
                  7.0e-46
Match length
                  128
% identity
NCBI Description
                 (AF039532) harpin induced gene 1 homolog [Oryza sativa]
```

Seq. No. 417474

Seq. ID uC-osroM202017h06b1

Method BLASTN



```
g1203831
NCBI GI
                  35
BLAST score
                  5.0e-10
E value
Match length
                  75
                  87
% identity
NCBI Description
                 Hordeum vulgare beta-D-glucan exohydrolase, isoenzyme
                  ExoII, mRNA, complete cds
                  417475
Seq. No.
                  uC-osroM202017h08a1
Seq. ID
                  BLASTN
Method
                  g780371
NCBI GI
                  267
BLAST score
                  1.0e-148
E value
Match length
                  279
% identity
                  99
NCBI Description Oryza sativa enolase mRNA, complete cds
                  417476
Seq. No.
                  uC-osroM202017h08b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3023713
BLAST score
                  636
                  2.0e-66
E value
                  140
Match length
                  90
% identity
NCBI Description
                  ENOLASE (2-PHOSPHOGLYCERATE DEHYDRATASE)
                   (2-PHOSPHO-D-GLYCERATE HYDRO-LYASE) (OSE1) >gi 780372
                   (U09450) enolase [Oryza sativa]
                  417477
Seq. No.
Seq. ID
                  uC-osroM202017h09b1
Method
                  BLASTX
NCBI GI
                  q1504012
BLAST score
                  161
E value
                   8.0e-11
Match length
                  108
% identity
                   33
                  (D86969) similar to Human zinc-finger protein,
NCBI Description
                  BR140(P1:JC2069) [Homo sapiens] >gi 5805248 gb AAD51905.1_
                   (AF127774) unknown [Homo sapiens]
                   417478
Seq. No.
Seq. ID
                  uC-osroM202017h10b1
Method
                   BLASTX
NCBI GI
                   q3643608
BLAST score
                   182
E value
                   1.0e-13
Match length
                   91
% identity
                   45
NCBI Description
                   (AC005395) hypothetical protein [Arabidopsis thaliana]
```

>gi_4874312_gb_AAD31374.1_AC006053 16 (AC006053)

hypothetical protein [Arabidopsis thaliana]

417479 Seq. No.

Seq. ID uC-osroM202017h11b1

Method BLASTX



NCBI GI g2088648 BLAST score 355 E value 2.0e-33 Match length 147 % identity 46

NCBI Description (AF002109) hypothetical protein [Arabidopsis thaliana]

Seq. No. 417480

Seq. ID uC-osroM202017h12a1

Method BLASTN
NCBI GI g2267005
BLAST score 266
E value 1.0e-148
Match length 266
% identity 100

NCBI Description Oryza sativa endosperm lumenal binding protein (BiP) mRNA,

complete cds

Seq. No. 417481

Seq. ID uC-osroM202017h12b1

Method BLASTX
NCBI GI g2267006
BLAST score 841
E value 2.0e-90
Match length 171
% identity 98

NCBI Description (AF006825) endosperm lumenal binding protein [Oryza sativa]

Seq. No. 417482

Seq. ID uC-osroM202018a02b1

Method BLASTX
NCBI GI g3608364
BLAST score 326
E value 2.0e-30
Match length 100
% identity 59

NCBI Description (AF019749) high-affinity nitrate transporter ACH2

[Arabidopsis thaliana]

Seq. No. 417483

Seq. ID uC-osroM202018a04b1

Method BLASTX
NCBI GI g3868754
BLAST score 743
E value 4.0e-79
Match length 141
% identity 98

NCBI Description (D64013) catalase [Oryza sativa]

Seq. No. 417484

Seq. ID uC-osroM202018a05b1

Method BLASTX
NCBI GI g3790581
BLAST score 215
E value 3.0e-17
Match length 51
% identity 65



(AF079179) RING-H2 finger protein RHB1a [Arabidopsis NCBI Description thaliana] 417485 Seq. No. uC-osroM202018a06b1 Seq. ID Method BLASTX g1351904 NCBI GI 349 BLAST score 5.0e-59 E value Match length 170 78 % identity NCBI Description BIFUNCTIONAL ASPARTOKINASE/HOMOSERINE DEHYDROGENASE 1, CHLOROPLAST PRECURSOR (AK-HD 1) (AK-HSDH 1) [INCLUDES: ASPARTOKINASE; HOMOSERINE DEHYDROGENASE] >gi 500851 (L33912) aspartate kinase-homoserine dehydrogenase [Zea mays] 417486 Seq. No. uC-osroM202018a09b1 Seq. ID BLASTX Method g1170714 NCBI GI BLAST score 846 4.0e-91 E value 169 Match length 93 % identity NCBI Description SHAGGY RELATED PROTEIN KINASE ASK-GAMMA >gi_541850_pir__S41597 protein kinase ASK-gamma (EC 2.7.1.-) - Arabidopsis thaliana >gi 456509 emb CAA53180 (X75431) ASK-gamma (Arabidopsis shaggy-related kinase) [Arabidopsis thaliana] >gi_2059329_emb_CAA73247_ (Y12710) shaggy-like kinase gamma [Arabidopsis thaliana] 417487 Seq. No. uC-osroM202018a10b1 Seq. ID Method BLASTX NCBI GI q82496 BLAST score 529 5.0e-54 E value 131 Match length 79 % identity NCBI Description phenylalanine ammonia-lyase (EC 4.3.1.5) - rice 417488 Seq. No. uC-osroM202018a11b1 Seq. ID Method

BLASTX NCBI GI q2342683 BLAST score 374 E value 7.0e - 36Match length 126 % identity

(AC000106) Contains similarity to Bos beta-mannosidase NCBI Description

(gb U46067). [Arabidopsis thaliana]

Seq. No. 417489

uC-osroM202018a12b1 Seq. ID

Method BLASTX NCBI GI g283008 BLAST score 765 E value 3.0e-88 Match length 167 % identity 95

NCBI Description sucrose synthase (EC 2.4.1.13) - rice

>gi 20366 emb CAA46017 (X64770) sucrose synthase [Oryza

sativa]

Seq. No. 417490

Seq. ID uC-osroM202018b05b1

Method BLASTX
NCBI GI g21699
BLAST score 234
E value 2.0e-19
Match length 66
% identity 67

NCBI Description (X66013) cathepsin B [Triticum aestivum]

Seq. No. 417491

Seq. ID uC-osroM202018b06b1

Method BLASTX
NCBI GI g2149640
BLAST score 694
E value 2.0e-73
Match length 154
% identity 86

NCBI Description (U91995) Argonaute protein [Arabidopsis thaliana]

>gi_5733867_gb_AAD49755.1_AC007932_3 (AC007932) Identical to gb_U91995 Argonaute protein from Arabidopsis thaliana. ESTs gb_H76075, gb_AA720232, gb_N65911 and gb_AA651494 come

from this gene

Seq. No. 417492

Seq. ID uC-osroM202018b07b1

Method BLASTX

NCBI GI g1170937

BLAST score 243

E value 2.0e-20

Match length 46
% identity 96

NCBI Description S-ADENOSYLMETHIONINE SYNTHETASE 1 (METHIONINE

ADENOSYLTRANSFERASE 1) (ADOMET SYNTHETASE 1)

>gi_450549_emb_CAA81481_ (Z26867) S-adenosyl methionine

synthetase [Oryza sativa]

Seq. No. 417493

Seq. ID uC-osroM202018b11b1

Method BLASTX
NCBI GI g1710401
BLAST score 514
E value 3.0e-52
Match length 122
% identity 81

NCBI Description RIBONUCLEOSIDE-DIPHOSPHATE REDUCTASE SMALL CHAIN

(RIBONUCLEOTIDE REDUCTASE) (R2 SUBUNIT)

>gi_1044912_emb_CAA63194_ (X92443) ribonucleotide reductase

R2 [Nicotiana tabacum]

NCBI GI

g100812

```
417494
Seq. No.
                  uC-osroM202018c01b1
Seq. ID
                  BLASTX
Method
                  g3135543
NCBI GI
BLAST score
                  663
                  1.0e-69
E value
                  138
Match length
                  93
% identity
                  (AF062393) aquaporin [Oryza sativa]
NCBI Description
                  417495
Seq. No.
                  uC-osroM202018c05b1
Seq. ID
                  BLASTX
Method
                  g4582468
NCBI GI
BLAST score
                  580
                  6.0e-60
E value
                  136
Match length
                  84
% identity
                  (AC007071) putative 40S ribosomal protein; contains
NCBI Description
                  C-terminal domain [Arabidopsis thaliana]
                   417496
Seq. No.
                   uC-osroM202018c06b1
Seq. ID
                  BLASTX
Method
NCBI GI
                   g5042408
                   419
BLAST score
E value
                   5.0e-41
                   148
Match length
                   55
% identity
                  (AC006193) very similar to alcohol dehydrogenase
NCBI Description
                   [Arabidopsis thaliana]
                   417497
Seq. No.
                   uC-osroM202018c09b1
Seq. ID
                   BLASTN
Method
                   g433815
NCBI GI
BLAST score
                   275
                   1.0e-153
E value
Match length
                   435
                   54
% identity
NCBI Description O.sativa gene for hydroxyproline-rich glycoprotein
                   417498
Seq. No.
                   uC-osroM202018c11b1
Seq. ID
                   BLASTX
Method
NCBI GI
                   g4220518
BLAST score
                   176
E value
                   1.0e-12
Match length
                   91
% identity
NCBI Description (AL035356) hypothetical protein [Arabidopsis thaliana]
                   417499
Seq. No.
                   uC-osroM202018c12b1
Seq. ID
Method
                   BLASTX
```



```
BLAST score 255
E value 5.0e-22
Match length 53
% identity 94
```

NCBI Description ubiquitin precursor - wheat (fragment)

>gi_21816_emb_CAA40138_ (X56803) ubiquitin [Triticum aestivum] >gi_21900_emb_CAA39938_ (X56601) ubiquitin

[Triticum aestivum]

Seq. No. 417500

Seq. ID uC-osroM202018d03b1

Method BLASTX
NCBI GI g6006869
BLAST score 260
E value 2.0e-22
Match length 76
% identity 74

NCBI Description (AC009540) putative cationic amino acid transporter

[Arabidopsis thaliana]

Seq. No. 417501

Seq. ID uC-osroM202018d05b1

Method BLASTX
NCBI GI g1172556
BLAST score 236
E value 1.0e-19
Match length 108
% identity 44

NCBI Description 36 KD OUTER MITOCHONDRIAL MEMBRANE PROTEIN PORIN

(VOLTAGE-DEPENDENT ANION-SELECTIVE CHANNEL PROTEIN) (VDAC) (POM 36) >gi_629729_pir__S46925 porin II, 36K - potato >gi_1076681_pir__B55364 porin (clone pPOM 36.2) - potato mitochondrion >gi_515360_emb_CAA56600_ (X80387) 36kDA porin

II [Solanum tuberosum]

Seq. No. 417502

Seq. ID uC-osroM202018d06b1

Method BLASTX
NCBI GI g1172556
BLAST score 296
E value 1.0e-26
Match length 129
% identity 46

NCBI Description 36 KD OUTER MITOCHONDRIAL MEMBRANE PROTEIN PORIN

(VOLTAGE-DEPENDENT ANION-SELECTIVE CHANNEL PROTEIN) (VDAC) (POM 36) >gi_629729_pir__S46925 porin II, 36K - potato >gi_1076681_pir__B55364 porin (clone pPOM 36.2) - potato mitochondrion >gi_515360_emb_CAA56600_ (X80387) 36kDA porin

II [Solanum tuberosum]

Seq. No. 417503

Seq. ID uC-osroM202018d07b1

Method BLASTX
NCBI GI g6016696
BLAST score 311
E value 3.0e-28
Match length 153

```
% identity
                  (AC009991) unknown protein [Arabidopsis thaliana]
NCBI Description
                  417504
Seq. No.
                  uC-osroM202018d09b1
Seq. ID
                  BLASTN
Method
NCBI GI
                  g218171
BLAST score
                  34
                  2.0e-09
E value
Match length
                  54
                  91
% identity
NCBI Description
                  Oryza sativa mRNA for type I light-harvesting chlorophyll
                  a/b binding protein of photosystem II (LHCPII), complete
                  417505
Seq. No.
                  uC-osroM202018d10b1
Seq. ID
Method
                  BLASTX
                  g6006864
NCBI GI
                  348
BLAST score
E value
                  1.0e-32
                  127
Match length
                  54
% identity
                  (AC009540) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  417506
Seq. ID
                  uC-osroM202018d12b1
                  BLASTX
Method
NCBI GI
                  q4510376
BLAST score
                  285
E value
                  2.0e-25
                  96
Match length
                  53
% identity
NCBI Description (AC007017) unknown protein [Arabidopsis thaliana]
Seq. No.
                  417507
Seq. ID
                  uC-osroM202018e05b1
Method
                  BLASTX
NCBI GI
                  q585778
BLAST score
                  466
E value
                  2.0e-46
Match length
                  89
% identity
                  96
                  GTP-BINDING NUCLEAR PROTEIN RAN2 >gi 453563 (L28714) Ran
NCBI Description
                  protein/TC4 protein [Solanum lycopersicum] >gi 453565
                  (L28715) Ran protein/TC4 protein [Solanum lycopersicum]
                  417508
Seq. No.
                  uC-osroM202018e06b1
Seq. ID
                  BLASTX
Method
NCBI GI
                  q2959370
BLAST score
                  238
E value
                  9.0e-20
                  109
Match length
                  39
% identity
```

NCBI Description (AL022117) hypothetical protein [Schizosaccharomyces pombe]

Seq. ID Method

```
417509
Seq. No.
Seq. ID
                  uC-osroM202018e07b1
Method
                  BLASTX
NCBI GI
                  g2244949
BLAST score
                  232
                  4.0e-19
E value
                  107
Match length
                  46
% identity
NCBI Description
                  (Z97339) cytochrome c oxidoreductase like protein
                   [Arabidopsis thaliana]
                  417510
Seq. No.
                  uC-osroM202018e08b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1136122
BLAST score
                  601
E value
                  4.0e-71
                  136
Match length
% identity
                  94
                  (X91807) alfa-tubulin [Oryza sativa]
NCBI Description
Seq. No.
                  417511
                  uC-osroM202018e11b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4220518
BLAST score
                  178
E value
                  7.0e-13
Match length
                  91
% identity
                  40
NCBI Description (AL035356) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  417512
                  uC-osroM202018e12b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1839188
BLAST score
                  631
E value
                  7.0e-66
Match length
                  148
% identity
                  83
NCBI Description (U86081) root hair defective 3 [Arabidopsis thaliana]
Seq. No.
                  417513
Seq. ID
                  uC-osroM202018f02b1
Method
                  BLASTX
NCBI GI
                  g1729971
BLAST score
                  561
E value
                  1.0e-57
Match length
                  147
% identity
                  78
NCBI Description
                  TONOPLAST INTRINSIC PROTEIN, GAMMA (GAMMA TIP)
                  (AQUAPORIN-TIP) >gi_1076745_pir__S52004 gamma-Tip protein -
                  rice >gi_473997_dbj_BAA05017 (D25534) gamma-Tip [Oryza
                  satival
Seq. No.
                  417514
```

54641

uC-osroM202018f03b1

BLASTX

```
NCBI GI
                  g3135611
                  398
BLAST score
                  1.0e-38
E value
Match length
                  143
                  55
% identity
                  (AF062485) cellulose synthase [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  417515
                  uC-osroM202018f06b1
Seq. ID
Method
                  BLASTX
                  g6063549
NCBI GI
BLAST score
                  357
                  1.0e-33
E value
Match length
                  134
% identity
                  50
                  (AP000615) EST AU070346(S12172) corresponds to a region of
NCBI Description
                   the predicted gene.; similar to AMP-binding protein.
                   (X94625) [Oryza sativa]
                   417516
Seq. No.
                   uC-osroM202018f09b1
Seq. ID
Method
                  BLASTX
NCBI GI
                   g2196672
BLAST score
                   568
                  1.0e-58
E value
Match length
                  122
% identity
                  87
NCBI Description
                  (Y08807) HMGd1 [Zea mays]
                   417517
Seq. No.
                   uC-osroM202018f11b1
Seq. ID
                   BLASTX
Method
                   g3128168
NCBI GI
                   294
BLAST score
                   2.0e-26
E value
                   95
Match length
                   58
% identity
NCBI Description
                  (AC004521) putative carboxyl-terminal peptidase
                   [Arabidopsis thaliana]
                   417518
Seq. No.
                   uC-osroM202018g01b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3004558
BLAST score
                   206
E value
                   3.0e-16
                   51
Match length
                   71
% identity
```

Seq. No. 417519

NCBI Description

Seq. ID uC-osroM202018g02b1

Method BLASTX
NCBI GI g5354158
BLAST score 523
E value 3.0e-53
Match length 137

(AC003673) peroxidase ATP22a [Arabidopsis thaliana]

% identity (AF149841) digalactosyldiacylglycerol synthase [Arabidopsis NCBI Description thaliana] >gi_5354160_gb_AAD42379.1_AF149842_1 (AF149842) digalactosyldiacylglycerol synthase [Arabidopsis thaliana] >gi 6041825 gb AAF02140.1_AC009918_12 (AC009918) digalactosyldiacylglycerol synthase [Arabidopsis thaliana] 417520 Seq. No. uC-osroM202018g09b1 Seq. ID BLASTX Method g4960024 NCBI GI 673 BLAST score 7.0e-71 E value 153 Match length % identity 82 (AF144079) S-adenosyl-L-methionine:L-methionine NCBI Description S-methyltransferase [Zea mays] 417521 Seq. No. uC-osroM202018h01b1 Seq. ID BLASTX Method g2662343 NCBI GI BLAST score 626 2.0e-65 E value 120 Match length 100 % identity NCBI Description (D63581) EF-1 alpha [Oryza sativa] 417522 Seq. No. uC-osroM202018h03b1 Seq. ID BLASTX Method g3023816 NCBI GI 680 BLAST score 1.0e-71 E value 147 Match length 90 % identity NCBI Description GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC >gi_968996 (U31676) glyceraldehyde-3-phosphate dehydrogenase [Oryza sativa] 417523 Seq. No. Seq. ID uC-osroM202018h04b1 Method BLASTX g1172818 NCBI GI BLAST score 518 9.0e-53 E value Match length 104 % identity 99 NCBI Description 40S RIBOSOMAL PROTEIN S16 >gi_538428 (L36313) ribosomal protein S16 [Oryza sativa] >gi_1096552_prf__2111468A ribosomal protein S16 [Oryza sativa]

110000

Seq. No.

Seq. ID uC-osroM202018h05b1

417524

Method BLASTX NCBI GI g1084461 BLAST score 472

```
3.0e-47
E value
Match length
                  133
                  71
% identity
                  RCc3 protein - rice >gi 786132 (L27208) RCc3 [Oryza sativa]
NCBI Description
                  417525
Seq. No.
                  uC-osroM202018h07b1
Seq. ID
                  BLASTX
Method
                  g182869
NCBI GI
                  275
BLAST score
                  2.0e-24
E value
                  95
Match length
                  52
% identity
                 (M12996) glucose-6-phosphate dehydrogenase [Homo sapiens]
NCBI Description
Seq. No.
                  417526
                  uC-osroM202018h08b1
Seq. ID
Method
                  BLASTX
                  q5725442
NCBI GI
                  337
BLAST score
                  2.0e-31
E value
Match length
                  168
                  45
% identity
                 (AL109787) putative protein [Arabidopsis thaliana]
NCBI Description
                  417527
                  uC-osroM202018h09b1
                  BLASTX
                  q584778
                  592
                  2.0e-61
E value
Match length
                  123
                  89
```

Seq. No. Seq. ID Method NCBI GI BLAST score

% identity

NCBI Description PHOSPHO-2-DEHYDRO-3-DEOXYHEPTONATE ALDOLASE 2 PRECURSOR

(PHOSPHO-2-KETO-3-DEOXYHEPTONATE ALDOLASE 2) (DAHP

SYNTHETASE 2) (3-DEOXY-D-ARABINO-HEPTULOSONATE 7-PHOSPHATE

SYNTHASE 2) >gi_542033_pir__S40412

2-dehydro-3-deoxyphosphoheptonate aldolase (EC 4.1.2.15) 2

precursor - tomato >gi_410488_emb_CAA79856_ (Z21793)

phospho-2-dehydro-3-deoxyheptonate aldolase [Lycopersicon

esculentum]

417528 Seq. No.

uC-osroM202018h10b1 Seq. ID

BLASTX Method q1172818 NCBI GI BLAST score 357 E value 7.0e - 34Match length 94 81 % identity

40S RIBOSOMAL PROTEIN S16 >gi_538428 (L36313) ribosomal NCBI Description

protein S16 [Oryza sativa] >qi 1096552 prf 2111468A

ribosomal protein S16 [Oryza sativa]

417529 Seq. No.

uC-osroM202019a04a1 Seq. ID

Method BLASTX

E value

1.0e-56

```
NCBI GI
                  q1184112
BLAST score
                   406
E value
                  1.0e-39
Match length
                  96
                  82
% identity
                  (U46138) Zn-induced protein [Oryza sativa]
NCBI Description
                   417530
Seq. No.
                  uC-osroM202019a04b1
Seq. ID
Method
                  BLASTN
                  g6016845
NCBI GI
BLAST score
                   303
                  1.0e-170
E value
Match length
                   435
% identity
                   93
NCBI Description Oryza sativa genomic DNA, chromosome 1, clone:P0711E10
Seq. No.
                   417531
                  uC-osroM202019a05b1
Seq. ID
                  BLASTX
Method
NCBI GI
                  g1168729
                   252
BLAST score
E value
                   8.0e-25
Match length
                  144
"% identity
                   47
                  CINNAMYL-ALCOHOL DEHYDROGENASE ELI3-1 (CAD)
NCBI Description
                   >gi 282867 pir S28044 ELI3-2 protein - Arabidopsis
                   thaliana >gi 16267 emb CAA48027 (X67816) Eli3-1
                   [Arabidopsis thaliana]
                   417532
Seq. No.
                   uC-osroM202019a06a1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g5833467
BLAST score
                   177
                   1.0e-12
E value
                   71
Match length
% identity
                   49
                  (AF158602) monodehydroascorbate reductase [Zantedeschia
NCBI Description
                   aethiopica]
                   417533
Seq. No.
                   uC-osroM202019a06b1
Seq. ID
Method
                  BLASTX
NCBI GI
                   g4704613
BLAST score
                   239
E value
                   3.0e-20
Match length
                   62
                   71
% identity
NCBI Description (AF109695) monodehydroascorbate reductase [Brassica juncea]
                   417534
Seq. No.
Seq. ID
                   uC-osroM202019a10a1
                  BLASTX
Method
NCBI GI
                   g3128168
BLAST score
                   553
```



Match length 134 % identity 69

NCBI Description (AC004521) putative carboxyl-terminal peptidase

[Arabidopsis thaliana]

Seq. No. 417535

Seq. ID uC-osroM202019a10b1

Method BLASTX NCBI GI q3128168 BLAST score 229 7.0e-19 E value Match length 80

% identity 54

NCBI Description (AC004521) putative carboxyl-terminal peptidase

[Arabidopsis thaliana]

Seq. No. 417536

Seq. ID uC-osroM202019a12b1

Method BLASTX NCBI GI q4587572 BLAST score 365 E value 3.0e-37 Match length 121

% identity 69

(AC006550) Similar to gb U70015 lysosomal trafficking NCBI Description

> regulator from Mus musculus and contains 2 PF 00400 WD40, G-beta repeats. ESTs gb T43386 and gb AA395236 come from

this gene. [Arabidopsis thaliana]

417537 Seq. No.

uC-osroM202019b01a1 Seq. ID

BLASTX Method g2497883 NCBI GI BLAST score 226 2.0e-18 E value 56 Match length 77 % identity

METALLOTHIONEIN-LIKE PROTEIN TYPE 1 >gi_1362174_pir__S57768 NCBI Description

metallothionein-like protein - rice >gi_687638 (U18404) metallothionein-like protein [Oryza satīva] >gi_1815626 (U43529) metallothionein-like type 1 [Oryza satīva]

>gi_4097154_gb_AAD10376.1_ (U46159) type 1 rice
metallothionein-like gene; Method: conceptual translation

supplied by author. [Oryza sativa]

Seq. No. 417538

Seq. ID uC-osroM202019b01b1

Method BLASTX NCBI GI q2497883 BLAST score 226 1.0e-18 E value Match length 56 % identity 75

NCBI Description METALLOTHIONEIN-LIKE PROTEIN TYPE 1 >gi_1362174_pir__S57768

metallothionein-like protein - rice >gi_687638 (U18404) metallothionein-like protein [Oryza satīva] >gi 1815626 (U43529) metallothionein-like type 1 [Oryza sativa]

>gi_4097154_gb_AAD10376.1_ (U46159) type 1 rice
metallothionein-like gene; Method: conceptual translation

supplied by author. [Oryza sativa]

Seq. No. 417539

uC-osroM202019b02a1 Seq. ID

Method BLASTX NCBI GI g3264607 BLAST score 266 E value 5.0e-23 54 Match length

85 % identity

(AF061509) shaggy kinase homolog [Zea mays] NCBI Description

417540 Seq. No.

uC-osroM202019b02b1 Seq. ID

BLASTX Method g1709129 NCBI GI BLAST score 218 2.0e-17 E value Match length 84 55 % identity

GLYCOGEN SYNTHASE KINASE-3 HOMOLOG MSK-3 NCBI Description

>gi 481018 pir S37642 protein kinase MSK-3 (EC 2.7.1.-) alfalfa >gi 313148 emb_CAA48472 (X68409) protein kinase

[Medicago sativa]

417541 Seq. No.

uC-osroM202019b03a1 Seq. ID

Method BLASTX NCBI GI q1184112 307 BLAST score 4.0e-28 E value 110 Match length % identity

NCBI Description (U46138) Zn-induced protein [Oryza sativa]

417542 Seq. No.

uC-osroM202019b04a1 Seq. ID

Method BLASTX NCBI GI g2245005 BLAST score 297 E value 1.0e-26 97 Match length % identity 62

NCBI Description (Z97341) hypothetical protein [Arabidopsis thaliana]

417543 Seq. No.

uC-osroM202019b05a1 Seq. ID

BLASTX Method NCBI GI q4206122 530 BLAST score E value 6.0e-54 Match length 197 52 % identity

NCBI Description (AF097667) protein phosphatase 2C homolog [Mesembryanthemum

crystallinum]

Seq. No. 417544

Seq. ID uC-osroM202019b06b1

Method BLASTX
NCBI GI g3790581
BLAST score 220
E value 1.0e-17
Match length 52
% identity 65

NCBI Description (AF079179) RING-H2 finger protein RHBla [Arabidopsis

thaliana]

Seq. No. 417545

Seq. ID uC-osroM202019b09b1

Method BLASTX
NCBI GI g417748
BLAST score 201
E value 2.0e-15
Match length 128
% identity 36

NCBI Description PROTEIN TRANSPORT PROTEIN SEC13 >gi_422187_pir__A45442

SEC13 protein - yeast (Saccharomyces cerevisiae) >gi_172559

(L05929) Sec13p [Saccharomyces cerevisiae] $>gi_54450\overline{1}$

(U14913) Sec13p [Saccharomyces cerevisiae]

Seq. No. 417546

Seq. ID uC-osroM202019b10b1

Method BLASTX
NCBI GI g1170714
BLAST score 767
E value 7.0e-82
Match length 157
% identity 92

NCBI Description SH

SHAGGY RELATED PROTEIN KINASE ASK-GAMMA

>gi_541850_pir__S41597 protein kinase ASK-gamma (EC
2.7.1.-) - Arabidopsis thaliana >gi_456509_emb_CAA53180_
(X75431) ASK-gamma (Arabidopsis shaggy-related kinase)
[Arabidopsis thaliana] >gi_2059329_emb_CAA73247_ (Y12710)

shaggy-like kinase gamma [Arabidopsis thaliana]

Seq. No. 417547

Seq. ID uC-osroM202019b12b1

Method BLASTX
NCBI GI g3395431
BLAST score 287
E value 9.0e-26
Match length 72
% identity 75

NCBI Description (AC004683) unknown protein [Arabidopsis thaliana]

Seq. No. 417548

Seq. ID uC-osroM202019c02a1

Method BLASTX
NCBI GI g2911042
BLAST score 561
E value 1.0e-57
Match length 180

```
% identity
                   62
                   (AL021961) Phosphoglycerate dehydrogenase - like protein
NCBI Description
                   [Arabidopsis thaliana]
                  417549
Seq. No.
                  uC-osroM202019c02b1
Seq. ID
Method
                  BLASTX
                  g2911042
NCBI GI
BLAST score
                  354
                  2.0e-33
E value
Match length
                  83
% identity
                  82
                   (AL021961) Phosphoglycerate dehydrogenase - like protein
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                   417550
                  uC-osroM202019c03a1
Seq. ID
Method
                  BLASTX
                  q1076288
NCBI GI
BLAST score
                   258
                   4.0e-22
E value
Match length
                  134
% identity
                   39
NCBI Description amino acid permease AAP3 - Arabidopsis thaliana
                   417551
Seq. No.
                  uC-osroM202019c06a1
Seq. ID
Method
                  BLASTX
                   g3927831
NCBI GI
                   172
BLAST score
                   4.0e-12
E value
                   45
Match length
                   69
% identity
                  (AC005727) similar to mouse ankyrin 3 [Arabidopsis
NCBI Description
                   thaliana]
                   417552
Seq. No.
Seq. ID
                   uC-osroM202019c07a1
Method
                   BLASTX
NCBI GI
                   q2952328
                   389
BLAST score
E value
                   2.0e-37
Match length
                   91
% identity
                  (AF049889) 1-aminocyclopropane-1-carboxylate oxidase [Oryza
NCBI Description
                   sativa]
Seq. No.
                   417553
Seq. ID
                   uC-osroM202019c07b1
Method
                   BLASTX
                   q2952328
NCBI GI
BLAST score
                   762
E value
                   3.0e-81
Match length
                   148
                   99
% identity
                  (AF049889) 1-aminocyclopropane-1-carboxylate oxidase [Oryza
NCBI Description
```

54649

sativa]

```
417554
Seq. No.
                  uC-osroM202019c08a1
Seq. ID
                  BLASTX
Method
                  q5679843
NCBI GI
                  513
BLAST score
                  5.0e-52
E value
                  101
Match length
                  100
% identity
                  (AJ243961) Putitive Ser/Thr protein kinase [Oryza sativa]
NCBI Description
                  417555
Seq. No.
                  uC-osroM202019c09a1
Seq. ID
                  BLASTX
Method
                  g1136122
NCBI GI
                  150
BLAST score
                  1.0e-09
E value
                  34
Match length
                  82
% identity
                  (X91807) alfa-tubulin [Oryza sativa]
NCBI Description
                  417556
Seq. No.
                  uC-osroM202019c09b1
Seq. ID
                  BLASTX
Method
                  g135435
NCBI GI
                   586
BLAST score
                   3.0e-67
E value
Match length
                  136
                   85
% identity
                  TUBULIN ALPHA CHAIN >gi_71573_pir__UBPGA tubulin alpha
NCBI Description
                   chain - pig
                   417557
Seq. No.
                   uC-osroM202019c11a1
Seq. ID
                   BLASTX
Method
NCBI GI
                   g2129578
BLAST score
                   166
                   2.0e-11
E value
                   43
Match length
                   72
% identity
                   dTDP-glucose 4-6-dehydratases homolog - Arabidopsis
NCBI Description
                   thaliana >gi_928932_emb_CAA89205_ (Z49239) homolog of
                   dTDP-glucose 4-6-dehydratases [Arabidopsis thaliana]
                   >gi 1585435 prf 2124427B diamide resistance gene
                   [Arabidopsis thaliana]
                   417558
Seq. No.
Seq. ID
                   uC-osroM202019c11b1
Method
                   BLASTX
                   q3522929
NCBI GI
                   795
BLAST score
                   4.0e-85
E value
Match length
                   157
% identity
                   (AC002535) putative dTDP-glucose 4-6-dehydratase
NCBI Description
                   [Arabidopsis thaliana] >gi_3738279 (AC005309) putative
                   dTDP-glucose 4-6-dehydratase [Arabidopsis thaliana]
```

Seq. ID

Method

417559 Seq. No. Seq. ID uC-osroM202019d03a1 Method BLASTX g4415908 NCBI GI BLAST score 441 E value 1.0e-43 Match length 120 % identity 69 NCBI Description (AC006282) unknown protein [Arabidopsis thaliana] 417560 Seq. No. Seq. ID uC-osroM202019d04a1 Method BLASTX NCBI GI g82734 BLAST score 458 E value 1.0e-45 Match length 92 29 % identity NCBI Description ubiquitin precursor - maize (fragment) >gi 226763 prf 1604470A poly-ubiquitin [Zea mays] Seq. No. 417561 uC-osroM202019d04b1 Seq. ID Method BLASTX NCBI GI g1332579 BLAST score 545 E value 4.0e-62 Match length 136 % identity 10 NCBI Description (X98063) polyubiquitin [Pinus sylvestris] Seq. No. 417562 uC-osroM202019d06a1 Seq. ID Method BLASTN NCBI GI g287400 BLAST score 35 E value 5.0e-10 Match length 55 % identity 91 NCBI Description Rice mRNA for peroxidase, complete cds Seq. No. 417563 Seq. ID uC-osroM202019d06b1 Method BLASTX NCBI GI g2388571 BLAST score 257 E value 4.0e-22 86 Match length % identity 62 NCBI Description (AC000098) Strong similarity to Arabidopsis peroxidase ATPEROX7A (gb X98321). [Arabidopsis thaliana] >qi 2738254 (U97684) peroxidase precursor [Arabidopsis thaliana] 417564 Seq. No.

54651

uC-osroM202019d07b1

BLASTX

```
NCBI GI
                  g3367591
BLAST score
                   176
                  2.0e-12
E value
Match length
                  86
                   41
% identity
                  (AL031135) putative protein [Arabidopsis thaliana]
NCBI Description
                   417565
Seq. No.
                  uC-osroM202019d08a1
Seq. ID
                  BLASTX
Method
                  g4455272
NCBI GI
                   259
BLAST score
                   3.0e-22
E value
                  114
Match length
% identity
                   41
                  (AL035527) subtilisin-like protease [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   417566
                  uC-osroM202019d08b1
Seq. ID
                  BLASTX
Method
NCBI GI
                   g4115926
                   360
BLAST score
E value
                   3.0e - 34
                   105
Match length
                   60
% identity
                  (AF118222) similar to the subtilase family of serine
NCBI Description
                  proteases (Pfam: PF00082, Score=50.7, E=4.7e-13, n=3)
                   [Arabidopsis thaliana] >gi_4539413_emb_CAB40046.1
                   (AL049524) putative subtilisin-like protease [Arabidopsis
                   thaliana]
                   417567
Seq. No.
                   uC-osroM202019d09a1
Seq. ID
                   BLASTX
Method
NCBI GI
                   g6006874
                   214
BLAST score
E value
                   5.0e-17
Match length
                   84
                   49
% identity
                   (ACO08153) putative UDP-glucuronosyltransferase, 5' partial
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                   417568
                   uC-osroM202019d10a1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3184291
BLAST score
                   162
E value
                   7.0e-11
Match length
                   102
% identity
                   42
                   (AC004136) putative DNA polymerase III gamma subunit
NCBI Description
                   [Arabidopsis thaliana]
```

Seq. No. 417569

Seq. ID uC-osroM202019d11b1

Method BLASTX NCBI GI g4704762

```
310
BLAST score
                  3.0e-28
E value
                  99
Match length
                  56
% identity
                  (AF128404) cellulase homolog [Nicotiana alata]
NCBI Description
                  417570
Seq. No.
                  uC-osroM202019d12b1
Seq. ID
                  BLASTX
Method
                  g4490736
NCBI GI
                  491
BLAST score
                  1.0e-50
E value
                  148
Match length
                   44
% identity
                  (AL035708) putative protein [Arabidopsis thaliana]
NCBI Description
                   417571
Seq. No.
                  uC-osroM202019e02a1
Seq. ID
                  BLASTN
Method
                   q394735
NCBI GI
                   487
BLAST score
                   0.0e+00
E value
                   513
Match length
                   99
% identity
NCBI Description Rice lip19 mRNA for basic/leucine zipper protein
                   417572
Seq. No.
                   uC-osroM202019e02b1
Seq. ID
                   BLASTN
Method
                   g394735
NCBI GI
                   465
BLAST score
                   0.0e + 00
E value
                   510
Match length
                   98
% identity
NCBI Description Rice lip19 mRNA for basic/leucine zipper protein
                   417573
Seq. No.
                   uC-osroM202019e04a1
Seq. ID
                   BLASTX
Method
                   g2688822
NCBI GI
                   358
BLAST score
                   8.0e-34
E value
Match length
                   99
                   70
% identity
                   [Prunus armeniaca]
```

NCBI Description (U93272) pyrophosphate-dependent phosphofructo-1-kinase

417574 Seq. No.

uC-osroM202019e04b1 Seq. ID

Method BLASTX a2688822 NCBI GI 394 BLAST score 4.0e-38 E value Match length 104 72 % identity

(U93272) pyrophosphate-dependent phosphofructo-1-kinase NCBI Description

[Prunus armeniaca]

```
Seq. No.
                  417575
                  uC-osroM202019e05a1
Seq. ID
                  BLASTX
Method
NCBI GI
                  g2651300
                  229
BLAST score
                  3.0e-19
E value
Match length
                  106
                   52
% identity
                   (AC002336) putative initiator tRNA
NCBI Description
                  phosphoribosyl-transferase [Arabidopsis thaliana]
Seq. No.
                   417576
                   uC-osroM202019e05b1
Seq. ID
                   BLASTX
Method
                   q2651300
NCBI GI
BLAST score
                   416
                   1.0e-40
E value
Match length
                   117
                   68
% identity
                  (AC002336) putative initiator tRNA
NCBI Description
                   phosphoribosyl-transferase [Arabidopsis thaliana]
                   417577
Seq. No.
                   uC-osroM202019e06a1
Seq. ID
                   BLASTX
Method
                   g4914402
NCBI GI
BLAST score
                   261
E value
                   1.0e-22
                   98
Match length
                   56
% identity
NCBI Description (AL050352) hypothetical protein [Arabidopsis thaliana]
                   417578
Seq. No.
                   uC-osroM202019e06b1
Seq. ID
                   BLASTX
Method
                   g4914402
NCBI GI
                   478
BLAST score
E value
                   5.0e-48
                   140
Match length
                   64
% identity
NCBI Description (AL050352) hypothetical protein [Arabidopsis thaliana]
                   417579
Seq. No.
                   uC-osroM202019e07b1
Seq. ID
                   BLASTX
Method
                   g6009909
NCBI GI
                   393
BLAST score
                   6.0e-38
E value
Match length
                   102
                   75
 % identity
NCBI Description (AB018242) histone H2A-like protein [Solanum melongena]
                   417580
 Seq. No.
                   uC-osroM202019e08b1
 Seq. ID
```

54654

BLASTX

g4758294

Method

NCBI GI

BLAST score 201 E value 5.0e-16 Match length 76 % identity 57

NCBI Description glutamyl-prolyl-tRNA synthetase

>gi_135104_sp_P07814_SYEP_HUMAN MULTIFUNCTIONAL AMINOACYL-TRNA SYNTHETASE [INCLUDES: GLUTAMYL-TRNA

SYNTHETASE (GLUTAMATE--TRNA LIGASE); PROLYL-TRNA SYNTHETASE

(PROLINE--TRNA LIGASE)] >gi_68554_pir__SYHUQT

glutamyl-prolyl-tRNA synthetase - human

>gi_31958_emb_CAA38224_ (X54326) glutaminyl-tRNA synthetase

[Homo sapiens]

Seq. No. 417581

Seq. ID uC-osroM202019e09a1

Method BLASTX
NCBI GI g3776573
BLAST score 356
E value 1.0e-33
Match length 89
% identity 69

NCBI Description (AC005388) Similar to nodulins and lipase homolog F14J9.5

gi_3482914 from Arabidopsis thaliana BAC gb_AC003970.
Alternate first exon from 72258 to 72509. [Arabidopsis

thaliana]

Seq. No. 417582

Seq. ID uC-osroM202019e09b1

Method BLASTX
NCBI GI g3776573
BLAST score 317
E value 4.0e-29
Match length 104
% identity 62

NCBI Description (AC005388) Similar to nodulins and lipase homolog F14J9.5

gi_3482914 from Arabidopsis thaliana BAC gb_AC003970. Alternate first exon from 72258 to 72509. [Arabidopsis

thaliana]

Seq. No. 417583

Seq. ID uC-osroM202019e10b1

Method BLASTX
NCBI GI g3805770
BLAST score 152
E value 9.0e-10
Match length 38
% identity 66

NCBI Description (U78721) ETTIN protein [Arabidopsis thaliana]

Seq. No. 417584

Seq. ID uC-osroM202019e11a1

Method BLASTX
NCBI GI g3551960
BLAST score 171
E value 6.0e-12
Match length 46
% identity 63

 $\mathcal{S}_{\widetilde{\mathcal{C}}}(V) = 0$

```
NCBI Description (AF082033) senescence-associated protein 15 [Hemerocallis
```

Seq. No. 417585

Seq. ID uC-osroM202019e11b1

Method BLASTX
NCBI GI g3551960
BLAST score 162
E value 1.0e-17
Match length 101
% identity 59

NCBI Description (AF082033) senescence-associated protein 15 [Hemerocallis

hybrid cultivar]

hybrid cultivar]

Seq. No. 417586

Seq. ID uC-osroM202019f01a1

Method BLASTN
NCBI GI g1778820
BLAST score 186
E value 1.0e-100
Match length 368

% identity 94
NCBI Description Oryza sativa S-adenosyl-L-methionine synthetase (pOS-SAMS2)

mRNA, complete cds

Seq. No. 417587

Seq. ID uC-osroM202019f01b1

Method BLASTX
NCBI GI g3024122
BLAST score 213
E value 7.0e-17
Match length 41
% identity 98

NCBI Description S-ADENOSYLMETHIONINE SYNTHETASE 2 (METHIONINE

ADENOSYLTRANSFERASE 2) (ADOMET SYNTHETASE 2) >gi_1778821 (U82833) S-adenosyl-L-methionine synthetase [Oryza sativa]

Seq. No. 417588

Seq. ID uC-osroM202019f02a1

Method BLASTN
NCBI GI g1778820
BLAST score 287
E value 1.0e-160
Match length 453
% identity 97

NCBI Description Oryza sativa S-adenosyl-L-methionine synthetase (pOS-SAMS2)

mRNA, complete cds

Seq. No. 417589

Seq. ID uC-osroM202019f02b1

Method BLASTX
NCBI GI g3024122
BLAST score 219
E value 1.0e-17
Match length 42
% identity 98

NCBI Description S-ADENOSYLMETHIONINE SYNTHETASE 2 (METHIONINE

ADENOSYLTRANSFERASE 2) (ADOMET SYNTHETASE 2) >gi_1778821 (U82833) S-adenosyl-L-methionine synthetase [Oryza sativa]

Seq. No. 417590

Seq. ID uC-osroM202019f03a1

Method BLASTX
NCBI GI g1351270
BLAST score 346
E value 1.0e-32
Match length 73
% identity 95

NCBI Description TRIOSEPHOSPHATE ISOMERASE, CYTOSOLIC (TIM)

>gi_478410_pir__JQ2255 triose-phosphate isomerase (EC
5.3.1.1) - rice >gi 169821 (M87064) triosephosphate

isomerase [Oryza sativa]

Seq. No. 417591

Seq. ID uC-osroM202019f03b1

Method BLASTX
NCBI GI g553107
BLAST score 310
E value 8.0e-50
Match length 108
% identity 81

NCBI Description (L04967) triosephosphate isomerase [Oryza sativa]

Seq. No. 417592

Seq. ID uC-osroM202019f04a1

Method BLASTX
NCBI GI g2982311
BLAST score 214
E value 4.0e-23
Match length 89
% identity 60

NCBI Description (AF051240) probable ubiquitin-conjugating enzyme E2 [Picea

mariana]

Seq. No. 417593

Seq. ID uC-osroM202019f06a1

Method BLASTX
NCBI GI g6016877
BLAST score 262
E value 2.0e-31
Match length 77
% identity 81

NCBI Description (AP000570) ESTs AU077642(E30706), AU077641(E30706)

correspond to a region of the predicted gene.; hypothetical

protein [Oryza sativa]

Seq. No. 417594

Seq. ID uC-osroM202019f06b1

Method BLASTX
NCBI GI g6016877
BLAST score 267
E value 2.0e-23
Match length 77
% identity 68



```
(AP000570) ESTs AU077642(E30706), AU077641(E30706)
NCBI Description
                  correspond to a region of the predicted gene.; hypothetical
                  protein [Oryza sativa]
                  417595
Seq. No.
                  uC-osroM202019f09a1
Seq. ID
                  BLASTX
Method
NCBI GI
                  q1203832
                  823
BLAST score
                  3.0e-88
E value
                  188
Match length
                  85
% identity
                  (U46003) beta-D-glucan exohydrolase, isoenzyme ExoII
NCBI Description
                  [Hordeum vulgare] >gi_1588407_prf _2208395A beta-D-glucan
                  exohydrolase [Hordeum vulgare]
                  417596
Seq. No.
                  uC-osroM202019f09b1
Seq. ID
Method
                  BLASTX
                  q1203832
NCBI GI
                  861
BLAST score
                  7.0e-93
E value
                  176
Match length
                   90
% identity
                  (U46003) beta-D-glucan exohydrolase, isoenzyme ExoII
NCBI Description
                   [Hordeum vulgare] >gi_1588407_prf__2208395A beta-D-glucan
                  exohydrolase [Hordeum vulgare]
Seq. No.
                   417597
                   uC-osroM202019f12a1
Seq. ID
                  BLASTX
Method
                   q836954
NCBI GI
BLAST score
                   369
                   3.0e-35
E value
Match length
                   139
                   55
% identity
                 (U20948) receptor protein kinase [Ipomoea trifida]
NCBI Description
Seq. No.
                   417598
                   uC-osroM202019f12b1
Seq. ID
Method
                   BLASTX
                   g836954
NCBI GI
                   173
BLAST score
                   2.0e-15
E value
                   88
Match length
                   55
% identity
NCBI Description (U20948) receptor protein kinase [Ipomoea trifida]
                   417599
Seq. No.
                   uC-osroM202019g02a1
Seq. ID
                   BLASTX
Method
                   g5668813
NCBI GI
                   218
BLAST score
                   1.0e-17
E value
                   144
Match length
```

NCBI Description (AC007519) Similar to gb_X77136 HSR203J protein from

37

% identity



Nicotiana tabacum and is a member of the PF_00135 Carboxylesterase family. ESTs gb_Z25688 and gb_F14025 come from this gene. [Arabidopsis thaliana]

Seq. No. 417600
Seq. ID uC-osroM202019g03a1
Method BLASTX
NCBI GI g1848225
BLAST score 237
E value 7.0e-20
Match length 50

% identity 78 NCBI Description (U88090) nonspecific lipid transfer protein [Hordeum

vulgare]

Seq. No. 417601

Seq. ID uC-osroM202019g04b1

Method BLASTX
NCBI GI g5903036
BLAST score 228
E value 1.0e-18
Match length 63
% identity 68

NCBI Description (AC008016) F6D8.5 [Arabidopsis thaliana]

Seq. No. 417602

Seq. ID uC-osroM202019g05b1

Method BLASTX
NCBI GI g4938491
BLAST score 159
E value 1.0e-10
Match length 137
% identity 31

NCBI Description (AL078464) hypothetical protein [Arabidopsis thaliana]

Seq. No. 417603

Seq. ID uC-osroM202019g06a1

Method BLASTX
NCBI GI g2058498
BLAST score 499
E value 2.0e-50
Match length 98
% identity 99

NCBI Description (U76029) hemoglobin 1 [Oryza sativa] >gi_2058500 (U76030)

hemoglobin 1 [Oryza sativa]

Seq. No. 417604

Seq. ID uC-osroM202019g06b1

Method BLASTX
NCBI GI g2058498
BLAST score 643
E value 5.0e-71
Match length 145
% identity 99

NCBI Description (U76029) hemoglobin 1 [Oryza sativa] >gi_2058500 (U76030)

hemoglobin 1 [Oryza sativa]

```
Seq. No.
                   417605
                  uC-osroM202019g07b1
Seq. ID
Method
                  BLASTX
                  g3036796
NCBI GI
                  211
BLAST score
                   5.0e-17
E value
Match length
                   91
                   45
% identity
                   (AL022373) putative protein [Arabidopsis thaliana]
NCBI Description
                   >gi 3805858_emb_CAA21478.1_ (AL031986) putative protein
                   [Arabidopsis thaliana]
                   417606
Seq. No.
                   \verb"uC-osroM202019g09b1"
Seq. ID
                   BLASTX
Method
                   g4938491
NCBI GI
BLAST score
                   159
                   1.0e-10
E value
Match length
                   137
                   31
% identity
                  (AL078464) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   417607
                   uC-osroM202019g11b1
Seq. ID
Method
                   BLASTX
                   g1323742
NCBI GI
                   208
BLAST score
E value
                   2.0e-16
                   125
Match length
                   36
% identity
NCBI Description (U32427) unknown [Triticum aestivum]
                   417608
Seq. No.
                   uC-osroM202019h01b1
Seq. ID
                   BLASTX
Method
                   g4886280
NCBI GI
                   253
BLAST score
E value
                   1.0e-21
                   114
Match length
                   42
% identity
NCBI Description (AL050300) putative protein [Arabidopsis thaliana]
                   417609
Seq. No.
                   uC-osroM202019h02b1
Seq. ID
                   BLASTX
Method
                   q4886280
NCBI GI
BLAST score
                   296
E value
                   1.0e-26
Match length
                   145
% identity
NCBI Description (AL050300) putative protein [Arabidopsis thaliana]
```

Seq. No. 417610

uC-osroM202019h04a1 Seq. ID

BLASTX Method NCBI GI g481477 BLAST score 494

BLAST score

195

```
7.0e-50
E value
                  99
Match length
                  17
% identity
                  ubiquitin precursor - rice >gi_416038_emb_CAA53665
NCBI Description
                  (X76064) polyubiquitin [Oryza sativa] >gi_1574944 (U37687)
                  polyubiquitin [Oryza sativa]
                  >gi_6013289_gb_AAF01315.1_AF184279_1 (AF184279)
                  polyubiquitin [Oryza sativa]
                  >gi_6013291_gb_AAF01316.1_AF184280_1 (AF184280)
                  polyubiquitin [Oryza sativa]
                  417611
Seq. No.
                  uC-osroM202019h04b1
Seq. ID
                  BLASTX
Method
                  g2760345
NCBI GI
                  680
BLAST score
                  1.0e-71
E value
                  136
Match length
                  28
% identity
                  (U84967) ubiquitin [Arabidopsis thaliana]
NCBI Description
                  417612
Seq. No.
                  uC-osroM202019h06a1
Seq. ID
                  BLASTX
Method
                  g3927836
NCBI GI
BLAST score
                  207
E value
                  3.0e-16
                  101
Match length
                  50
% identity
                 (AC005727) unknown protein [Arabidopsis thaliana]
NCBI Description
                  417613
Seq. No.
                  uC-osroM202019h06b1
Seq. ID
                  BLASTX
Method
NCBI GI
                  q3927836
BLAST score
                   162
E value
                   5.0e-11
Match length
                   34
                   79
% identity
NCBI Description (AC005727) unknown protein [Arabidopsis thaliana]
Seq. No.
                   417614
                   uC-osroM202019h07a1
Seq. ID
                   BLASTN
Method
                   q5091496
NCBI GI
                   40
BLAST score
E value
                   3.0e-13
Match length
                   83
% identity
                   88
NCBI Description Oryza sativa genomic DNA, chromosome 6, clone P0680A03,
                   complete sequence
Seq. No.
                   417615
                   uC-osroM202019h08b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g399940
```

```
E value
                  4.0e-15
                  103
Match length
% identity
                  48
                  HEAT SHOCK 70 KD PROTEIN, MITOCHONDRIAL PRECURSOR
NCBI Description
                  >gi 100004_pir__S25005 heat shock protein, 70K - kidney
                  bean >gi 22636 emb CAA47345 (X66874) 70 kDa heat shock
                  protein [Phaseolus vulgaris]
                  417616
Seq. No.
                  uC-osroM202019h09a1
Seq. ID
                  BLASTX
Method
NCBI GI
                  q169363
                  277
BLAST score
                  2.0e-24
E value
Match length
                  61
                  79
% identity
                 (M75856) PVPR3 [Phaseolus vulgaris]
NCBI Description
                  417617
Seq. No.
                  uC-osroM202019h09b1
Seq. ID
Method
                  BLASTX
                  g4836932
NCBI GI
BLAST score
                  174
                  2.0e-12
E value
                  111
Match length
                  37
% identity
                 (AC006085) Unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  417618
                  uC-osroM202019h10a1
Seq. ID
                  BLASTX
Method
                  g4960024
NCBI GI
                  357
BLAST score
                   9.0e-34
E value
                  91
Match length
                   77
% identity
                  (AF144079) S-adenosyl-L-methionine:L-methionine
NCBI Description
                   S-methyltransferase [Zea mays]
                   417619
Seq. No.
                  uC-osroM202019h10b1
Seq. ID
                   BLASTX
Method
                   g4960024
NCBI GI
                   473
BLAST score
                   1.0e-52
E value
                   129
Match length
                   77
% identity
                  (AF144079) S-adenosyl-L-methionine:L-methionine
NCBI Description
                   S-methyltransferase [Zea mays]
                   417620
Seq. No.
Seq. ID
                   uC-osroM202019h11b1
Method
                   BLASTX
                   g542200
NCBI GI
                   160
BLAST score
                   1.0e-10
E value
```

54662

63

Match length

```
% identity
                  hypothetical protein - garden asparagus
NCBI Description
                  >gi_452714_emb_CAA54526_ (X77320) unknown [Asparagus
                  officinalis]
                  417621
Seq. No.
                  uC-osroM202020a01b1
Seq. ID
                  BLASTN
Method
                  g5042437
NCBI GI
BLAST score
                  46
                  1.0e-16
E value
Match length
                  90
                  89
% identity
NCBI Description Oryza sativa BAC T49B20 genomic sequence, complete sequence
                  417622
Seq. No.
                  uC-osroM202020a03a1
Seq. ID
                  BLASTX
Method
                  q1816444
NCBI GI
BLAST score
                  657
                  5.0e-69
E value
                  137
Match length
                   93
% identity
                  (AB000801) chalcone synthase [Oryza sativa]
NCBI Description
                   417623
Seq. No.
                   uC-osroM202020a03b1
Seq. ID
                   BLASTX
Method
                   g3860333
NCBI GI
                   176
BLAST score
                   1.0e-12
E value
                   106
Match length
                   40
% identity
                  (AJ012693) basic blue copper protein [Cicer arietinum]
NCBI Description
                   417624
Seq. No.
                   uC-osroM202020a04b1
Seq. ID
                   BLASTX
Method
                   g5804782
NCBI GI
                   279
BLAST score
                   5.0e-36
E value
                   122
Match length
                   68
% identity
NCBI Description (AB017480) chloroplast FtsH protease [Nicotiana tabacum]
                   417625
Seq. No.
                   uC-osroM202020a05a1
Seq. ID
Method
                   BLASTX
```

Method BLASTX
NCBI GI g2239083
BLAST score 178
E value 8.0e-13
Match length 70
% identity 44

NCBI Description (Z84383) anthranilate N-hydroxycinnamoyl/benzoyltransferase [Dianthus caryophyllus] >gi 2239087 emb CAB06429 (Z84385)

anthranilate N-hydroxycinnamoyl/benzoyltransferase

[Dianthus caryophyllus]

417626 Seq. No. uC-osroM202020a06a1 Seq. ID BLASTN Method g1816443 NCBI GI 46 BLAST score 1.0e-16 E value 66 Match length 92 % identity NCBI Description Oryza sativa mRNA for chalcone synthase, complete cds 417627 Seq. No. uC-osroM202020a06b1 Seq. ID BLASTX Method g1621467 NCBI GI 315 BLAST score 6.0e-29 E value 86 Match length 64 % identity (U73106) laccase [Liriodendron tulipifera] NCBI Description 417628 Seq. No. uC-osroM202020a07a1 Seq. ID BLASTN Method g3789951 NCBI GI 112 BLAST score E value 6.0e-56 Match length 314 82 % identity Oryza sativa chlorophyll a/b-binding protein presursor NCBI Description (Cab27) mRNA, nuclear gene encoding chloroplast protein, complete cds 417629 Seq. No. uC-osroM202020a07b1 Seq. ID Method BLASTX NCBI GI q4574742 313 BLAST score 1.0e-28 E value Match length 116 % identity NCBI Description (AF135270) fragmin A [Physarum polycephalum] 417630 Seq. No. uC-osroM202020a09a1 Seq. ID Method BLASTX NCBI GI g561873 320 BLAST score 1.0e-29 E value Match length 61 % identity 95 NCBI Description (L37289) chitinase [Oryza sativa]

54664

417631

BLASTX

g2331131

uC-osroM202020a09b1

Seq. No.

Seq. ID

Method

NCBI GI

```
433
BLAST score
                  6.0e-43
E value
                  89
Match length
                  97
% identity
                  (AF010579) glycine-rich protein [Oryza sativa]
NCBI Description
                  417632
Seq. No.
                  uC-osroM202020a10a1
Seq. ID
                  BLASTX
Method
NCBI GI
                  g3831453
BLAST score
                  192
                  2.0e-14
E value
                  65
Match length
                  49
% identity
                  (AC005700) unknown protein [Arabidopsis thaliana]
NCBI Description
                  417633
Seq. No.
                  uC-osroM202020a10b1
Seq. ID
                  BLASTX
Method
                  g2454602
NCBI GI
BLAST score
                  469
                  6.0e-47
E value
                  112
Match length
                  73
% identity
                  (AF016327) Barperm1 [Hordeum vulgare]
NCBI Description
Seq. No.
                  417634
                  uC-osroM202020a11a1
Seq. ID
                  BLASTX
Method
                  g3393062
NCBI GI
BLAST score
                  517
E value
                  2.0e-52
                  135
Match length
                  70
% identity
                  (Y17386) putative In2.1 protein [Triticum aestivum]
NCBI Description
Seq. No.
                  417635
                  uC-osroM202020a12b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4835766
BLAST score
                  271
E value
                   1.0e-23
Match length
                   57
                   88
% identity
NCBI Description
                  (AC007202) Contains similarity to gb AB017693 transfactor
                   (WERBP-1) from Nicotiana tabacum. ESTs gb_H39299,
                  gb_T41875, gb_H38232 and gb_N38325 come from this gene.
                   [Arabidopsis thaliana]
                   417636
Seq. No.
                  uC-osroM202020b01b1
Seq. ID
```

Method BLASTX
NCBI GI g3023816
BLAST score 603
E value 1.0e-62
Match length 133
% identity 89



NCBI Description GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC >gi_968996 (U31676) glyceraldehyde-3-phosphate dehydrogenase [Oryza sativa]

Seq. No. 417637

Seq. ID uC-osroM202020b02b1

Method BLASTX
NCBI GI g112957
BLAST score 210
E value 1.0e-16
Match length 144
% identity 32

NCBI Description ALPHA-ACTININ 3, NON MUSCULAR (F-ACTIN CROSS LINKING

PROTEIN) >gi_71570_pir__FADOAA alpha-actinin - slime mold (Dictyostelium discoideum) >gi_7178_emb_CAA68685_ (Y00689) alpha-actinin (AA 1 - 862) [Dictyostelium discoideum]

Seq. No. 417638

Seq. ID uC-osroM202020b04b1

Method BLASTX
NCBI GI g3789942
BLAST score 379
E value 2.0e-36
Match length 78
% identity 20

NCBI Description (AF093505) polyubiquitin [Saccharum hybrid cultivar

H32-8560]

Seq. No. 417639

Seq. ID uC-osroM202020b05b1

Method BLASTX
NCBI GI g4454032
BLAST score 215
E value 5.0e-20
Match length 124

% identity 38

NCBI Description (AL035394) putative protein [Arabidopsis thaliana]

Seq. No. 417640

Seq. ID uC-osroM202020b08b1

Method BLASTX
NCBI GI g3023816
BLAST score 577
E value 1.0e-59
Match length 129
% identity 88

NCBI Description GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC

>gi 968996 (U31676) glyceraldehyde-3-phosphate

dehydrogenase [Oryza sativa]

Seq. No. 417641

Seq. ID uC-osroM202020b09a1

Method BLASTX
NCBI GI g733454
BLAST score 193
E value 1.0e-14
Match length 59

% identity (U23188) chlorophyll a/b-binding apoprotein CP26 precursor NCBI Description [Zea mays] 417642 Seq. No. uC-osroM202020b10b1 Seq. ID Method BLASTN q3282393 NCBI GI BLAST score 349 0.0e + 00E value Match length 399 97 % identity NCBI Description Oryza sativa aie2 mRNA, partial cds 417643 Seq. No. uC-osroM202020b11a1 Seq. ID Method BLASTX g4126809 NCBI GI BLAST score 428 E value 4.0e-42 83 Match length 53 % identity NCBI Description (AB017042) glyoxalase I [Oryza sativa] Seq. No. 417644 uC-osroM202020b11b1 Seq. ID Method BLASTX a4539453 NCBI GI 285 BLAST score 2.0e-25 E value Match length 133 43 % identity NCBI Description (AL049500) putative protein [Arabidopsis thaliana]

Seq. No. 417645

Seq. ID uC-osroM202020c01a1

Method BLASTN
NCBI GI 94406131
BLAST score 212
E value 1.0e-115
Match length 384
% identity 89

NCBI Description Oryza sativa MADS box protein (MADS16) mRNA, complete cds

Seq. No. 417646

Seq. ID uC-osroM202020c01b1

Method BLASTX
NCBI GI g1203832
BLAST score 249
E value 3.0e-21
Match length 62
% identity 76

NCBI Description (U46003) beta-D-glucan exohydrolase, isoenzyme ExoII

[Hordeum vulgare] >gi_1588407_prf__2208395A beta-D-glucan

exohydrolase [Hordeum vulgare]

Seq. No. 417647

```
uC-osroM202020c02b1
Seq. ID
Method
                  BLASTX
                  g2462733
NCBI GI
                  344
BLAST score
                  2.0e-32
E value
                  134
Match length
                  56
% identity
NCBI Description
```

(AC002292) Putative enoyl-CoA hydratase/isomerase

[Arabidopsis thaliana]

Seq. No. 417648

uC-osroM202020c03b1 Seq. ID

Method BLASTX g399942 NCBI GI 143 BLAST score 7.0e-09 E value Match length 129 36 % identity

CHLOROPLAST STROMA 70 KD HEAT SHOCK-RELATED PROTEIN NCBI Description

PRECURSOR >gi_421881_pir__S32818 heat shock protein, 70K, chloroplast - garden pea >gi_169023 (L03299) 70 kDa heat shock protein [Pisum sativum] >gi_871515_emb_CAA49147_ (X69213) Psst70 (stress 70 protein) [Pisum sativum]

417649 Seq. No.

uC-osroM202020c04b1 Seq. ID

Method BLASTX NCBI GI q131773 BLAST score 609 2.0e-63 E value Match length 141 % identity 89

40S RIBOSOMAL PROTEIN S14 (CLONE MCH2) NCBI Description

>gi 82724 pir B30097 ribosomal protein S14 (clone MCH2) -

maize

Seq. No. 417650

uC-osroM202020c05b1 Seq. ID

Method BLASTX g5541709 NCBI GI BLAST score 562 E value 7.0e-58 Match length 148 % identity 72

NCBI Description (AL096860) putative protein [Arabidopsis thaliana]

Seq. No. 417651

Seq. ID uC-osroM202020c06a1

Method BLASTX NCBI GI g3142292 BLAST score 276 E value 3.0e-24Match length 65 75 % identity

NCBI Description (AC002411) Contains similarity to tetratricopeptide repeat

protein gb U46571 from home sapiens. EST gb Z47802 and gb Z48402 come from this gene. [Arabidopsis thaliana]

```
417652
Seq. No.
Seq. ID
                  uC-osroM202020c07a1
Method
                  BLASTX
NCBI GI
                  g2130069
BLAST score
                   225
E value
                   3.0e-18
                   55
Match length
                   84
% identity
                  catalase (EC 1.11.1.6) catA - rice
NCBI Description
                   >gi_1261858_dbj_BAA06232_ (D29966) catalase [Oryza sativa]
Seq. No.
                   417653
                   uC-osroM202020c10b1
Seq. ID
Method
                   BLASTX
                   g1402920
NCBI GI
BLAST score
                   312
                   2.0e-28
E value
Match length
                   99
                   61
% identity
NCBI Description (X98321) peroxidase [Arabidopsis thaliana]
                   417654
Seq. No.
                   uC-osroM202020c11a1
Seq. ID
Method
                   BLASTN
NCBI GI
                   a3075487
BLAST score
                   44
                   2.0e-15
E value
                   132
Match length
% identity
                   91
NCBI Description Oryza sativa chlorophyll a/b-binding protein (RCABP69)
                   mRNA, complete cds
                   417655
Seq. No.
                   uC-osroM202020c11b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   q4803944
BLAST score
                   173
E value
                   3.0e-12
Match length
                   43
% identity
                   70
NCBI Description (AC006264) putative C2-domain protein (prosite: PD0C00380)
                   [Arabidopsis thaliana]
                   417656
Seq. No.
Seq. ID
                   uC-osroM202020c12b1
Method
                   BLASTX
                   q6056199
NCBI GI
BLAST score
                   303
E value
                   2.0e-27
Match length
                   109
                   53
% identity
NCBI Description (AC009400) unknown protein [Arabidopsis thaliana]
                   417657
Seq. No.
                   \verb"uC-osroM202020d01b1"
Seq. ID
```

54669

BLASTX

Method

Seq. No.

Seq. ID

417662

uC-osroM202020d05a1

NCBI GI g5731756 BLAST score 285 1.0e-25 E value 95 Match length 57 % identity (AL109819) putative protein [Arabidopsis thaliana] NCBI Description Seq. No. 417658 uC-osroM202020d02a1 Seq. ID BLASTX Method NCBI GI g2501190 BLAST score 161 7.0e-11 E value Match length 51 71 % identity NCBI Description THIAMINE BIOSYNTHETIC ENZYME 1-2 PRECURSOR >gi_2130147_pir__S61420 thiamine biosynthetic enzyme thi1-2 - maize >qi 596080 (U17351) thiamine biosynthetic enzyme [Zea mays] 417659 Seq. No. uC-osroM202020d03b1 Seq. ID Method BLASTX NCBI GI g417154 BLAST score 582 E value 2.0e-60 Match length 120 99 % identity HEAT SHOCK PROTEIN 82 >gi_100685_pir__S25541 heat shock NCBI Description protein 82 - rice (strain Taichung Native One) >gi_20256_emb_CAA77978_ (Z11920) heat shock protein 82 (HSP82) [Oryza sativa] 417660 Seq. No. uC-osroM202020d04a1 Seq. ID Method BLASTX NCBI GI q2435522 BLAST score 362 E value 2.0e-34 Match length 115 % identity 59 NCBI Description (AF024504) contains similarity to other AMP-binding enzymes [Arabidopsis thaliana] 417661 Seq. No. uC-osroM202020d04b1 Seq. ID Method BLASTX NCBI GI g2262159 BLAST score 236 1.0e-19 E value Match length 50 % identity (AC002329) predicted protein similar to S.pombe protein NCBI Description C5H10.03 [Arabidopsis thaliana]

Match length

89

```
BLASTX
Method
NCBI GI
                  q5081779
BLAST score
                  449
                  1.0e-44
E value
Match length
                  90
                  90
% identity
                 (AF150630) cellulose synthase [Gossypium hirsutum]
NCBI Description
                  417663
Seq. No.
                  uC-osroM202020d10b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g82496
                  631
BLAST score
                  6.0e-66
E value
                  141
Match length
% identity
                  87
NCBI Description phenylalanine ammonia-lyase (EC 4.3.1.5) - rice
                   417664
Seq. No.
                  uC-osroM202020d11b1
Seq. ID
                  BLASTX
Method
NCBI GI
                  g5912424
                  526
BLAST score
                  1.0e-53
E value
                  149
Match length
                  72
% identity
NCBI Description (AJ242970) BTF3b-like factor [Arabidopsis thaliana]
                   417665
Seq. No.
                  uC-osroM202020d12a1
Seq. ID
Method
                  BLASTN
                  g2984708
NCBI GI
BLAST score
                   40
                   5.0e-13
E value
                   80
Match length
                   88
% identity
NCBI Description
                  Zea mays DnaJ-related protein ZMDJ1 (mdJ1) gene, complete
                   cds >gi 5996689 gb AR066473.1_AR066473 Sequence 2 from
                  patent US
                   417666
Seq. No.
Seq. ID
                   uC-osroM202020e01b1
                   BLASTX
Method
                   q1184112
NCBI GI
BLAST score
                   175
                   1.0e-12
E value
Match length
                   57
% identity
NCBI Description (U46138) Zn-induced protein [Oryza sativa]
                   417667
Seq. No.
Seq. ID
                   uC-osroM202020e02a1
Method
                   BLASTX
NCBI GI
                   g320617
BLAST score
                   393
                   5.0e-38
E value
```

% identity NCBI Description chlorophyll a/b-binding protein II precursor - rice >gi 227612_prf__1707316B chlorophyll a/b binding protein 2 [Oryza sativa] 417668 Seq. No. Seq. ID uC-osroM202020e02b1 Method BLASTX NCBI GI q2392895 BLAST score 494 E value 7.0e-50 Match length 151 14 % identity (AF017056) brassinosteroid insensitive 1 [Arabidopsis NCBI Description thaliana] >gi_5042156_emb_CAB44675.1_ (AL078620) brassinosteroid insensitive 1 gene (BRI1) [Arabidopsis thaliana] 417669 Seq. No. Seq. ID uC-osroM202020e04b1 Method BLASTX NCBI GI q3023713 BLAST score 624 E value 4.0e-65 Match length 122 % identity 100 ENOLASE (2-PHOSPHOGLYCERATE DEHYDRATASE) NCBI Description (2-PHOSPHO-D-GLYCERATE HYDRO-LYASE) (OSE1) >gi 780372 (U09450) enolase [Oryza sativa] Seq. No. 417670 uC-osroM202020e05a1 Seq. ID Method BLASTX NCBI GI q482311 BLAST score 420 E value 3.0e-41Match length 83 100 % identity photosystem II oxygen-evolving complex protein 1 - rice NCBI Description (strain Nihonbare) >gi 739292 prf 2002393A oxygen-evolving complex protein 1 [Oryza sativa] 417671 Seq. No. Seq. ID uC-osroM202020e06b1 Method BLASTX NCBI GI q4099408 BLAST score 637 1.0e-66 E value Match length 136 88 % identity NCBI Description (U86763) delta-type tonoplast intrinsic protein [Triticum aestivum]

Seq. No. 417672

Seq. ID uC-osroM202020e07b1

Method BLASTX NCBI GI g2130073

663 BLAST score 1.0e-69 E value 133 Match length 96 % identity

fructose-bisphosphate aldolase (EC 4.1.2.13) isoenzyme C-1, cytosolic - rice >gi_786178_dbj_BAA08845_ (D50307) aldolase NCBI Description

C-1 [Oryza sativa] >gi_790970_dbj_BAA08830_ (D50301)

aldolase C-1 [Oryza sativa]

417673 Seq. No.

uC-osroM202020e08a1 Seq. ID

BLASTX Method g4098272 NCBI GI 275 BLAST score 3.0e-24E value Match length 54 96 % identity

(U76558) alpha-tubulin [Triticum aestivum] NCBI Description

417674 Seq. No.

uC-osroM202020e09b1 Seq. ID

BLASTX Method g1361979 NCBI GI 188 BLAST score 5.0e-14 E value 96 Match length 38 % identity

serine O-acetyltransferase (EC 2.3.1.30) - watermelon NCBI Description

>gi_1350550_dbj_BAA12843_ (D85624) serine acetyltransferase
[Citrullus lanatus] >gi_1841312_dbj_BAA08479_ (D49535)

serine acetyltransferase. [Citrullus lanatus] >gi_2337772_dbj_BAA21827_ (AB006530) serine

acetyltransferase [Citrullus lanatus]

417675 Seq. No.

uC-osroM202020e10b1 Seq. ID

Method BLASTX q4454050 NCBI GI 325 BLAST score 5.0e-30 E value 84 Match length % identity

NCBI Description (AL035394) putative protein [Arabidopsis thaliana]

417676 Seq. No.

uC-osroM202020e12b1 Seq. ID

Method BLASTX NCBI GI g2618686 BLAST score 288 1.0e-25 E value Match length 156 39 % identity

NCBI Description (AC002510) hypothetical protein [Arabidopsis thaliana]

417677 Seq. No.

uC-osroM202020f05b1 Seq. ID

Method BLASTX

g5732048 NCBI GI 189 BLAST score 4.0e-14E value 77 Match length 45 % identity (AF147262) contains similarity to the Pfam family PF00646 -NCBI Description F-box domain; score=10.1, E=1.2, N=1 [Arabidopsis thaliana] 417678 Seq. No. uC-osroM202020f06a1 Seq. ID BLASTN Method g4097337 NCBI GI 397 BLAST score 0.0e+00E value Match length 461 97 % identity Oryza sativa metallothionein-like protein mRNA, complete NCBI Description cds 417679 Seq. No. uC-osroM202020f06b1 Seq. ID BLASTN Method q11957 NCBI GI 442 BLAST score 0.0e+00E value Match length 472 49 % identity NCBI Description Rice complete chloroplast genome 417680 Seq. No. uC-osroM202020f07b1 Seq. ID Method BLASTX g6091750 NCBI GI 585 BLAST score 1.0e-60 E value 150 Match length % identity NCBI Description (AC009992) unknown protein [Arabidopsis thaliana] 417681 Seq. No. Seq. ID uC-osroM202020f08b1 Method BLASTN q471330 NCBI GI 143 BLAST score 1.0e-74 E value 163 Match length

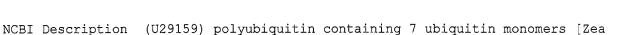
% identity 98

NCBI Description O.sativa Adhl gene, 5' flanking region

417682 Seq. No.

Seq. ID uC-osroM202020f09a1

Method BLASTX NCBI GI q902584 BLAST score 233 E value 2.0e-19 Match length 53 % identity 13



Seq. No. 417683

Seq. ID uC-osroM202020f10b1

mays]

Method BLASTX
NCBI GI g2983997
BLAST score 215
E value 4.0e-17
Match length 80
% identity 47

NCBI Description (AE000749) hypothetical protein [Aquifex aeolicus]

Seq. No. 417684

Seq. ID uC-osroM202020f11b1

Method BLASTX
NCBI GI g1351209
BLAST score 492
E value 1.0e-49
Match length 118
% identity 81

NCBI Description T-COMPLEX PROTEIN 1, DELTA SUBUNIT (TCP-1-DELTA)

(CCT-DELTA) >gi_993037 (U25697) CCT-4 [Caenorhabditis elegans] >gi_3878120_emb_CAA88861.1_ (Z49068) similar to T-complex protein; cDNA EST EMBL:Z14357 comes from this gene; cDNA EST EMBL:Z14529 comes from this gene; cDNA EST EMBL:D73565 comes from this gene; cDNA EST EMBL:D70995

comes from this gene; cDNA EST yk503

Seq. No. 417685

Seq. ID uC-osroM202020f12b1

Method BLASTX
NCBI GI g3023816
BLAST score 622
E value 7.0e-65
Match length 137
% identity 88

NCBI Description GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC

>gi 968996 (U31676) glyceraldehyde-3-phosphate

dehydrogenase [Oryza sativa]

Seq. No. 417686

Seq. ID uC-osroM202020g01a1

Method BLASTX
NCBI GI g347855
BLAST score 386
E value 3.0e-37
Match length 92
% identity 83

NCBI Description (L21753) glucose transporter [Saccharum hybrid cultivar

H65-7052]

Seq. No. 417687

Seq. ID uC-osroM202020g01b1

Method BLASTX
NCBI GI g1491638
BLAST score 219

E value

```
1.0e-17
E value
Match length
                   78
                   51
% identity
                  (X99922) male sterility protein 2 [Brassica napus]
NCBI Description
                   417688
Seq. No.
                  uC-osroM202020g04a1
Seq. ID
                  BLASTX
Method
                   g322854
NCBI GI
                   286
BLAST score
                   1.0e-25
E value
                   66
Match length
                   88
% identity
NCBI Description
                  pollen-specific protein - rice >gi_20310_emb_CAA78897_
                   (Z16402) pollen specific gene [Oryza sativa]
                   417689
Seq. No.
                   uC-osroM202020q04b1
Seq. ID
                   BLASTX
Method
NCBI GI
                   g5732035
                   358
BLAST score
                   6.0e - 34
E value
                   153
Match length
                   55
% identity
                  (AF160760) contains similarity to Pfam family PF0040 - WD
NCBI Description
                   domain, G-beta repeat; score=10.8, E=3.2, N-2 [Arabidopsis
                   thaliana]
                   417690
Seq. No.
                   uC-osroM202020q05a1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2894304
BLAST score
                   325
                   4.0e-30
E value
                   84
Match length
                   21
% identity
NCBI Description
                  (AJ223328) polyubiquitin [Nicotiana tabacum]
                   >gi_3334645_emb_CAA07773_ (AJ007936) polyubiquitin
                   [Gibberella pulicaris]
                   417691
Seq. No.
Seq. ID
                   uC-osroM202020g05b1
Method
                   BLASTX
NCBI GI
                   g2130069
BLAST score
                   718
                   4.0e-76
E value
Match length
                   139
% identity
                   97
NCBI Description
                  catalase (EC 1.11.1.6) catA - rice
                   >gi_1261858_dbj_BAA06232_ (D29966) catalase [Oryza sativa]
Seq. No.
                   uC-osroM202020g07a1
Seq. ID
Method
                   BLASTN
NCBI GI
                   g6041757
BLAST score
                   376
                   0.0e + 00
```

Match length 412 % identity 98

NCBI Description Genomic Sequence For Oryza sativa Clone 10P20, Lemont

Strain, Complete Sequence, complete sequence

Seq. No. 417693

Seq. ID uC-osroM202020g07b1

Method BLASTX
NCBI GI g4314388
BLAST score 432
E value 1.0e-42
Match length 128
% identity 63

NCBI Description (AC006232) hypothetical protein [Arabidopsis thaliana]

Seq. No. 417694

Seq. ID uC-osroM202020g08b1

Method BLASTX
NCBI GI 94454043
BLAST score 493
E value 8.0e-50
Match length 146
% identity 66

NCBI Description (AL035394) putative receptor kinase [Arabidopsis thaliana]

Seq. No. 417695

Seq. ID uC-osroM202020g09b1

Method BLASTX
NCBI GI g4538941
BLAST score 357
E value 8.0e-34
Match length 138
% identity 56

NCBI Description (AL049483) NPR1 like protein [Arabidopsis thaliana]

Seq. No. 417696

Seq. ID uC-osroM202020g10b1

Method BLASTX
NCBI GI g129591
BLAST score 473
E value 1.0e-47
Match length 112
% identity 82

NCBI Description PHENYLALANINE AMMONIA-LYASE >gi 295824 emb CAA34226 (X16099) phenylalanine ammonia-lyase [Oryza sativa]

Seq. No. 417697

Seq. ID uC-osroM202020g11b1

Method BLASTX
NCBI GI g3790102
BLAST score 561
E value 9.0e-58
Match length 151
% identity 72

NCBI Description (AF095521) pyrophosphate-dependent phosphofructokinase

alpha subunit [Citrus X paradisi]

```
417698
Seq. No.
Seq. ID
                   uC-osroM202020h01a1
                   BLASTX
Method
NCBI GI
                   q729944
BLAST score
                   188
                   4.0e-14
E value
Match length
                   51
                   61
% identity
NCBI Description
                   POLLEN ALLERGEN ZEA M 1 (ZEA M I) >gi 478272 pir JC1524
                   major allergen mI protein - maize >gi_293902 (L14271) Zea
                   mI [Zea mays]
                   417699
Seq. No.
                   uC-osroM202020h03b1
Seq. ID
Method
                   BLASTX
                   q5732035
NCBI GI
                   186
BLAST score
                   2.0e-25
E value
                   122
Match length
% identity
                   (AF160760) contains similarity to Pfam family PF0040 - WD
NCBI Description
                    domain, G-beta repeat; score=10.8, E=3.2, N-2 [Arabidopsis
                   thaliana]
                    417700
Seq. No.
Seq. ID
                   uC-osroM202020h04b1
Method
                   BLASTX
NCBI GI
                    q1076809
BLAST score
                    616
                    3.0e-64
E value
Match length
                    139
% identity
                   H+-transporting ATPase (EC 3.6.1.35) - maize
NCBI Description
                    >gi_758355_emb_CAA59800_ (X85805) H(+)-transporting ATPase
                    [Zea mays]
Seq. No.
                    417701
                    uC-osroM202020h05a1
Seq. ID
Method
                    BLASTX
NCBI GI
                    g2499931
BLAST score
                    228
E value
                    1.0e-18
Match length
                    61
                    70
% identity
                   ADENINE PHOSPHORIBOSYLTRANSFERASE 2 (APRT)
NCBI Description
                    >gi_2129534_pir__S71272 adenine phosphoribosyltransferase (EC 2.4.2.7) - Arabidopsis thaliana
                    >gi_1321681_emb_CAA65609_ (X96866) adenine phosphoribosyltransferase [Arabidopsis thaliana]
                    >gi 5902383 gb AAD55485.1 AC009322 25 (AC009322) adenine
                    phosphoribosyltransferase [Arabidopsis thaliana]
                    417702
Seq. No.
                    uC-osroM202020h05b1
Seq. ID
```

54678

 ${\tt BLASTX}$

669

g119150

Method NCBI GI

BLAST score

E value

2.0e-14

```
E value
                   2.0e-70
Match length
                   128
                   98
% identity
NCBI Description
                   ELONGATION FACTOR 1-ALPHA (EF-1-ALPHA)
                   >gi_82081_pir__S10507 translation elongation factor eEF-1
                   alpha chain - tomato >gi_19273_emb_CAA32618_ (X14449) EF 1-alpha (AA 1-448) [Lycopersicon esculentum]
                   >gi_295810_emb_CAA37212_ (X53043) elongation factor 1-alpha
                   [Lycopersicon esculentum]
Seq. No.
                   417703
Seq. ID
                   uC-osroM202020h06b1
Method
                   BLASTX
NCBI GI
                   q4938497
BLAST score
                   475
                   1.0e-47
E value
Match length
                   148
                   63
% identity
NCBI Description (AL078465) isp4 like protein [Arabidopsis thaliana]
                   417704
Seq. No.
Seq. ID
                   uC-osroM202020h07a1
Method
                   BLASTX
NCBI GI
                   q4582468
BLAST score
                   248
E value
                   3.0e-21
Match length
                   63
                   73
% identity
NCBI Description (AC007071) putative 40S ribosomal protein; contains
                   C-terminal domain [Arabidopsis thaliana]
Seq. No.
                   417705
                   uC-osroM202020h08a1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g1143864
BLAST score
                   270
E value
                   1.0e-23
                   58
Match length
                   86
% identity
NCBI Description (U28047) beta glucosidase [Oryza sativa]
                   417706
Seq. No.
                   uC-osroM202020h08b1
Seq. ID
                   BLASTX
Method
NCBI GI
                   g4678308
BLAST score
                   399
E value
                   9.0e-39
                   128
Match length
% identity
NCBI Description (AL049655) putative protein [Arabidopsis thaliana]
                   417707
Seq. No.
Seq. ID
                   uC-osroM202020h10b1
                   BLASTN
Method
NCBI GI
                   g5042437
BLAST score
                   42
```



Match length 90 % identity 88

NCBI Description Oryza sativa BAC T49B20 genomic sequence, complete sequence

Seq. No. 417708

Seq. ID uC-osroM202021a02b1

Method BLASTX
NCBI GI g115829
BLAST score 416
E value 6.0e-52
Match length 136
% identity 76

NCBI Description CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR

(CAB) (LHCP) >gi_99364_pir__JW0040 light-harvesting

chlorophyll $28.5\overline{\text{K}}$ apoprotein (photosystem II) - green alga (Dunaliella tertiolecta) >gi_167985 (M60049) 28.5 kDa LHCII

apoprotein [Dunaliella tertiolecta]

Seq. No. 417709

Seq. ID uC-osroM202021a05b1

Method BLASTX
NCBI GI g2293480
BLAST score 428
E value 4.0e-42
Match length 84

% identity 99

NCBI Description (AF011331) glycine-rich protein [Oryza sativa]

Seq. No. 417710

Seq. ID uC-osroM202021a07b1

Method BLASTX
NCBI GI g6103623
BLAST score 970
E value 1.0e-105
Match length 187
% identity 98

NCBI Description (AF172094) actin [Picea rubens]

Seq. No. 417711

Seg. ID uC-osroM202021a08b1

Method BLASTX
NCBI GI g1890573
BLAST score 562
E value 2.0e-61
Match length 147
% identity 82

NCBI Description (X93173) xyloglucan endotransglycosylase (XET) [Hordeum

vulgare]

Seq. No. 417712

Seq. ID uC-osroM202021a10b1

Method BLASTX
NCBI GI g2894534
BLAST score 837
E value 5.0e-90
Match length 165
% identity 97

NCBI Description (AJ224327) aquaporin [Oryza sativa] 417713 Seq. No. Seq. ID uC-osroM202021a12b1 Method BLASTX g3236248 NCBI GI BLAST score 347 E value 9.0e-33 Match length 105 % identity 66 NCBI Description (AC004684) unknown protein [Arabidopsis thaliana] Seq. No. 417714 Seq. ID uC-osroM202021b01b1 Method BLASTX g2209332 NCBI GI BLAST score 717 E value 6.0e - 76Match length 153 89 % identity NCBI Description (U89272) chloroplast membrane protein ALBINO3 [Arabidopsis thaliana] >gi_3927828 (AC005727) chloroplast membrane protein ALBINO3 [Arabidopsis thaliana] Seq. No. 417715 Seq. ID uC-osroM202021b04b1 Method BLASTX NCBI GI q1502430 BLAST score 501 E value 1.0e-50 Match length 125 % identity NCBI Description (U62331) phosphate transporter [Arabidopsis thaliana] >gi_2564661 (AF022872) phosphate transporter [Arabidopsis thaliana] >gi_3869206_dbj_BAA34398_ (AB016166) Phosphate Transporter 4 [Arabidopsis thaliana] >gi_3928081 (AC005770) phosphate transporter, AtPT2 [Arabidopsis thaliana] Seq. No. 417716 Seq. ID uC-osroM202021b05b1 Method BLASTX NCBI GI g1502430 BLAST score 171 E value 3.0e-12 Match length 96 % identity NCBI Description (U62331) phosphate transporter [Arabidopsis thaliana] >gi_2564661 (AF022872) phosphate transporter [Arabidopsis

thaliana] >gi_3869206_dbj_BAA34398_ (AB016166) Phosphate Transporter 4 [Arabidopsis thaliana] >gi_3928081 (AC005770)

phosphate transporter, AtPT2 [Arabidopsis thaliana]

Seq. No. 417717

Seq. ID uC-osroM202021b07b1

Method BLASTX NCBI GI g121950 BLAST score 178

```
E value
                   8.0e-13
                  55
Match length
                   65
% identity
                  HISTONE H1 >gi 22321 emb CAA40362 (X57077) H1 histone [Zea
NCBI Description
                  mays]
                   417718
Seq. No.
                  uC-osroM202021b08b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g5734639
BLAST score
                   391
                  1.0e-37
E value
Match length
                  77
                  100
% identity
                  (AP000391) ESTs AU056036(S20239), C72753(E2173),
NCBI Description
                  AU056035(S20239) correspond to a region of the predicted
                  gene.; Similar to putative cytochrome P-450 (AC003680)
                   [Oryza sativa]
                   417719
Seq. No.
Seq. ID
                  uC-osroM202021b09b1
Method
                  BLASTX
NCBI GI
                  g1203832
BLAST score
                  352
E value
                   4.0e-33
                  84
Match length
% identity
                  80
NCBI Description
                  (U46003) beta-D-glucan exohydrolase, isoenzyme ExoII
                   [Hordeum vulgare] >gi_1588407_prf__2208395A beta-D-glucan
                  exohydrolase [Hordeum vulgare]
                   417720
Seq. No.
Seq. ID
                  uC-osroM202021b10b1
Method
                  BLASTX
NCBI GI
                   q2696221
BLAST score
                   432
E value
                   1.0e-42
Match length
                  134
% identity
                   64
NCBI Description (D55708) chitinase [Oryza sativa]
Seq. No.
                   417721
Seq. ID
                  uC-osroM202021b12b1
Method
                  BLASTX
NCBI GI
                  g2245057
BLAST score
                  302
                  2.0e-27
E value
Match length
                  104
                   56
% identity
NCBI Description (Z97342) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   417722
```

Seq. ID uC-osroM202021c05b1

Method BLASTX
NCBI GI g5453379
BLAST score 470
E value 5.0e-47

Match length 120 % identity 73

NCBI Description (AF155124) bacterial-induced peroxidase precursor

[Gossypium hirsutum]

Seq. No. 417723

Seq. ID uC-osroM202021c07b1

Method BLASTX
NCBI GI g121332
BLAST score 275
E value 5.0e-24
Match length 75
% identity 80

NCBI Description GLUTAMINE SYNTHETASE ROOT ISOZYME (GLUTAMATE--AMMONIA

LIGASE) (CLONE LAMBDA-GS8) >gi_68590_pir__AJRZQB

glutamate--ammonia ligase (EC 6.3.1.2) beta, cytosolic - rice >gi 20358 emb CAA32460 (X14244) cytosolic glutamine

syntethase (AA 1-357) [Oryza sativa]

Seq. No. 417724

Seq. ID uC-osroM202021c09b1

Method BLASTX
NCBI GI g1752734
BLAST score 389
E value 2.0e-37
Match length 193
% identity 43

NCBI Description (D78510) beta-glucan-elicitor receptor [Glycine max]

Seq. No. 417725

Seq. ID uC-osroM202021c10b1

Method BLASTX
NCBI GI g1752734
BLAST score 231
E value 4.0e-19
Match length 130
% identity 41

NCBI Description (D78510) beta-glucan-elicitor receptor [Glycine max]

Seq. No. 417726

Seq. ID uC-osroM202021c12b1

Method BLASTN
NCBI GI g3986152
BLAST score 168
E value 1.0e-89
Match length 232
% identity 93

NCBI Description Oryza sativa gene for plastidic ATP sulfurylase, complete

cds

Seq. No. 417727

Seq. ID uC-osroM202021d02b1

Method BLASTX
NCBI GI g2894534
BLAST score 770
E value 3.0e-82
Match length 152

```
% identity
                  (AJ224327) aquaporin [Oryza sativa]
NCBI Description
                  417728
Seq. No.
                  uC-osroM202021d05b1
Seq. ID
                  BLASTX
Method
NCBI GI
                  q82496
BLAST score
                  567
                  2.0e-58
E value
Match length
                  131
                  84
% identity
NCBI Description phenylalanine ammonia-lyase (EC 4.3.1.5) - rice
                  417729
Seq. No.
                  uC-osroM202021d07b1
Seq. ID
                  BLASTX
Method
                  q1362162
NCBI GI
                   443
BLAST score
                  9.0e-44
E value
                  126
Match length
                   66
% identity
                  beta-glucosidase BGQ60 precursor - barley >gi_804656
NCBI Description
                   (L41869) beta-glucosidase [Hordeum vulgare]
Seq. No.
                   417730
                  uC-osroM202021d09b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g5912424
BLAST score
                   569
E value
                   1.0e-58
Match length
                   161
% identity
                   73
NCBI Description (AJ242970) BTF3b-like factor [Arabidopsis thaliana]
                   417731
Seq. No.
Seq. ID
                   uC-osroM202021d10b1
Method
                  BLASTX
NCBI GI
                   q3482918
BLAST score
                   463
E value
                   3.0e-46
Match length
                   109
% identity
                  (AC003970) Similar to ATP-citrate-lyase [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   417732
Seq. ID
                   uC-osroM202021d11b1
Method
                   BLASTX
                   q4008156
NCBI GI
BLAST score
                   576
E value
                   1.0e-59
Match length
                   135
```

% identity 85
NCBI Description (AB008845) NADH dependent Glutamate Synthase [Oryza sativa]

Seq. No. 417733

Seq. ID uC-osroM202021e02b1

Method BLASTX NCBI GI g3746431 818 BLAST score 9.0e-88 E value Match length 189 82 % identity (AF038585) pyruvate dehydrogenase kinase isoform 1; PDK1 NCBI Description [Zea mays] 417734 Seq. No. Seq. ID uC-osroM202021e05b1 Method BLASTX NCBI GI g3641836 BLAST score 223 2.0e-21 E value Match length 148 34 % identity (AL023094) putative serine/threonine protein kinase NCBI Description [Arabidopsis thaliana] 417735 Seq. No. uC-osroM202021e06b1 Seq. ID Method BLASTX NCBI GI g2130073 BLAST score 714 1.0e-75 E value Match length 142 99 % identity fructose-bisphosphate aldolase (EC 4.1.2.13) isoenzyme C-1, NCBI Description cytosolic - rice >gi_786178_dbj_BAA08845_ (D50307) aldolase C-1 [Oryza sativa] $>\overline{g}i 7909\overline{7}0 d\overline{b}j BAA088\overline{3}0$ (D50301) aldolase C-1 [Oryza sativa] 417736 Seq. No. Seq. ID uC-osroM202021e09b1 Method BLASTX NCBI GI q6056376 BLAST score 607

E value 4.0e-63 Match length 160 69 % identity

NCBI Description (AC009894) Similar to serine/threonine kinases [Arabidopsis

thaliana]

Seq. No. 417737

Seq. ID uC-osroM202021e11b1

Method BLASTX NCBI GI g3894168 BLAST score 148 E value 3.0e-15Match length 115 % identity

(AC005312) similar to phloem-specific lectin [Arabidopsis NCBI Description

thaliana]

Seq. No. 417738

Seq. ID uC-osroM202021f04b1 Method BLASTX
NCBI GI g3695403
BLAST score 577
E value 1.0e-59
Match length 131
% identity 84

NCBI Description (AF096373) contains similarity to the pfkB family of carbohydrate kinases (Pfam: PF00294, E=1.6e-75)

[Arabidopsis thaliana] >gi_4538955_emb_CAB39779.1

(AL049488) fructokinase-like protein [Arabidopsis thaliana]

Seq. No. 417739

Seq. ID uC-osroM202021f05b1

Method BLASTX
NCBI GI g5541709
BLAST score 341
E value 7.0e-32
Match length 119
% identity 65

NCBI Description (AL096860) putative protein [Arabidopsis thaliana]

Seq. No. 417740

Seq. ID uC-osroM202021f06b1

Method BLASTX
NCBI GI g4185515
BLAST score 556
E value 4.0e-57
Match length 139
% identity 77

NCBI Description (AF102824) actin depolymerizing factor 6 [Arabidopsis thaliana] >gi 6007773 gb AAF01035.1 AF183576 1 (AF183576)

actin depolymerizing factor 6 [Arabidopsis thaliana]

Seq. No. 417741

Seq. ID uC-osroM202021f07b1

Method BLASTX
NCBI GI 94588001
BLAST score 277
E value 1.0e-24
Match length 125
% identity 50

NCBI Description (AF085279) hypothetical Ser-Thr protein kinase [Arabidopsis

thaliana]

Seq. No. 417742

Seq. ID uC-osroM202021f09b1

Method BLASTX
NCBI GI g475048
BLAST score 495
E value 6.0e-50
Match length 151
% identity 65

NCBI Description (X72581) tonoplast intrinsic protein gamma (gamma-TIP)

[Arabidopsis thaliana]

Seq. No. 417743

Seq. ID uC-osroM202021f10b1

Seq. No.

Seq. ID

417748

uC-osroM202021h04b1

Method BLASTX NCBI GI a4582468 BLAST score 655 E value 1.0e-68 Match length 152 % identity 88 (AC007071) putative 40S ribosomal protein; contains NCBI Description C-terminal domain [Arabidopsis thaliana] Seq. No. 417744 Seq. ID uC-osroM202021f11b1 Method BLASTX NCBI GI q1747296 BLAST score 791 E value 5.0e-86 Match length 173 % identity 95 NCBI Description (D45384) vacuolar H+-pyrophosphatase [Oryza sativa] >gi 3298476 dbj BAA31524 (AB012766) ovp2 [Oryza sativa] Seq. No. 417745 uC-osroM202021f12b1 Seq. ID Method BLASTX NCBI GI g2149640 BLAST score 729 E value 2.0e-77 Match length 176 % identity NCBI Description (U91995) Argonaute protein [Arabidopsis thaliana] >gi_5733867_gb_AAD49755.1_AC007932_3 (AC007932) Identical to gb_U91995 Argonaute protein from Arabidopsis thaliana. ESTs gb_H76075, gb_AA720232, gb N65911 and gb AA651494 come from this gene Seq. No. 417746 Seq. ID uC-osroM202021q07b1 Method BLASTX NCBI GI g1208496 BLAST score 318 E value 4.0e-29 Match length 104 % identity 64 NCBI Description (D38124) EREBP-3 [Nicotiana tabacum] Seq. No. 417747 Seq. ID uC-osroM202021g08b1 Method BLASTX NCBI GI g1217967 BLAST score 210 E value 1.0e-16 Match length 85 % identity NCBI Description (X96431) high affinity sulphate transporter [Hordeum vulgare]



```
BLASTX
Method
                  g283008
NCBI GI
                  499
BLAST score
                  2.0e-50
E value
                  122
Match length
                  84
% identity
                  sucrose synthase (EC 2.4.1.13) - rice
NCBI Description
                  >gi_20366_emb_CAA46017_ (X64770) sucrose synthase [Oryza
                  sativa]
                  417749
Seq. No.
                  uC-osroM202021h06b1
Seq. ID
                  BLASTX
Method
NCBI GI
                  g553107
                  281
BLAST score
                  1.0e-27
E value
                  101
Match length
                  70
% identity
                  (L04967) triosephosphate isomerase [Oryza sativa]
NCBI Description
                   417750
Seq. No.
                  uC-osroM202021h08b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g100001
BLAST score
                   362
E value
                   2.0e-34
Match length
                  115
                   57
% identity
                  endopeptidase C1 - kidney bean >gi 1345573 emb CAA40073_
NCBI Description
                   (X56753) endopeptidase (EP-C1) [Phaseolus vulgaris]
Seq. No.
                   417751
                  uC-osroM202021h10b1
Seq. ID
Method
                  BLASTX
NCBI GI
                   q3360289
BLAST score
                   290
E value
                   7.0e-26
                   94
Match length
                   61
% identity
NCBI Description
                   (AF023164) leucine-rich repeat transmembrane protein kinase
                   1 [Zea mays]
                   417752
Seq. No.
Seq. ID
                   uC-osroM202022a01b1
Method
                   BLASTX
NCBI GI
                   q5882749
BLAST score
                   236
E value
                   1.0e-19
Match length
                   101
% identity
                   54
                   (AC008263) Contains 2 PF 00612 IQ calmodulin-binding motif
NCBI Description
                   domains. [Arabidopsis thaliana]
```

Seq. No. 417753

Seq. ID uC-osroM202022a04b1

Method BLASTX NCBI GI g1620896



```
BLAST score
                   5.0e-42
E value
Match length
                   105
                   81
% identity
                   (D87956) protein involved in sexual development
NCBI Description
                    [Schizosaccharomyces pombe] >gi 2408048 emb CAB16251
                   (Z99164) hypothetical protein [Schizosaccharomyces pombe]
                   417754
Seq. No.
                   uC-osroM202022a05b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g1946372
BLAST score
                   152
E value
                   2.0e-10
                   42
Match length
                   88
% identity
                   (U93215) yeast hypothetical protein YDB1 SCHPO isolog
NCBI Description
                   [Arabidopsis thaliana]
                   417755
Seq. No.
Seq. ID
                   uC-osroM202022a06b1
Method
                   BLASTX
NCBI GI
                   q2493321
                   327
BLAST score
E value
                   2.0e-30
                   92
Match length
% identity
                   67
NCBI Description L-ASCORBATE OXIDASE PRECURSOR (ASCORBASE) (ASO)
                   >gi 2129952 pir S66353 L-ascorbate oxidase (EC 1.10.3.3)
                   precursor - common tobacco >gi 599594 dbj BAA07734_
                    (D43624) ascorbate oxidase precursor [Nicotiana tabacum]
                   417756
Seq. No.
                   uC-osroM202022a07b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   q1729971
BLAST score
                   348
                    6.0e-33
E value
Match length
                    99
                    73
% identity
                   TONOPLAST INTRINSIC PROTEIN, GAMMA (GAMMA TIP)
NCBI Description
                   (AQUAPORIN-TIP) >gi_1076745_pir__S52004 gamma-Tip protein - rice >gi_473997_dbj_BAA05017_ (D25534) gamma-Tip [Oryza
                   sativa]
                    417757
Seq. No.
Seq. ID
                    uC-osroM202022a08b1
Method
                   BLASTX
NCBI GI
                    g2499488
BLAST score
                    261
E value
                    5.0e-23
                   78
Match length
```

% identity 64

NCBI Description PYROPHOSPHATE--FRUCTOSE 6-PHOSPHATE 1-PHOSPHOTRANSFERASE ALPHA SUBUNIT (PFP) (6-PHOSPHOFRUCTOKINASE (PYROPHOSPHATE))

(PYROPHOSPHATE-DEPENDENT 6-PHOSPHOFRUCTOSE-1-KINASE)

(PPI-PFK) >gi_483547_emb_CAA83682_ (Z32849)



pyrophosphate-dependent phosphofructokinase alpha subunit
[Ricinus communis]

Seq. No. 417758

Seq. ID uC-osroM202022a10b1

Method BLASTX
NCBI GI g2244749
BLAST score 418
E value 4.0e-41
Match length 104
% identity 75

NCBI Description (Z97335) hydroxymethyltransferase [Arabidopsis thaliana]

Seq. No. 417759

Seq. ID uC-osroM202022a12b1

Method BLASTX
NCBI GI g3894168
BLAST score 254
E value 6.0e-22
Match length 108
% identity 44

NCBI Description (AC005312) similar to phloem-specific lectin [Arabidopsis

thaliana]

Seq. No. 417760

Seq. ID uC-osroM202022b01b1

Method BLASTN
NCBI GI g2773153
BLAST score 325
E value 0.0e+00
Match length 365
% identity 98

NCBI Description Oryza sativa abscisic acid- and stress-inducible protein

(Asr1) mRNA, complete cds

Seq. No. 417761

Seq. ID uC-osroM202022b03b1

Method BLASTX
NCBI GI g4761580
BLAST score 372
E value 8.0e-36
Match length 76
% identity 88

NCBI Description (AF129424) profilin [Pyrus communis]

Seq. No. 417762

Seq. ID uC-osroM202022b04b1

Method BLASTX
NCBI GI 94741844
BLAST score 307
E value 4.0e-28
Match length 67
% identity 97

NCBI Description (AF112964) small GTP-binding protein [Triticum aestivum]

Seq. No. 417763

Seq. ID uC-osroM202022b05b1

Seq. ID

```
Method
                  BLASTX
NCBI GI
                  q1402918
BLAST score
                  206
E value
                  9.0e-20
Match length
                  67
                  73
% identity
NCBI Description
                  (X98320) peroxidase [Arabidopsis thaliana]
                  >gi_1429215_emb_CAA67310_ (X98774) peroxidase ATP6a
                  [Arabidopsis thaliana]
Seq. No.
                  417764
Seq. ID
                  uC-osroM202022b10b1
Method
                  BLASTX
NCBI GI
                  q2130072
BLAST score
                  496
E value
                  3.0e-50
Match length
                  116
                  84
% identity
NCBI Description
                  ferredoxin--nitrite reductase (EC 1.7.7.1) - rice
                  >gi_809514_dbj_BAA09122_ (D50556) ferredoxin-nitrite
                  reductase [Oryza sativa]
Seq. No.
                  417765
Seq. ID
                  uC-osroM202022b12b1
Method
                  BLASTN
NCBI GI
                  q5042437
BLAST score
                  130
E value
                  1.0e-66
Match length
                  238
% identity
                  89
NCBI Description Oryza sativa BAC T49B20 genomic sequence, complete sequence
                  417766
Seq. No.
Seq. ID
                  uC-osroM202022c02b1
Method
                  BLASTX
NCBI GI
                  q129591
BLAST score
                  318
E value
                  2.0e-29
                  84
Match length
                  75
% identity
NCBI Description PHENYLALANINE AMMONIA-LYASE >gi 295824 emb CAA34226
                  (X16099) phenylalanine ammonia-lyase [Oryza sativa]
                  417767
Seq. No.
                  uC-osroM202022c04b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1076746
BLAST score
                  638
E value
                  8.0e-67
Match length
                  123
                  99
% identity
NCBI Description heat shock protein 70 - rice (fragment)
                  >gi 763160 emb CAA47948 (X67711) heat shock protein 70
                  [Oryza sativa]
Seq. No.
                  417768
```

54691

uC-osroM202022c05b1

```
BLASTX
Method
NCBI GI
                  q3759184
BLAST score
                  153
E value
                  5.0e-10
                  82
Match length
                  37
% identity
NCBI Description (AB018441) phi-1 [Nicotiana tabacum]
                  417769
Seq. No.
                  uC-osroM202022c08b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1800223
                  333
BLAST score
                  2.0e-31
E value
Match length
                  151
% identity
                  49
NCBI Description (U65018) mannosyltransferase [Dictyostelium discoideum]
Seq. No.
                  417770
Seq. ID
                  uC-osroM202022c11b1
Method
                  BLASTN
                  g6063530
NCBI GI
BLAST score
                  37
E value
                  4.0e-11
                  49
Match length
                  94
% identity
NCBI Description Oryza sativa genomic DNA, chromosome 3, clone:P0043E01
                  417771
Seq. No.
                  uC-osroM202022d01b1
Seq. ID
Method
                  BLASTN
NCBI GI
                  q5257255
BLAST score
                  72
E value
                  3.0e-32
Match length
                  218
% identity
                  84
NCBI Description Oryza sativa genomic DNA, chromosome 8, clone:P0026F07
                   417772
Seq. No.
                  uC-osroM202022d02b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2943792
BLAST score
                  645
E value
                  1.0e-67
Match length
                  136
% identity
NCBI Description (AB006809) PV72 [Cucurbita sp.]
                   417773
Seq. No.
                  uC-osroM202022d03b1
Seq. ID
                  BLASTX
Method
```

Method BLASTX
NCBI GI g2244749
BLAST score 420
E value 2.0e-41
Match length 129
% identity 60

NCBI Description (Z97335) hydroxymethyltransferase [Arabidopsis thaliana]

```
Seq. No.
                   417774
Seq. ID
                   uC-osroM202022d04b1
Method
                   BLASTX
NCBI GI
                   g5689613
BLAST score
                   180
E value
                   3.0e-13
Match length
                   75
% identity
                   55
NCBI Description (AJ242807) cellulase [Brassica napus]
                   417775
Seq. No.
                   uC-osroM202022d05b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   q2662343
BLAST score
                   563
E value
                   2.0e-60
Match length
                   119
% identity
                   96
NCBI Description (D63581) EF-1 alpha [Oryza sativa]
                   417776
Seq. No.
Seq. ID
                   uC-osroM202022d06b1
Method
                   BLASTX
NCBI GI
                   g2492487
BLAST score
                   414
E value
                   1.0e-40
                   85
Match length
% identity
                   95
NCBI Description 14-3-3-LIKE PROTEIN B (14-3-3B) >gi 1070354 emb CAA63658
                   (X93170) Hv14-3-3b [Hordeum vulgare]
                   417777
Seq. No.
Seq. ID
                   uC-osroM202022d07b1
Method
                   BLASTX
NCBI GI
                   g120668
BLAST score
                   750
                   7.0e-80
E value
                   161
Match length
% identity
                   91
NCBI Description GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC
                   >gi_82399_pir__A24159 glyceraldehyde-3-phosphate
dehydrogenase (EC 1.2.1.12), cytosolic - barley (fragment)
                   >gi_167044 (M36650) glyceraldehyde-3-phosphate
                   dehydrogenase [Hordeum vulgare] >gi_225347_prf__1301218A
                   dehydrogenase, glyceraldehydephosphate [Hordeum vulgare var.
                   distichum]
                   417778
Seq. No.
Seq. ID
                   uC-osroM202022d08b1
Method
                   BLASTX
NCBI GI
                   g1632831
BLAST score
                   566
E value
                   2.0e-58
Match length
                   132
% identity
                   82
NCBI Description (Z49698) orf [Ricinus communis]
```

417779 Seq. No. uC-osroM202022d10b1 Seq. ID Method BLASTX g4097547 NCBI GI 308 BLAST score E value 3.0e-28 Match length 126 53 % identity (U64906) ATFP3 [Arabidopsis thaliana] NCBI Description 417780 Seq. No. uC-osroM202022e02b1 Seq. ID BLASTX Method NCBI GI a1778372 BLAST score 424 1.0e-41 E value 119 Match length 69 % identity NCBI Description (U77679) asparagine synthetase 1 [Glycine max] 417781 Seq. No. uC-osroM202022e03b1 Seq. ID Method BLASTX NCBI GI q2827552 BLAST score 207 2.0e-16 E value 55 Match length 71 % identity NCBI Description (AL021635) predicted protein [Arabidopsis thaliana] 417782 Seq. No. uC-osroM202022e05b1 Seq. ID Method BLASTX NCBI GI q6006879 BLAST score 307 E value 5.0e-28 91 Match length % identity 64 (AC008153) putative eukaryotic translation initiation NCBI Description factor 3 subunit [Arabidopsis thaliana] 417783 Seq. No. uC-osroM202022e06b1 Seq. ID Method BLASTX NCBI GI g2130089 397 BLAST score 1.0e-38 E value 88 Match length 90 % identity

2-oxoglutarate/malate translocator (clone OMT103), NCBI Description

mitochondrial membrane - proso millet
>gi_1100743_dbj_BAA08105_ (D45075) 2-oxoglutarate/malate

translocator [Panicum miliaceum]

Seq. No. 417784

Seq. ID uC-osroM202022e07b1

```
BLASTX
Method
NCBI GI
                  q4204859
                  392
BLAST score
E value
                  6.0e-38
Match length
                  156
                  53
% identity
                 (U55859) heat shock protein 80 [Triticum aestivum]
NCBI Description
                  417785
Seq. No.
                  uC-osroM202022e10b1
Seq. ID
Method
                  BLASTX
                  q2224663
NCBI GI
BLAST score
                  449
                  2.0e-44
E value
                  147
Match length
% identity
                  65
NCBI Description (AB002359) KIAA0361 [Homo sapiens]
                  417786
Seq. No.
                  uC-osroM202022f01b1
Seq. ID
Method
                  BLASTN
NCBI GI
                  q303852
BLAST score
                  47
                  6.0e-18
E value
                  55
Match length
                  96
% identity
NCBI Description Rice mRNA for ribosomal protein L3, complete cds
                   417787
Seq. No.
                  uC-osroM202022f02b1
Seq. ID
Method
                  BLASTX
                  q1203832
NCBI GI
                   219
BLAST score
                   7.0e-18
E value
                   56
Match length
% identity
NCBI Description
                  (U46003) beta-D-glucan exohydrolase, isoenzyme ExoII
                   [Hordeum vulgare] >gi_1588407_prf__2208395A beta-D-glucan
                   exohydrolase [Hordeum vulgare]
                   417788
Seq. No.
                   uC-osroM202022f03b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g4510430
BLAST score
                   460
E value
                   6.0e-46
Match length
                   112
% identity
                   78
                  (AC006929) unknown protein, 3' partial [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   417789
                   uC-osroM202022f04b1
Seq. ID
                   BLASTX
Method
                   g3128210
NCBI GI
BLAST score
                   441
```

54695

7.0e-44

E value

Match length 112 72 % identity

NCBI Description (AC004077) putative cytochrome P450 protein [Arabidopsis thaliana] >gi 3337378 (AC004481) putative cytochrome P450

protein [Arabidopsis thaliana]

Seq. No. 417790

Seq. ID uC-osroM202022f07b1

Method BLASTX NCBI GI q129591 BLAST score 408 E value 6.0e-40 Match length 100 80 % identity

PHENYLALANINE AMMONIA-LYASE >qi 295824 emb CAA34226 NCBI Description (X16099) phenylalanine ammonia-lyase [Oryza sativa]

417791 Seq. No.

Seq. ID uC-osroM202022f08b1

Method BLASTX NCBI GI q99492 BLAST score 397 E value 1.0e-38 Match length 100 76 % identity

chlorophyll a/b-binding protein (cab-6) precursor Japanese black pine >gi_20939_emb_CAA43907_ (X61915) NCBI Description

chlorophyll a/b-binding protein [Pinus thunbergii]

Seq. No. 417792

uC-osroM202022f09b1 Seq. ID

Method BLASTX NCBI GI g2662343 BLAST score 527 E value 4.0e-61

Match length 122 98 % identity

NCBI Description (D63581) EF-1 alpha [Oryza sativa]

417793 Seq. No.

uC-osroM202022f10b1 Seq. ID

BLASTX Method NCBI GI g1053047 BLAST score 587 E value 7.0e-61 Match length 117 % identity 100

(U38425) histone H3 [Glycine max] >gi 1053049 (U38426) NCBI Description

histone H3 [Glycine max] >gi 1053051 (U38427) histone H3

[Glycine max]

417794 Seq. No.

Seq. ID uC-osroM202022f11b1

BLASTX Method NCBI GI q5453379 BLAST score 302 E value 2.0e-27

```
tch length 84
```

Match length 84 % identity 68

NCBI Description (AF155124) bacterial-induced peroxidase precursor

[Gossypium hirsutum]

Seq. No. 417795

Seq. ID uC-osroM202022g02b1

Method BLASTN
NCBI GI 9460988
BLAST score 289
E value 1.0e-162
Match length 289
% identity 100

NCBI Description O.sativa (Arborio) Beta Tubulin mRNA, clone OSTB-34

Seq. No. 417796

Seq. ID uC-osroM202022g03b1

Method BLASTX
NCBI GI g3219758
BLAST score 499
E value 8.0e-51
Match length 97
% identity 96

NCBI Description ACTIN 66 >gi 1498374 (U60485) actin [Solanum tuberosum]

Seq. No. 417797

Seq. ID uC-osroM202022g06b1

Method BLASTX
NCBI GI g729480
BLAST score 522
E value 3.0e-53
Match length 102
% identity 98

NCBI Description FERREDOXIN--NADP REDUCTASE, ROOT ISOZYME PRECURSOR (FNR)

>gi_435647_dbj_BAA04232_ (D17410) ferredoxin-NADP+
reductase [Oryza sativa] >gi_902936_dbj_BAA07479.1_
(D38445) root ferredoxin-NADP+ reductase [Oryza sativa]
>gi_1096932_prf__2113196A ferredoxin-NADP oxidoreductase

[Oryza sativa]

Seq. No. 417798

Seg. ID uC-osroM202022g07b1

Method BLASTX
NCBI GI g1346013
BLAST score 436
E value 5.0e-43
Match length 100
% identity 78

NCBI Description 12 KD FK506-BINDING PROTEIN (FKBP) (PEPTIDYL-PROLYL

CIS-TRANS ISOMERASE) (PPIASE) (MACROLIDE BINDING PROTEIN) >gi_1079073_pir__S54139 FK506-binding protein - fruit fly (Drosophila melanogaster) >gi_784978_emb_CAA88904_ (Z49079) FK506-binding protein [Drosophila melanogaster] >gi_1209722

(U41441) macrolide binding protein [Drosophila

melanogaster]

Seq. No. 417799

NCBI GI

BLAST score

q129916

627

```
uC-osroM202022g10b1
Seq. ID
Method
                  BLASTX
                  q4406780
NCBI GI
BLAST score
                  487
E value
                  4.0e-49
                  116
Match length
                  77
% identity
                  (AC006532) putative multispanning membrane protein
NCBI Description
                  [Arabidopsis thaliana]
                  417800
Seq. No.
                  uC-osroM202022g11b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4063746
BLAST score
                  396
E value
                  5.0e-40
                  119
Match length
                  72
% identity
NCBI Description (AC005851) nodulin-like protein [Arabidopsis thaliana]
                  417801
Seq. No.
                  uC-osroM202022h05b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1706328
BLAST score
                  629
                  8.0e-66
E value
Match length
                  131
                  95
% identity
                  PYRUVATE DECARBOXYLASE ISOZYME 2 (PDC) >gi 1009710 (U27350)
NCBI Description
                  pyruvate decarboxylase 2 [Oryza sativa] >gi 1777455
                  (U38199) pyruvate decarboxylase 2 [Oryza sativa]
                  417802
Seq. No.
                  uC-osroM202023a01b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3135543
BLAST score
                  486
E value
                  4.0e-49
Match length
                  114
% identity
                  84
NCBI Description (AF062393) aquaporin [Oryza sativa]
                   417803
Seq. No.
                  uC-osroM202023a02b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3786012
BLAST score
                  263
E value
                  9.0e-23
                  89
Match length
                  53
% identity
NCBI Description (AC005499) putative acid phosphatase [Arabidopsis thaliana]
                   417804
Seq. No.
                  uC-osroM202023a04b1
Seq. ID
Method
                  BLASTX
```

```
2.0e-65
E value
                  133
Match length
                  92
% identity
                 PHOSPHOGLYCERATE KINASE, CYTOSOLIC >gi_66911_pir_
NCBI Description
                  phosphoglycerate kinase (EC 2.7.2.3), cytosolic - wheat
                  >gi_21835_emb_CAA33302_ (X15232) phosphoglycerate kinase
                  (AA 1 - 401) [Triticum aestivum]
                  417805
Seq. No.
                  uC-osroM202023a07b1
Seq. ID
                  BLASTX
```

Method BLASTX
NCBI GI g2829913
BLAST score 384
E value 6.0e-37
Match length 102
% identity 75

NCBI Description (AC002291) putative carboxyphosphonoenolpyruvate mutase

[Arabidopsis thaliana]

Method BLASTX
NCBI GI g5051773
BLAST score 226
E value 2.0e-18
Match length 159
% identity 38

NCBI Description (AL078637) putative protein [Arabidopsis thaliana]

Seq. No. 417807

Seq. ID uC-osroM202023a09b1

Method BLASTX
NCBI GI g4982522
BLAST score 596
E value 8.0e-62
Match length 161
% identity 70

NCBI Description (AC000107) F17F8.28 [Arabidopsis thaliana]

Seq. No. 417808

Seq. ID uC-osroM202023a10b1

Method BLASTX
NCBI GI g1084461
BLAST score 285
E value 2.0e-25
Match length 71
% identity 77

NCBI Description RCc3 protein - rice >gi_786132 (L27208) RCc3 [Oryza sativa]

Seq. No. 417809

Seq. ID uC-osroM202023a11b1

Method BLASTX
NCBI GI g549063
BLAST score 650
E value 4.0e-68
Match length 139
% identity 92



NCBI Description TRANSLATIONALLY CONTROLLED TUMOR PROTEIN HOMOLOG (TCTP)

>gi_1072464_pir__A38958 IgE-dependent histamine-releasing
factor homolog - rice >gi_303835_dbj_BAA02151_ (D12626)

21kd polypeptide [Oryza sativa]

Seq. No. 417810

Seq. ID uC-osroM202023b02b1

Method BLASTX
NCBI GI g1352186
BLAST score 369
E value 3.0e-35
Match length 132
% identity 52

NCBI Description ALLENE OXIDE SYNTHASE PRECURSOR (HYDROPEROXIDE DEHYDRASE)

(CYTOCHROME P450 74A) >gi_404866 (U00428) allene oxide

synthase [Linum usitatissimum]

Seq. No. 417811

Seq. ID uC-osroM202023b03b1

Method BLASTX
NCBI GI g2130072
BLAST score 669
E value 2.0e-70
Match length 147
% identity 88

NCBI Description ferredoxin--nitrite reductase (EC 1.7.7.1) - rice

>gi_809514_dbj_BAA09122_ (D50556) ferredoxin-nitrite

reductase [Oryza sativa]

Seq. No. 417812

Seq. ID uC-osroM202023b06b1

Method BLASTX
NCBI GI g1172977
BLAST score 605
E value 7.0e-63
Match length 150
% identity 81

NCBI Description 60S RIBOSOMAL PROTEIN L18 >gi_606970 (U15741) cytoplasmic

ribosomal protein L18 [Arabidopsis thaliana]

Seq. No. 417813

Seq. ID uC-osroM202023b07b1

Method BLASTN
NCBI GI g5815409
BLAST score 517
E value 0.0e+00
Match length 529
% identity 99

NCBI Description Oryza sativa blast and wounding induced mitogen-activated

protein kinase (BWMK1) mRNA, complete cds

Seq. No. 417814

Seq. ID uC-osroM202023b09b1

Method BLASTX
NCBI GI g5230728
BLAST score 427
E value 6.0e-42

96 Match length % identity

(AF089851) peroxisomal copper-containing amine oxidase NCBI Description

[Glycine max]

417815 Seq. No.

uC-osroM202023b11b1 Seq. ID

Method BLASTX NCBI GI q3023816 BLAST score 650 E value 3.0e-68 Match length 143 % identity 88

GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC NCBI Description

>gi 968996 (U31676) glyceraldehyde-3-phosphate

dehydrogenase [Oryza sativa]

417816 Seq. No.

uC-osroM202023b12b1 Seq. ID

Method BLASTX NCBI GI q417882 508 BLAST score E value 2.0e-51 Match length 106 % identity 96

TRANSCRIPTION INITIATION FACTOR TFIID-2 (TATA-BOX FACTOR 2) NCBI Description

(TATA SEQUENCE-BINDING PROTEIN 2) (TBP-2)

>gi 422014_pir__S30216 transcription initiation factor IID

- wheat >gi_21877_emb_CAA79268_ (Z18804) DNA binding protein [Triticum aestivum] >gi_170778 (L07604) DNA-binding

protein [Triticum aestivum]

Seq. No. 417817

uC-osroM202023c01b1 Seq. ID

Method BLASTX g3169719 NCBI GI BLAST score 553 E value 1.0e-56 Match length 140 74 % identity

NCBI Description (AF007109) similar to yeast dcpl [Arabidopsis thaliana]

Seq. No. 417818

Seq. ID uC-osroM202023c06b1

Method BLASTX NCBI GI g2370232 BLAST score 567 E value 2.0e-58 Match length 114 93 % identity

NCBI Description (AJ001341) putative acyl-CoA oxidase [Hordeum vulgare]

417819 Seq. No.

Seq. ID uC-osroM202023c07b1

Method BLASTN NCBI GI q5734616 313 BLAST score

Seq. ID Method

```
E value
                  1.0e-176
Match length
                  442
% identity
                  99
NCBI Description Oryza sativa genomic DNA, chromosome 6, clone:P0538C01
Seq. No.
                  417820
                  uC-osroM202023c09b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2832643
BLAST score
                  179
E value
                  5.0e-13
Match length
                  103
% identity
NCBI Description (AL021710) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  417821
                  uC-osroM202023c10b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2244813
BLAST score
                  315
E value
                  7.0e-29
Match length
                  129
% identity
                  50
NCBI Description
                  (Z97336) acylaminoacyl-peptidase like protein [Arabidopsis
                  thaliana]
                  417822
Seq. No.
Seq. ID
                  uC-osroM202023c12b1
Method
                  BLASTX
NCBI GI
                  g2498312
BLAST score
                  185
E value
                  1.0e-13
                  96
Match length
% identity
                  41
NCBI Description PROBABLE DIHYDROPYRIMIDINE DEHYDROGENASE [NADP+] (DPD)
                  (DIHYDROURACIL DEHYDROGENASE) (DIHYDROTHYMINE
                  DEHYDROGENASE) >gi 1049458 (U39742) coded for by C. elegans
                  cDNA yk28e9.3; coded for by C. elegans cDNA yk28e9.5; coded
                  for by C. elegans cDNA yk28h9.3; coded for by C. elegans
                  cDNA yk28h9.5; coded for by C. elegans cDNA yk40e4.5; coded
                  for by C. elegans cDNA yk5h3.5;
Seq. No.
                  417823
Seq. ID
                  uC-osroM202023d01b1
Method
                  BLASTX
NCBI GI
                  g1706325
BLAST score
                  507
E value
                  2.0e-51
Match length
                  103
% identity
                  97
NCBI Description
                 PYRUVATE DECARBOXYLASE ISOZYME 1 (PDC) >gi 476286 (U07339)
                  pyruvate decarboxylase 1 [Oryza sativa] >gi 1098559
                  (U26660) pyruvate decarboxylase [Oryza sativa]
Seq. No.
                  417824
```

54702

uC-osroM202023d03b1

BLASTX

NCBI GI g1351974
BLAST score 734
E value 6.0e-78
Match length 145
% identity 99

NCBI Description ADP-RIBOSYLATION FACTOR >gi_1076788_pir__S49325

ADP-ribosylation factor - maize >gi_1076789_pir__S53486 ADP-ribosylation factor - maize >gi_556686_emb_CAA56351_

(X80042) ADP-ribosylation factor [Zea mays]

Seq. No. 417825

Seq. ID uC-osroM202023d04b1

Method BLASTX
NCBI GI g5103831
BLAST score 294
E value 2.0e-26
Match length 107
% identity 56

NCBI Description (AC007591) ESTs gb_H37032, gb_R6425, gb_Z34651, gb_N37268,

gb AA713172 and gb Z34241 come from this gene. [Arabidopsis

thaliana]

Seq. No. 417826

Seq. ID uC-osroM202023d06b1

Method BLASTX
NCBI GI g2501578
BLAST score 300
E value 5.0e-27
Match length 66
% identity 89

NCBI Description ETHYLENE-INDUCIBLE PROTEIN HEVER >gi 2129913 pir S60047

ethylene-responsive protein 1 - Para rubber tree

>gi 1209317 (M88254) ethylene-inducible protein [Hevea

brasiliensis]

Seq. No. 417827

Seq. ID uC-osroM202023d07b1

Method BLASTX
NCBI GI g2501578
BLAST score 265
E value 6.0e-23
Match length 63
% identity 86

NCBI Description ETHYLENE-INDUCIBLE PROTEIN HEVER >gi_2129913_pir__S60047

ethylene-responsive protein 1 - Para rubber tree

>gi_1209317 (M88254) ethylene-inducible protein [Hevea

brasiliensis]

Seq. No. 417828

Seq. ID uC-osroM202023d08b1

Method BLASTX
NCBI GI g4938503
BLAST score 354
E value 2.0e-33
Match length 90
% identity 40

NCBI Description (AL078465) hnRNP-like protein [Arabidopsis thaliana]

```
417829
Seq. No.
Seq. ID
                  uC-osroM202023d12b1
Method
                  BLASTX
NCBI GI
                  q1843440
BLAST score
                  158
                  1.0e-10
E value
Match length
                  85
% identity
                  38
NCBI Description (Z70521) unknown [Cucumis melo]
                  417830
Seq. No.
                  uC-osroM202023e02b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1706260
BLAST score
                  332
                  6.0e-31
E value
Match length
                  90
                  69
% identity
NCBI Description CYSTEINE PROTEINASE 1 PRECURSOR >gi 2118131_pir__S59597
                  cysteine proteinase 1 precursor - maize
                  >gi_643597_dbj_BAA08244_ (D45402) cysteine proteinase [Zea
                  mays]
                  417831
Seq. No.
Seq. ID
                  uC-osroM202023e03b1
Method
                  BLASTX
NCBI GI
                  q1747296
BLAST score
                  806
E value
                  2.0e-86
Match length
                  168
% identity
                  92
NCBI Description (D45384) vacuolar H+-pyrophosphatase [Oryza sativa]
                  >gi 3298476 dbj BAA31524 (AB012766) ovp2 [Oryza sativa]
Seq. No.
                  417832
                  uC-osroM202023e07b1
Seq. ID
                  BLASTX
Method
NCBI GI
                  q2293480
BLAST score
                  437
E value
                  3.0e-43
                  85
Match length
                  100
% identity
NCBI Description (AF011331) glycine-rich protein [Oryza sativa]
Seq. No.
                  417833
Seq. ID
                  uC-osroM202023e08b1
Method
                  BLASTX
NCBI GI
                  q2982448
BLAST score
                  276
E value
                  3.0e-24
Match length
                  131
% identity
NCBI Description (AL022224) putative protein [Arabidopsis thaliana]
Seq. No.
                  417834
                  uC-osroM202023e10b1
Seq. ID
```

Method

NCBI GI

E value

BLAST score

BLASTX

497

g2129579

4.0e-50

```
Method
                   BLASTX
NCBI GI
                   q1724110
BLAST score
                   388
E value
                   2.0e-37
Match length
                   115
                   60
% identity
                   (U79770) cinnamyl-alcohol dehydrogenase Eli3
NCBI Description
                   [Mesembryanthemum crystallinum]
                   417835
Seq. No.
                   uC-osroM202023f01b1
Seq. ID
Method
                  BLASTX
NCBI GI
                   q4185143
BLAST score
                   338
E value
                   8.0e-32
Match length
                   96
                   67
% identity
NCBI Description
                   (AC005724) putative signal recognition particle receptor
                  beta subunit [Arabidopsis thaliana]
                   417836
Seq. No.
Seq. ID
                   uC-osroM202023f02b1
Method
                  BLASTX
NCBI GI
                   q478740
BLAST score
                   175
E value
                   1.0e-12
Match length
                   32
% identity
                   100
NCBI Description phenylalanine ammonia-lyase (EC 4.1.3.5) - rice
                   417837
Seq. No.
                   uC-osroM202023f03b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g5668762
BLAST score
                   268
E value
                   2.0e-23
Match length
                   86
                   58
% identity
NCBI Description (AC005916) EST gb N65787 comes from this gene. [Arabidopsis
                   thaliana]
                   417838
Seq. No.
Seq. ID
                   uC-osroM202023f04b1
Method
                   BLASTN
NCBI GI
                   g6006355
BLAST score
                   203
E value
                   1.0e-110
Match length
                   367
% identity
                   99
NCBI Description Oryza sativa genomic DNA, chromosome 6, clone:P0493C11
                   417839
Seq. No.
Seq. ID
                   uC-osroM202023f05b1
```

```
Match length
                   124
% identity
NCBI Description
                  Dwarfl protein - Arabidopsis thaliana >gi 516043 (U12400)
                   Dwarf1 [Arabidopsis thaliana]
                   417840
Seq. No.
                   uC-osroM202023f07b1
Seq. ID
Method
                  BLASTN
NCBI GI
                   g2114206
BLAST score
                  257
E value
                   1.0e-142
Match length
                   265
% identity
                   99
NCBI Description Oryza sativa DNA for glutaredoxin, complete cds
                  417841
Seq. No.
                  uC-osroM202023f08b1
Seq. ID
Method
                  BLASTN
                  g20094
NCBI GI
BLAST score
                   136
E value
                   8.0e-71
Match length
                   136
                   100
% identity
NCBI Description
                  O.sativa RSs2 gene for sucrose-UDP glucosyltransferase
                   (isozyme 2)
Seq. No.
                   417842
Seq. ID
                   uC-osroM202023f10b1
Method
                  BLASTX
NCBI GI
                   g3142292
BLAST score
                   522
E value
                   4.0e-53
Match length
                   135
                   77
% identity
NCBI Description
                  (AC002411) Contains similarity to tetratricopeptide repeat
                  protein gb_U46571 from home sapiens. EST gb Z47802 and
                  gb_Z48402 come from this gene. [Arabidopsis thaliana]
                   417843
Seq. No.
Seq. ID
                  uC-osroM202023f11b1
Method
                  BLASTX
NCBI GI
                   g294845
BLAST score
                   377
E value
                   4.0e-36
Match length
                  110
% identity
                   65
NCBI Description
                   (L13655) membrane protein [Saccharum hybrid cultivar
                  H65-7052]
Seq. No.
                   417844
Seq. ID
                  uC-osroM202023g03b1
Method
                  BLASTN
NCBI GI
                  g2114206
BLAST score
                  130
E value
                  7.0e-67
Match length
                  162
```

96

% identity

```
NCBI Description Oryza sativa DNA for glutaredoxin, complete cds
                  417845
Seq. No.
Seq. ID
                  uC-osroM202023g07b1
Method
                  BLASTX
                  g3122858
NCBI GI
BLAST score
                  210
E value
                  1.0e-16
Match length
                  74
% identity
                  59
NCBI Description D-3-PHOSPHOGLYCERATE DEHYDROGENASE PRECURSOR (PGDH)
                  >gi_2189964_dbj_BAA20405_ (AB003280) Phosphoglycerate
                  dehydrogenase [Arabidopsis thaliana]
                   >gi_2804258_dbj_BAA24440_ (AB010407) phosphoglycerate
                  dehydrogenase [Arabidopsis thaliana]
                  417846
Seq. No.
                  uC-osroM202023g08b1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g2114206
BLAST score
                  291
E value
                  1.0e-162
                  327
Match length
                  97
% identity
NCBI Description Oryza sativa DNA for glutaredoxin, complete cds
Seq. No.
                  417847
Seq. ID
                  uC-osroM202023q09b1
Method
                  BLASTX
NCBI GI
                  g129591
BLAST score
                  345
E value
                  2.0e-32
Match length
                  64
                  100
% identity
NCBI Description PHENYLALANINE AMMONIA-LYASE >gi_295824_emb_CAA34226_
                   (X16099) phenylalanine ammonia-lyase [Oryza sativa]
Seq. No.
                  417848
Seq. ID
                  uC-osroM202023g11b1
Method
                  BLASTX
NCBI GI
                  q2935338
BLAST score
                  426
E value
                  8.0e-42
Match length
                  101
% identity
                  81
NCBI Description
                  (AF043297) poly(A) binding protein RB47 [Chlamydomonas
                  reinhardtii]
Seq. No.
                  417849
Seq. ID
                  uC-osroM202023h05b1
Method
                  BLASTX
NCBI GI
                  g4325339
BLAST score
                  192
E value
                  2.0e-14
Match length
                  145
                  30
% identity
NCBI Description (AF128392) No definition line found [Arabidopsis thaliana]
```

Seq. No.

Seq. ID

417855

uC-osroM202024a05b1

417850 Seq. No. Seq. ID uC-osroM202023h09b1 Method BLASTX NCBI GI q1172571 BLAST score 776 E value 6.0e-83 Match length 155 % identity 92 PHOSPHOENOLPYRUVATE CARBOXYKINASE [ATP] NCBI Description >gi_1076277_pir__S52637 phosphoenolpyruvate carboxykinase (ATP) (EC 4.1.1.49) - cucumber >gi_567102 (L31899) phosphoenolpyruvate carboxykinase [Cucumis sativus] Seq. No. 417851 Seq. ID uC-osroM202023h10b1 Method BLASTX NCBI GI g1208496 BLAST score 257 E value 4.0e-22 Match length 99 57 % identity NCBI Description (D38124) EREBP-3 [Nicotiana tabacum] 417852 Seq. No. uC-osroM202024a01a1 Seq. ID Method BLASTX NCBI GI q4126809 BLAST score 258 E value 2.0e-22 Match length 51 % identity 98 NCBI Description (AB017042) glyoxalase I [Oryza sativa] Seq. No. 417853 Seq. ID uC-osroM202024a04a1 Method BLASTX NCBI GI q2341061 BLAST score 170 E value 5.0e-12 Match length 39 87 % identity NCBI Description (U73459) translational initiation factor eIF-4A [Zea mays] Seq. No. 417854 uC-osroM202024a04b1 Seq. ID Method BLASTX NCBI GI g4406783 BLAST score 591 E value 2.0e-61 Match length 136 % identity 81 (AC006532) putative glutamate decarboxylase [Arabidopsis NCBI Description thaliana]

Method BLASTX NCBI GI q6094242 BLAST score 353 E value 3.0e - 33Match length 93 68 % identity

NCBI Description PUTATIVE SELENIUM-BINDING PROTEIN

>gi_2244759_emb_CAB10182.1 (Z97335) selenium-binding

protein like [Arabidopsis thaliana]

Seq. No. 417856

uC-osroM202024a06a1 Seq. ID

Method BLASTX NCBI GI q1345809 BLAST score 458 E value 6.0e-46Match length 106 % identity

NCBI Description CHALCONE SYNTHASE (NAREGENIN-CHALCONE SYNTHASE)

>gi_2117713_pir__S58190 naringenin-chalcone synthase (EC
2.3.1.74) - rice >gi_927491_emb_CAA61955_ (X89859)

naringenin-chalcone synthase [Oryza sativa]

Seq. No. 417857

uC-osroM202024a06b1 Seq. ID

Method BLASTX NCBI GI q2130073 BLAST score 279 E value 5.0e-40 Match length 129 % identity 72

NCBI Description fructose-bisphosphate aldolase (EC 4.1.2.13) isoenzyme C-1,

cytosolic - rice >gi_786178_dbj_BAA08845_ (D50307) aldolase

C-1 [Oryza sativa] \overline{g} i 7909 $\overline{7}$ 0 d \overline{b} j BAA088 $\overline{3}$ 0 (D50301)

aldolase C-1 [Oryza sativa]

417858 Seq. No.

uC-osroM202024a07b1 Seq. ID

Method BLASTX NCBI GI g4240305 BLAST score 144 E value 7.0e-09 50 Match length 58 % identity

NCBI Description (AB020715) KIAA0908 protein [Homo sapiens]

Seq. No. 417859

Seq. ID uC-osroM202024a08b1

Method BLASTX NCBI GI g1136122 BLAST score 711 E value 3.0e-75Match length 133 98 % identity

NCBI Description (X91807) alfa-tubulin [Oryza sativa]

Seq. No. 417860

```
uC-osroM202024a09a1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2130069
BLAST score
                  200
                  2.0e-15
E value
Match length
                  39
                  97
% identity
NCBI Description catalase (EC 1.11.1.6) catA - rice
                  >gi_1261858_dbj_BAA06232_ (D29966) catalase [Oryza sativa]
                  417861
Seq. No.
Seq. ID
                  uC-osroM202024a10b1
Method
                  BLASTX
NCBI GI
                  q3024122
BLAST score
                  471
E value
                  4.0e-58
Match length
                  117
                  99
% identity
NCBI Description S-ADENOSYLMETHIONINE SYNTHETASE 2 (METHIONINE
                  ADENOSYLTRANSFERASE 2) (ADOMET SYNTHETASE 2) >gi 1778821
                  (U82833) S-adenosyl-L-methionine synthetase [Oryza sativa]
                   417862
Seq. No.
                  uC-osroM202024b01b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1519249
BLAST score
                  646
E value
                  1.0e-67
                  134
Match length
% identity
NCBI Description (U65956) GF14-b protein [Oryza sativa]
                   417863
Seq. No.
                  uC-osroM202024b02a1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q439879
BLAST score
                  222
E value
                   5.0e-18
Match length
                   46
% identity
NCBI Description (L15194) [Golden delicious apple fruit expressed mRNA,
                   complete cds.], gene product [Malus domestica]
Seq. No.
                   417864
                   uC-osroM202024b02b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g4204300
                   295
BLAST score
E value
                   2.0e-26
Match length
                  100
% identity
                   60
NCBI Description (AC003027) Unknown protein [Arabidopsis thaliana]
                   417865
Seq. No.
Seq. ID
                   uC-osroM202024b03a1
Method
                   BLASTX
NCBI GI
                  g6016873
```



BLAST score 217 E value 2.0e-18 Match length 73 % identity 75

NCBI Description (AP000570) EST AU078346(E30133) corresponds to a region of the predicted gene.; Similar to zinc inducible protein.

(AF022734) [Oryza sativa]

Seq. No. 417866

Seq. ID uC-osroM202024b03b1

Method BLASTX
NCBI GI g115587
BLAST score 432
E value 1.0e-42
Match length 92
% identity 93

NCBI Description PHOSPHOENOLPYRUVATE CARBOXYLASE 1 (PEPCASE) (CP21)

>gi_418801_pir__S31159 phosphoenolpyruvate carboxylase (EC
4.1.1.31) CP21 - sorghum >gi_21630_emb_CAA39197_ (X55664)

phosphoenolpyruvate carboxylase [Sorghum bicolor] >gi_22615_emb_CAA46267_ (X65137) phosphoenolpyruvate

carboxylase [Sorghum bicolor]

Seq. No. 417867

Seq. ID uC-osroM202024b04b1

Method BLASTX
NCBI GI g2979553
BLAST score 152
E value 7.0e-10
Match length 54
% identity 54

NCBI Description (AC003680) hypothetical protein [Arabidopsis thaliana]

Seq. No. 417868

Seq. ID uC-osroM202024b07b1

Method BLASTX
NCBI GI g231587
BLAST score 353
E value 2.0e-33
Match length 126
% identity 62

NCBI Description ATP SYNTHASE BETA CHAIN, MITOCHONDRIAL PRECURSOR

>gi_283001_pir__S25304 H+-transporting ATP synthase (EC
3.6.1.34) beta chain precursor, mitochondrial - rice
>gi_218147_dbj_BAA01372_ (D10491) mitochondrial F1-ATPase

[Oryza sativa]

Seq. No. 417869

Seq. ID uC-osroM202024b08b1

Method BLASTX
NCBI GI g5919185
BLAST score 319
E value 2.0e-29
Match length 112
% identity 59

NCBI Description (AF183809) arabinogalactan protein Pop14A9 [Populus alba x

Populus tremula]

Seq. ID

```
417870
Seq. No.
Seq. ID
                   uC-osroM202024b10b1
Method
                   BLASTX
NCBI GI
                   q5453379
BLAST score
                   253
E value
                   1.0e-21
                   91
Match length
% identity
                   57
                   (AF155124) bacterial-induced peroxidase precursor
NCBI Description
                   [Gossypium hirsutum]
                   417871
Seq. No.
                   uC-osroM202024b11b1
Seq. ID
Method
                   BLASTN
NCBI GI
                   q218182
BLAST score
                   155
                   1.0e-81
E value
Match length
                   246
% identity
                   93
NCBI Description Rice mRNA for oryzain beta (EC 3.4.22)
Seq. No.
                   417872
Seq. ID
                   uC-osroM202024b12b1
Method
                   BLASTX
NCBI GI
                   q1729971
BLAST score
                   414
                   1.0e-40
E value
Match length
                   113
                    74
% identity
NCBI Description TONOPLAST INTRINSIC PROTEIN, GAMMA (GAMMA TIP)
                   (AQUAPORIN-TIP) >gi_1076745_pir__S52004 gamma-Tip protein - rice >gi_473997_dbj_BAA05017_ (D25534) gamma-Tip [Oryza
                   sativa]
Seq. No.
                    417873
Seq. ID
                   uC-osroM202024c03a1
Method
                   BLASTX
NCBI GI
                   g1184112
BLAST score
                   436
E value
                    3.0e-43
Match length
                   116
                   76
% identity
NCBI Description (U46138) Zn-induced protein [Oryza sativa]
Seq. No.
                   417874
Seq. ID
                   uC-osroM202024c05b1
                   BLASTX
Method
NCBI GI
                   g169757
BLAST score
                   513
E value
                   2.0e-52
                   106
Match length
% identity
                    96
NCBI Description (M36469) alcohol dehydrogenase (adh2) [Oryza sativa]
Seq. No.
                   417875
```

uC-osroM202024c06b1



Method BLASTX
NCBI GI g2497953
BLAST score 153
E value 1.0e-13
Match length 69
% identity 57

NCBI Description MOLYBDOPTERIN BIOSYNTHESIS CNX1 PROTEIN (MOLYBDENUM COFACTOR BIOSYNTHESIS ENZYME CNX1) >gi_1263314 (L47323) molybdenum cofactor biosynthesis enzyme [Arabidopsis thaliana] >gi_4469123_emb_CAB38312_ (AJ236870) molybdenum

cofactor biosynthesis enzyme [Arabidopsis thaliana]

Seq. No. 417876

Seq. ID uC-osroM202024c07b1

Method BLASTN
NCBI GI g5734616
BLAST score 48
E value 6.0e-18
Match length 204
% identity 83

NCBI Description Oryza sativa genomic DNA, chromosome 6, clone:P0538C01

Seq. No. 417877

Seq. ID uC-osroM202024c11a1

Method BLASTX
NCBI GI g3236248
BLAST score 632
E value 4.0e-66
Match length 151
% identity 80

NCBI Description (AC004684) unknown protein [Arabidopsis thaliana]

Seq. No. 417878

Seq. ID uC-osroM202024c11b1

Method BLASTX
NCBI GI g537437
BLAST score 175
E value 2.0e-18
Match length 88
% identity 56

NCBI Description (U12637) cysteine proteinase [Hemerocallis hybrid cultivar]

Seq. No. 417879

Seq. ID uC-osroM202024d01a1

Method BLASTX
NCBI GI g2662310
BLAST score 201
E value 1.0e-15
Match length 38
% identity 100

NCBI Description (AB009307) bpw1 [Hordeum vulgare]

Seq. No. 417880

Seq. ID uC-osroM202024d02a1

Method BLASTN NCBI GI g218171 BLAST score 91 E value 2.0e-43 Match length 320 % identity

NCBI Description Oryza sativa mRNA for type I light-harvesting chlorophyll

a/b binding protein of photosystem II (LHCPII), complete

417881 Seq. No.

Seq. ID uC-osroM202024d03a1

Method BLASTX NCBI GI q729135 152 BLAST score 6.0e-10 E value 42 Match length % identity 71

NCBI Description CAFFEIC ACID 3-O-METHYLTRANSFERASE

(S-ADENOSYSL-L-METHIONINE: CAFFEIC ACID

3-O-METHYLTRANSFERASE) (COMT) >gi_283034_pir__ S28612 catechol O-methyltransferase (EC 2.1.1.6) - maize >gi_168532 (M73235) O-methyltransferase [Zea mays]

417882 Seq. No.

Seq. ID uC-osroM202024d04b1

Method BLASTX NCBI GI q1729971 BLAST score 405 1.0e-39 E value Match length 108 76 % identity

TONOPLAST INTRINSIC PROTEIN, GAMMA (GAMMA TIP) NCBI Description

(AQUAPORIN-TIP) >gi_1076745_pir__S52004 gamma-Tip protein -

rice >gi 473997_dbj_BAA05017_ (D25534) gamma-Tip [Oryza

sativa]

Seq. No. 417883

uC-osroM202024d05a1 Seq. ID

Method BLASTN NCBI GI q4105602 BLAST score 299 E value 1.0e-167 Match length 331 98 % identity

NCBI Description Oryza sativa metallothionein (MTe) gene, complete cds

417884 Seq. No.

Seq. ID uC-osroM202024d08a1

Method BLASTX NCBI GI q132105 BLAST score 193 9.0e-15 E value Match length 36 100 % identity

RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR NCBI Description

(RUBISCO SMALL SUBUNIT C) >gi 68094 pir RKRZS9

ribulose-bisphosphate carboxy $\overline{\text{lase}}$ ($\overline{\text{EC}}$ 4.1.1.39) small chain precursor (clone pOSSS1139) - rice >gi 218208 dbj BAA00538_

(D00643) small subunit of ribulose-1,5-bisphosphate

carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa] >gi_226375_prf__1508256A ribulose bisphosphate carboxylase S [Oryza sativa]

Seq. No. 417885

Seq. ID uC-osroM202024d10a1

Method BLASTN
NCBI GI g20321
BLAST score 123
E value 9.0e-63
Match length 243
% identity 88

NCBI Description Oryza sativa RAc1 mRNA for actin

Seq. No. 417886

Seq. ID uC-osroM202024d10b1

Method BLASTX
NCBI GI g3342804
BLAST score 276
E value 2.0e-24
Match length 56
% identity 95

NCBI Description (AF061839) putative 6-phosphogluconate dehydrogenase [Zea

mays]

Seq. No. 417887

Seq. ID uC-osroM202024d11b1

Method BLASTX
NCBI GI g2130073
BLAST score 217
E value 7.0e-18
Match length 61
% identity 69

NCBI Description fructose-bisphosphate aldolase (EC 4.1.2.13) isoenzyme C-1,

cytosolic - rice >gi 786178 dbj BAA08845 (D50307) aldolase

C-1 [Oryza sativa] $\overline{gi_790970_dbj_BAA08830_}$ (D50301)

aldolase C-1 [Oryza sativa]

Seq. No. 417888

Seq. ID uC-osroM202024e01b1

Method BLASTX
NCBI GI 94006829
BLAST score 570
E value 7.0e-59
Match length 136
% identity 82

NCBI Description (AC005970) putative protein kinase [Arabidopsis thaliana]

Seq. No. 417889

Seq. ID uC-osroM202024e02b1

Method BLASTX
NCBI GI g1747296
BLAST score 391
E value 7.0e-38
Match length 122
% identity 66

```
(D45384) vacuolar H+-pyrophosphatase [Oryza sativa]
NCBI Description
                  >gi 3298476 dbj BAA31524 (AB012766) ovp2 [Oryza sativa]
                  417890
Seq. No.
                  uC-osroM202024e05a1
Seq. ID
                  BLASTN
Method
NCBI GI
                  q2331130
BLAST score
                  68
E value
                  1.0e-29
Match length
                  266
                  79
% identity
NCBI Description Oryza sativa glycine-rich protein (OSGRP1) mRNA, complete
Seq. No.
                  417891
Seq. ID
                  uC-osroM202024e05b1
                  BLASTX
Method
NCBI GI
                  g2388580
BLAST score
                  256
E value
                  9.0e-31
                  91
Match length
% identity
                  65
NCBI Description (AC000098) Similar to Sequence 10 from patent 5477002
                  (gb 1253956). [Arabidopsis thaliana]
                  417892
Seq. No.
Seq. ID
                  uC-osroM202024e06a1
Method
                  BLASTN
NCBI GI
                  g6041757
BLAST score
                  342
E value
                  0.0e+00
                  410
Match length
% identity
                  96
NCBI Description Genomic Sequence For Oryza sativa Clone 10P20, Lemont
                  Strain, Complete Sequence, complete sequence
                  417893
Seq. No.
Seq. ID
                  uC-osroM202024e06b1
Method
                  BLASTX
NCBI GI
                  g3132470
BLAST score
                  262
E value
                  1.0e-22
                  146
Match length
% identity
                  41
NCBI Description (AC003096) unknown protein [Arabidopsis thaliana]
Seq. No.
                  417894
                  uC-osroM202024e09b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3421413
BLAST score
                  215
E value
                  3.0e-17
Match length
                  51
% identity
NCBI Description
                  (AF081922) protein phosphatase 2A 55 kDa B regulatory
```

54716

subunit [Oryza sativa] >gi_3421415 (AF081923) protein phosphatase 2A 55 kDa B regulatory subunit [Oryza sativa]

417895 Seq. No. Seq. ID uC-osroM202024e10b1 Method BLASTX NCBI GI g4926827 BLAST score 327 E value 3.0e-30 Match length 106 % identity 64 NCBI Description (AC004135) T17H7.12 [Arabidopsis thaliana] 417896 Seq. No. Seq. ID uC-osroM202024e11b1 Method BLASTX NCBI GI q2459447 BLAST score 502 E value 7.0e-51Match length 134 % identity 68 NCBI Description (AC002332) putative Mlo protein [Arabidopsis thaliana] Seq. No. 417897 uC-osroM202024f02b1 Seq. ID Method BLASTX NCBI GI g3790100 BLAST score 348 E value 8.0e-33 Match length 102 70 % identity NCBI Description (AF095520) pyrophosphate-dependent phosphofructokinase beta subunit [Citrus X paradisi] Seq. No. 417898 Seq. ID uC-osroM202024f03a1 Method BLASTN NCBI GI g2662340 BLAST score 289 E value 1.0e-161 Match length 309 98 % identity NCBI Description Oryza sativa mRNA for EF-1 alpha, complete cds 417899 Seq. No. Seq. ID uC-osroM202024f04b1 Method BLASTX g129591 NCBI GI BLAST score 540 E value 2.0e-55 Match length 119

% identity 90

NCBI Description PHENYLALANINE AMMONIA-LYASE >gi 295824 emb CAA34226

(X16099) phenylalanine ammonia-lyase [Oryza sativa]

Seq. No. 417900

Seq. ID uC-osroM202024f09b1

Method BLASTX NCBI GI g4926827



BLAST score 182 E value 8.0e-26 Match length 87 % identity 76

NCBI Description (AC004135) T17H7.12 [Arabidopsis thaliana]

Seq. No. 417901

Seq. ID uC-osroM202024f11a1

Method BLASTX
NCBI GI g5852089
BLAST score 202
E value 1.0e-15
Match length 43
% identity 79

NCBI Description (AL117264) zwh12.1 [Oryza sativa]

Seq. No. 417902

Seq. ID uC-osroM202024f12b1

Method BLASTX
NCBI GI g1351974
BLAST score 578
E value 9.0e-60
Match length 112
% identity 100

NCBI Description ADP-RIBOSYLATION FACTOR >gi_1076788_pir__S49325

ADP-ribosylation factor - maize >gi_1076789_pir_S53486 ADP-ribosylation factor - maize >gi_556686_emb_CAA56351_

(X80042) ADP-ribosylation factor [Zea mays]

Seq. No. 417903

Seq. ID uC-osroM202024g02b1

Method BLASTX
NCBI GI g2245378
BLAST score 441
E value 6.0e-44
Match length 102
% identity 79

NCBI Description (U83245) auxin response factor 1 [Arabidopsis thaliana] >gi 5080809 gb AAD39318.1 AC007258 7 (AC007258) auxin

response factor 1 [Arabidopsis thaliana]

Seq. No. 417904

Seq. ID uC-osroM202024g04a1

Method BLASTN
NCBI GI g5734616
BLAST score 119
E value 3.0e-60
Match length 307
% identity 85

NCBI Description Oryza sativa genomic DNA, chromosome 6, clone:P0538C01

Seq. No. 417905

Seq. ID uC-osroM202024g05a1

Method BLASTX
NCBI GI g5734639
BLAST score 294
E value 2.0e-26

Match length 57 % identity 98

NCBI Description (AP000391) ESTs AU056036(S20239), C72753(E2173),

AU056035(S20239) correspond to a region of the predicted gene.; Similar to putative cytochrome P-450 (AC003680)

[Oryza sativa]

Seq. No. 417906

Seq. ID uC-osroM202024g06a1

Method BLASTX
NCBI GI g1362086
BLAST score 279
E value 1.0e-24
Match length 61
% identity 92

NCBI Description 5-methyltetrahydropteroyltriglutamate--homocysteine

S-methyltransferase (EC 2.1.1.14) - Madagascar periwinkle

>gi_2129919_pir__S65957

5-methyltetrahydropteroyltriglutamate--homocysteine

S-methyltransferase (EC 2.1.1.14) - Madagascar periwinkle >gi_886471_emb_CAA58474_ (X83499) methionine synthase

[Catharanthus roseus]

Seq. No. 417907

Seq. ID uC-osroM202024g07b1

Method BLASTN
NCBI GI g2239259
BLAST score 45
E value 5.0e-16
Match length 49
% identity 98

NCBI Description Zea mays mRNA for cinnamoyl CoA reductase

Seq. No. 417908

Seq. ID uC-osroM202024g09b1

Method BLASTX
NCBI GI 93873699
BLAST score 192
E value 2.0e-14
Match length 116
% identity 41

NCBI Description (Z73102) predicted using Genefinder; Similarity to viral

non-structural proteins (SW:POLN EEVV3); cDNA EST

EMBL:D65747 comes from this gene; cDNA EST EMBL:D69295 comes from this gene; cDNA EST EMBL:C10380 comes from this

gene

Seq. No. 417909

Seq. ID uC-osroM202024g10a1

Method BLASTX
NCBI GI g3341511
BLAST score 361
E value 3.0e-34
Match length 104
% identity 75

NCBI Description (AJ231134) cinnamoyl-CoA reductase [Saccharum officinarum]

Seq. No. 417910

Seq. ID uC-osroM202024g11b1

Method BLASTX
NCBI GI g1184774
BLAST score 535
E value 1.0e-54
Match length 128
% identity 80

NCBI Description (U45856) cytosolic glyceroldehyde-3-phosphate dehydrogenase

GAPC3 [Zea mays]

Seq. No. 417911

Seq. ID uC-osroM202024h02b1

Method BLASTX
NCBI GI g2130073
BLAST score 655
E value 8.0e-69
Match length 131
% identity 98

NCBI Description fructose-bisphosphate aldolase (EC 4.1.2.13) isoenzyme C-1,

cytosolic - rice >gi_786178_dbj_BAA08845_ (D50307) aldolase

C-1 [Oryza sativa] $> gi_790970_dbj_BAA08830_ (D50301)$

aldolase C-1 [Oryza sativa]

Seq. No. 417912

Seq. ID uC-osroM202024h04a1

Method BLASTX
NCBI GI g1352347
BLAST score 271
E value 1.0e-23
Match length 69
% identity 77

NCBI Description ELONGATION FACTOR 1-BETA A1 (EF-1-BETA)

>gi_480620_pir__S37103 translation elongation factor eEF-1
beta-A1 chain - Arabidopsis thaliana (cv. Colombia)
>gi 398608 emb CAA52751 (X74733) elongation factor-1 beta

A1 [Arabidopsis thaliana]

Seq. No. 417913

Seq. ID uC-osroM202024h04b1

Method BLASTX
NCBI GI g4758294
BLAST score 333
E value 4.0e-31
Match length 104
% identity 56

NCBI Description glutamyl-prolyl-tRNA synthetase

>gi_135104_sp_P07814_SYEP_HUMAN_MULTIFUNCTIONAL AMINOACYL-TRNA_SYNTHETASE [INCLUDES: GLUTAMYL-TRNA

SYNTHETASE (GLUTAMATE--TRNA LIGASE); PROLYL-TRNA SYNTHETASE

(PROLINE--TRNA LIGASE)] >gi 68554 pir SYHUQT

glutamyl-prolyl-tRNA synthetase - human

>gi_31958 emb CAA38224 (X54326) glutaminyl-tRNA synthetase

[Homo sapiens]

Seq. No. 417914

Seq. ID uC-osroM202024h05b1

Method BLASTX NCBI GI g2055230 BLAST score 223 E value 3.0e-18 Match length 103 % identity 53

NCBI Description (AB000130) SRC2 [Glycine max]

Seq. No. 417915

Seq. ID uC-osroM202024h06a1

Method BLASTX NCBI GI q3047104 BLAST score 154 E value 6.0e-10 Match length 55 % identity 58

NCBI Description (AF058919) No definition line found [Arabidopsis thaliana]

Seq. No. 417916

Seq. ID uC-osroM202024h06b1

Method BLASTX NCBI GI g3786011 BLAST score 325 E value 4.0e-30 Match length 105 % identity 64

NCBI Description (AC005499) putative elongation factor [Arabidopsis

thaliana]

417917 Seq. No.

Seq. ID uC-osroM202024h07b1

Method BLASTX NCBI GI q2979553 BLAST score 185 E value 1.0e-13 Match length 61 % identity

NCBI Description (AC003680) hypothetical protein [Arabidopsis thaliana]

417918 Seq. No.

Seq. ID uC-osroM202024h08a1

Method BLASTN NCBI GI g5852170 BLAST score 159 E value 5.0e-84 Match length 288 % identity 94

NCBI Description Oryza sativa indica(GLA4) genomic DNA, chromosome 4, BAC

clone:t17804

Seq. No. 417919

Seq. ID uC-osroM202024h08b1

Method BLASTX NCBI GI g3882018 BLAST score 215 E value 4.0e-17 Match length 88

```
% identity
NCBI Description (Y18377) cytokinin oxidase [Zea mays]
Seq. No.
                  417920
                  uC-osroM202024h09a1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g5852170
BLAST score
                  34
E value
                  2.0e-09
Match length
                  106
% identity
                  83
NCBI Description Oryza sativa indica(GLA4) genomic DNA, chromosome 4, BAC
                  clone:t17804
Seq. No.
                  417921
Seq. ID
                  uC-osroM202024h10b1
Method
                  BLASTX
NCBI GI
                  q3643594
BLAST score
                  578
E value
                  9.0e-60
Match length
                  134
% identity
                  78
NCBI Description (AC005395) unknown protein [Arabidopsis thaliana]
Seq. No.
                  417922
Seq. ID
                  uC-osroM202024h12b1
Method
                  BLASTX
NCBI GI
                  q3786011
BLAST score
                  161
E value
                  4.0e-11
Match length
                  69
                  57
% identity
NCBI Description (AC005499) putative elongation factor [Arabidopsis
                  thaliana]
                  417923
Seq. No.
                  uC-osroM202025a02b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4914402
BLAST score
                  155
E value
                  2.0e-10
Match length
                  63
% identity
NCBI Description (AL050352) hypothetical protein [Arabidopsis thaliana]
                  417924
Seq. No.
Seq. ID
                  uC-osroM202025a03a1
Method
                  BLASTX
NCBI GI
                  g1871186
BLAST score
                  196
E value
                  6.0e-15
Match length
                  55
% identity
NCBI Description (U90439) protein kinase isolog [Arabidopsis thaliana]
```

Seq. No. 417925

Seq. ID uC-osroM202025a07b1



Method BLASTX NCBI GI q1170937 BLAST score 581 E value 4.0e-60 Match length 111 100 % identity

NCBI Description S-ADENOSYLMETHIONINE SYNTHETASE 1 (METHIONINE ADENOSYLTRANSFERASE 1) (ADOMET SYNTHETASE 1)

>gi_450549_emb_CAA81481_ (Z26867) S-adenosyl methionine

synthetase [Oryza sativa]

417926 Seq. No.

Seq. ID uC-osroM202025a08a1

Method BLASTX NCBI GI a3763932 BLAST score 165 E value 3.0e-11 Match length 45 % identity 69

NCBI Description (AC004450) putative protein kinase [Arabidopsis thaliana]

417927 Seq. No.

Seq. ID uC-osroM202025a08b1

Method BLASTX NCBI GI q1305549 BLAST score 430 E value 2.0e-42 Match length 129 70 % identity

NCBI Description (U55874) asparagine synthetase [Glycine max]

Seq. No. 417928

Seq. ID uC-osroM202025a09b1

Method BLASTX NCBI GI q5679684 BLAST score 468 E value 7.0e-47Match length 94

% identity 100

NCBI Description (AJ243828) phosphatase 2A regulatory A subunit [Oryza sativa] >gi_5679686_emb_CAB51804.1_ (AJ243829) protein

phosphatase 2A A subunit [Oryza sativa]

Seq. No. 417929

Seq. ID uC-osroM202025a10b1

Method BLASTX NCBI GI g129916 BLAST score 507 E value 2.0e-51 Match length 113 % identity 89

PHOSPHOGLYCERATE KINASE, CYTOSOLIC >gi_66911_pir__TVWTGY phosphoglycerate kinase (EC 2.7.2.3), cytosolic - wheat NCBI Description

>gi_21835_emb_CAA33302 (X15232) phosphoglycerate kinase

(AA 1 - 401) [Triticum aestivum]

Seq. No. 417930

Method

NCBI GI

BLAST score

BLASTX

173

q5730130

```
uC-osroM202025b02a1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g5360658
BLAST score
                  175
                  7.0e-94
E value
                  199
Match length
                  97
% identity
NCBI Description
                  Oryza sativa OsASA2 mRNA for anthranilate synthase alpha 2
                  subunit, complete cds
                  417931
Seq. No.
Seq. ID
                  uC-osroM202025b02b1
Method
                  BLASTX
NCBI GI
                  g2632254
BLAST score
                  195
E value
                  4.0e-31
                  81
Match length
% identity
                  91
NCBI Description (Y12465) serine/threonine kinase [Sorghum bicolor]
                  417932
Seq. No.
Seq. ID
                  uC-osroM202025b04b1
Method
                  BLASTX
NCBI GI
                  g4204300
                  259
BLAST score
E value
                  2.0e-22
Match length
                  93
                  53
% identity
NCBI Description (AC003027) Unknown protein [Arabidopsis thaliana]
                  417933
Seq. No.
Seq. ID
                  uC-osroM202025b05b1
Method
                  BLASTX
NCBI GI
                  g3023816
BLAST score
                  217
                  5.0e-23
E value
                  135
Match length
% identity
                  39
NCBI Description GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC
                  >gi 968996 (U31676) glyceraldehyde-3-phosphate
                  dehydrogenase [Oryza sativa]
                  417934
Seq. No.
Seq. ID
                  uC-osroM202025b06a1
Method
                  BLASTX
NCBI GI
                  g1236961
BLAST score
                  387
E value
                  2.0e-37
Match length
                  103
% identity
                  64
NCBI Description (U50201) prunasin hydrolase precursor [Prunus serotina]
                  417935
Seq. No.
Seq. ID
                  uC-osroM202025b06b1
```

54724

```
E value
                  3.0e-12
Match length
                  98
                  48
% identity
NCBI Description (AL109796) putative protein [Arabidopsis thaliana]
                  417936
Seq. No.
                  uC-osroM202025b07b1
Seq. ID
                  BLASTX
Method
NCBI GI
                  q1076821
BLAST score
                  308
                  5.0e-28
E value
Match length
                  82
% identity
                  72
NCBI Description probable 1-acyl-glycerol-3-phosphate acyltransferase -
                  maize >gi 575960_emb_CAA82638_ (Z29518)
                  1-acyl-glycerol-3-phosphate acyltransferase (putative) [Zea
                  mays]
                  417937
Seq. No.
Seq. ID
                  uC-osroM202025b09b1
                  BLASTX
Method
NCBI GI
                  q2058498
BLAST score
                  322
                  4.0e-31
E value
                  82
Match length
                  82
% identity
NCBI Description (U76029) hemoglobin 1 [Oryza sativa] >gi_2058500 (U76030)
                  hemoglobin 1 [Oryza sativa]
                  417938
Seq. No.
Seq. ID
                  uC-osroM202025b10b1
Method
                  BLASTX
NCBI GI
                  q2119278
BLAST score
                  716
                  5.0e-76
E value
                  131
Match length
                  99
% identity
NCBI Description tubulin beta-1 chain - rice
                  417939
Seq. No.
                  uC-osroM202025b11b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g586339
```

Method BLASTX
NCBI GI g586339
BLAST score 145
E value 4.0e-09
Match length 54
% identity 46

NCBI Description PEROXISOMAL-COENZYME A SYNTHETASE >gi 626794 pir S46098

probable AMP-binding protein - yeast (Saccharomyces

cerevisiae) >gi 536615 emb CAA85185 (Z36091) ORF YBR222c

[Saccharomyces cerevisiae]

Seq. No. 417940

Seq. ID uC-osroM202025b12b1

Method BLASTX NCBI GI g478740 BLAST score 250

```
8.0e-23
E value
Match length
                   64
% identity
                   82
NCBI Description phenylalanine ammonia-lyase (EC 4.1.3.5) - rice
                   417941
Seq. No.
                  uC-osroM202025c02b1
Seq. ID
Method
                  BLASTX
NCBI GI
                   q2414622
BLAST score
                   261
E value
                   2.0e-22
Match length
                  126
                   42
% identity
NCBI Description
                  (Z99259) conserved protein [Schizosaccharomyces pombe]
                   417942
Seq. No.
                   uC-osroM202025c03b1
Seq. ID
Method
                  BLASTX
NCBI GI
                   g3341513
BLAST score
                   288
E value
                   9.0e-26
Match length
                   91
% identity
                   62
NCBI Description
                  (AJ231135) cinnamyl alcohol dehydrogenase [Saccharum
                   officinarum]
                   417943
Seq. No.
Seq. ID
                   uC-osroM202025c05b1
Method
                  BLASTX
NCBI GI
                   g1353516
BLAST score
                   303
E value
                   2.0e-27
Match length
                   83
% identity
                   69
NCBI Description (U38651) sugar transporter [Medicago truncatula]
                   417944
Seq. No.
                   uC-osroM202025c06b1
Seq. ID
Method
                  BLASTX
NCBI GI
                   g4768831
BLAST score
                   241
E value
                   4.0e-20
Match length
                   131
                   38
% identity
NCBI Description (AF116827) unknown [Homo sapiens]
                   417945
Seq. No.
                   uC-osroM202025c08a1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g671740
BLAST score
                   240
E value
                   3.0e-20
                   47
Match length
                   98
% identity
NCBI Description
                  (X84730) ribulose-bisphosphate carboxylase [synthetic
                   construct]
```

```
Seq. No.
                  417946
Seq. ID
                  uC-osroM202025c08b1
Method
                  BLASTX
NCBI GI
                  g2702268
BLAST score
                  274
E value
                  4.0e-24
Match length
                  67
% identity
                  78
NCBI Description (AC003033) putative cellulase [Arabidopsis thaliana]
                  417947
Seq. No.
Seq. ID
                  uC-osroM202025c09b1
Method
                  BLASTX
NCBI GI
                  q2058498
BLAST score
                  570
E value
                  7.0e-59
Match length
                  118
% identity
                  98
NCBI Description (U76029) hemoglobin 1 [Oryza sativa] >gi_2058500 (U76030)
                  hemoglobin 1 [Oryza sativa]
Seq. No.
                  417948
Seq. ID
                  uC-osroM202025c10a1
Method
                  BLASTX
NCBI GI
                  g1170937
BLAST score
                  329
E value
                  1.0e-30
Match length
                  66
% identity
                  94
NCBI Description S-ADENOSYLMETHIONINE SYNTHETASE 1 (METHIONINE
                  ADENOSYLTRANSFERASE 1) (ADOMET SYNTHETASE 1)
                  >gi 450549_emb_CAA81481_ (Z26867) S-adenosyl methionine
                  synthetase [Oryza sativa]
Seq. No.
                  417949
Seq. ID
                  uC-osroM202025c10b1
Method
                  BLASTX
NCBI GI
                  q121528
BLAST score
                  559
E value
                  2.0e-57
Match length
                  139
                  79
% identity
NCBI Description GOS9 PROTEIN >gi 100683 pir S19115 GOS9 protein - rice
                  >gi_20242 emb CAA36189 (X51909) GOS9 [Oryza sativa]
Seq. No.
                  417950
Seq. ID
                  uC-osroM202025c11b1
Method
                  BLASTX
NCBI GI
                  g2130072
BLAST score
                  548
E value
                  3.0e-56
Match length
                  124
% identity
                  85
NCBI Description ferredoxin--nitrite reductase (EC 1.7.7.1) - rice
```

reductase [Oryza sativa]

>gi_809514_dbj_BAA09122 (D50556) ferredoxin-nitrite

Seq. ID

```
Seq. No.
                  417951
Seq. ID
                  uC-osroM202025c12a1
Method
                  BLASTX
NCBI GI
                  g3548818
BLAST score
                  219
E value
                  1.0e-17
Match length
                  72
% identity
                  54
NCBI Description (AC005313) unknown protein [Arabidopsis thaliana]
Seq. No.
                  417952
Seq. ID
                  uC-osroM202025c12b1
Method
                  BLASTX
NCBI GI
                  q4206122
BLAST score
                  318
E value
                  3.0e-29
Match length
                  81
% identity
                  75
NCBI Description (AF097667) protein phosphatase 2C homolog [Mesembryanthemum
                  crystallinum]
Seq. No.
                  417953
Seq. ID
                  uC-osroM202025d01b1
Method
                  BLASTX
NCBI GI
                  q4454018
BLAST score
                  268
E value
                  2.0e-23
Match length
                  115
% identity
                  42
NCBI Description (AL035396) SRG1-like protein [Arabidopsis thaliana]
                  417954
Seq. No.
Seq. ID
                  uC-osroM202025d02b1
Method
                  BLASTX
NCBI GI
                  g121349
BLAST score
                  651
E value
                  9.0e-69
Match length
                  150
% identity
                  84
NCBI Description GLUTAMINE SYNTHETASE SHOOT ISOZYME (GLUTAMATE--AMMONIA
                  LIGASE) (CLONE LAMBDA-GS28) >gi 20368 emb CAA32461
                  (X14245) cytosolic glutamine synthetase (AA 1-356) [Oryza
                  sativa]
Seq. No.
                  417955
Seq. ID
                  uC-osroM202025d04b1
Method
                  BLASTX
NCBI GI
                  g3334320
BLAST score
                  667
E value
                  4.0e-70
Match length
                  134
                  95
% identity
NCBI Description 40S RIBOSOMAL PROTEIN SA (P40) >gi 2444420 (AF020553)
                  ribosome-associated protein p40 [Glycine max]
Seq. No.
                  417956
```

uC-osroM202025d05b1

Method BLASTX NCBI GI g1076820 BLAST score 748 E value 1.0e-79 Match length 158 % identity 89 NCBI Description phosphoglycerate mutase (EC 5.4.2.1) - maize Seq. No. 417957 Seq. ID uC-osroM202025d08b1 Method BLASTX NCBI GI q4218535 BLAST score 504 E value 4.0e-51 Match length 117 78 % identity

NCBI Description (AJ010829) GRAB1 protein [Triticum sp.]

Seq. No. 417958

Seq. ID uC-osroM202025d09b1

Method BLASTX
NCBI GI 94217999
BLAST score 565
E value 3.0e-58
Match length 133
% identity 79

NCBI Description (AC006135) putative ubiquitin--protein ligase

(ubiquitin-conjugating enzyme) [Arabidopsis thaliana]

Seq. No. 417959

Seq. ID uC-osroM202025d10b1

Method BLASTX
NCBI GI g2829913
BLAST score 363
E value 2.0e-34
Match length 98
% identity 73

NCBI Description (AC002291) putative carboxyphosphonoenolpyruvate mutase

[Arabidopsis thaliana]

Seq. No. 417960

Seq. ID uC-osroM202025d12a1

Method BLASTX
NCBI GI g2500380
BLAST score 495
E value 6.0e-50
Match length 105
% identity 87

NCBI Description 60S RIBOSOMAL PROTEIN L44 >gi_2119128_pir__JC4923 ribosomal

protein RL44 - upland cotton >gi 1553129 (U64677) ribosomal protein L44 isoform a [Gossypium hirsutum] >gi 1553131 (U64678) ribosomal protein L44 isoform b [Gossypium

hirsutum]

Seq. No. 417961

Seq. ID uC-osroM202025e05b1

Method BLASTX



NCBI GI g899610 BLAST score 245 E value 2.0e-21 Match length 77 % identity 67

NCBI Description (U29383) acidic ribosomal protein P2 [Zea mays]

Seq. No. 417962

Seq. ID uC-osroM202025e06a1

Method BLASTX
NCBI GI g2913893
BLAST score 220
E value 9.0e-18
Match length 63
% identity 70

NCBI Description (AB011368) LIP5 [Oryza sativa]

Seq. No. 417963

Seq. ID uC-osroM202025e08b1

Method BLASTX
NCBI GI g5020215
BLAST score 341
E value 6.0e-32
Match length 157
% identity 44

NCBI Description (AF149917) acyl CoA reductase [Simmondsia chinensis]

>gi 5020217 gb AAD38040.1 AF149918 1 (AF149918) acyl CoA

reductase [synthetic construct]

Seq. No. 417964

Seq. ID uC-osroM202025e09b1

Method BLASTX
NCBI GI g1172635
BLAST score 518
E value 1.0e-52

Match length 108 % identity 96

NCBI Description 26S PROTEASE REGULATORY SUBUNIT 4 HOMOLOG (TAT-BINDING PROTEIN HOMOLOG 2) >gi 556558 dbj BAA04615 (D17789) rice

homologue of Tat binding protein [Oryza sativa]

Seq. No. 417965

Seq. ID uC-osroM202025e10b1

Method BLASTX
NCBI GI g419789
BLAST score 320
E value 2.0e-29
Match length 100
% identity 62

NCBI Description hypothetical protein - potato

Seq. No. 417966

Seq. ID uC-osroM202025e11b1

Method BLASTX
NCBI GI g2462265
BLAST score 368
E value 4.0e-35

```
92
Match length
                  73
% identity
NCBI Description (Y12793) patatin-like protein [Cucumis sativus]
                  417967
Seq. No.
                  uC-osroM202025e12a1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g2331140
BLAST score
                  253
E value
                  1.0e-140
Match length
                  404
% identity
                  96
NCBI Description Oryza sativa water-stress inducible protein (WSI) mRNA,
                  complete cds
                   417968
Seq. No.
                  uC-osroM202025f01b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2662343
BLAST score
                  532
E value
                  2.0e-54
Match length
                  102
                  99
% identity
NCBI Description (D63581) EF-1 alpha [Oryza sativa]
Seq. No.
                  417969
                  uC-osroM202025f02a1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4097573
BLAST score
                  149
E value
                  2.0e-09
Match length
                  60
% identity
                   43
NCBI Description (U64917) GMFP7 [Glycine max]
Seq. No.
                   417970
Seq. ID
                  uC-osroM202025f03b1
                  BLASTX
Method
NCBI GI
                  g1504012
BLAST score
                  214
E value
                   6.0e-17
Match length
                  124
                   36
% identity
                  (D86969) similar to Human zinc-finger protein,
NCBI Description
                  BR140(P1:JC2069) [Homo sapiens] >gi 5805248 gb_AAD51905.1_
                   (AF127774) unknown [Homo sapiens]
                   417971
Seq. No.
                  uC-osroM202025f08a1
Seq. ID
Method
                  BLASTN
NCBI GI
                   g20280
BLAST score
                   323
E value
                   0.0e + 00
Match length
                   393
% identity
                   95
```

NCBI Description Rice gene for phenylalanine ammonia-lyase (EC 4.3.1.5)

Match length

% identity

80

```
Seq. No.
                  417972
                  uC-osroM202025f08b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3241943
BLAST score
                  621
E value
                  8.0e-65
Match length
                  147
                  77
% identity
NCBI Description (AC004625) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  417973
                  uC-osroM202025f09a1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q549063
BLAST score
                  484
E value
                  1.0e-48
Match length
                  94
                  98
% identity
NCBI Description
                  TRANSLATIONALLY CONTROLLED TUMOR PROTEIN HOMOLOG (TCTP)
                  >gi_1072464_pir__A38958 IgE-dependent histamine-releasing
                  factor homolog - rice >gi_303835_dbj_BAA02151_ (D12626)
                  21kd polypeptide [Oryza sativa]
Seq. No.
                  417974
Seq. ID
                  uC-osroM202025f09b1
Method
                  BLASTX
NCBI GI
                  q1076668
BLAST score
                  353
E value
                  2.0e-33
Match length
                  71
% identity
                  89
                  NADH dehydrogenase (EC 1.6.99.3) - potato
NCBI Description
                  >gi_639834_emb_CAA58823_ (X83999) NADH dehydrogenase
                  [Solanum tuberosum]
                  417975
Seq. No.
                  uC-osroM202025f10b1
Seq. ID
                  BLASTX
Method
NCBI GI
                  q1351974
BLAST score
                  443
E value
                  7.0e-44
                  91
Match length
                  96
% identity
NCBI Description ADP-RIBOSYLATION FACTOR >gi 1076788_pir__S49325
                  ADP-ribosylation factor - maize >gi 1076789_pir__S53486
                  ADP-ribosylation factor - maize >gi 556686 emb CAA56351
                  (X80042) ADP-ribosylation factor [Zea mays]
                  417976
Seq. No.
Seq. ID
                  uC-osroM202025f12b1
Method
                  BLASTX
NCBI GI
                  g1769887
BLAST score
                  344
E value
                  2.0e-32
```

NCBI Description (X95736) amino acid permease 6 [Arabidopsis thaliana]

417977 Seq. No. Seq. ID uC-osroM202025q02a1 Method BLASTN NCBI GI g4959460 BLAST score 43 E value 8.0e-15 Match length 120 92 % identity NCBI Description Zea mays RACB small GTP binding protein mRNA, complete cds Seq. No. 417978 Seq. ID uC-osroM202025g03a1 Method BLASTX NCBI GI q416731 BLAST score 152 E value 7.0e-10 75 Match length % identity 44 NCBI Description POLLEN SPECIFIC PROTEIN C13 PRECURSOR >gi 82655 pir JQ1107 18.3K protein precursor, pollen - maize >gi_255569_bbs_113677 (S44171) pollen specific protein [Zea mays=corn, Peptide, 170 aa] [Zea mays] >gi_1588669_prf__2209273A Zm13 [Zea mays] Seq. No. 417979 Seq. ID uC-osroM202025g04a1 Method BLASTN NCBI GI g786177 BLAST score 34 E value 2.0e-09 Match length 130 % identity 82 NCBI Description Rice DNA for aldolase C-1, complete cds Seq. No. 417980 Seq. ID uC-osroM202025g05b1 Method BLASTX NCBI GI g3924603 BLAST score 207 E value 3.0e-16 Match length 60 % identity NCBI Description (AF069442) putative WD-repeat protein [Arabidopsis thaliana] 417981 Seq. No. Seq. ID uC-osroM202025g06b1 Method BLASTX NCBI GI q3522942 BLAST score 306 8.0e-28 E value 106 Match length

NCBI Description (AC004411) hypothetical protein [Arabidopsis thaliana]

Seq. No. 417982

62

% identity

Seq. ID uC-osroM202025q08b1 Method BLASTX NCBI GI g3894214 BLAST score 424 E value 2.0e-46 Match length 167 % identity 66 NCBI Description (D83726) elongation factor 1 beta 2 [Oryza sativa] >gi 3894216 dbj BAA34599 (D83727) elongation factor 1 beta 2 [Oryza sativa] 417983 Seq. No. Seq. ID uC-osroM202025g09a1 Method BLASTX NCBI GI g3378493 BLAST score 252 E value 2.0e-21 Match length 118 % identity 45 NCBI Description (AJ007579) cysteine proteinase [Ribes nigrum] Seq. No. 417984 Seq. ID uC-osroM202025g10a1 Method BLASTX NCBI GI q2497953 BLAST score 352 E value 3.0e-33 Match length 89 % identity 79 NCBI Description MOLYBDOPTERIN BIOSYNTHESIS CNX1 PROTEIN (MOLYBDENUM COFACTOR BIOSYNTHESIS ENZYME CNX1) >gi_1263314 (L47323) molybdenum cofactor biosynthesis enzyme [Arabidopsis thaliana] >gi_4469123_emb_CAB38312_ (AJ236870) molybdenum cofactor biosynthesis enzyme [Arabidopsis thaliana] Seq. No. 417985 Seq. ID uC-osroM202025q12b1 Method BLASTX NCBI GI g425685 BLAST score 224 E value 3.0e-18 Match length 146 % identity 36 NCBI Description thimet oligopeptidase=soluble angiotensin II-binding protein homolog (EC 3.4.24.15) [rats, testis, Peptide, 687 aa] Seq. No. 417986 Seq. ID uC-osroM202025h03b1

Method BLASTX
NCBI GI g5441896
BLAST score 557
E value 3.0e-57
Match length 141
% identity 86

NCBI Description (AP000367) ESTs D23521(C2939),C22481(C2939) correspond to a region of the predicted gene.; Similar to serine/threonine

```
protein kinase like protein. (AL022140) [Oryza sativa]
Seq. No.
                  417987
                  uC-osroM202025h04b1
Seq. ID
Method
                  BLASTN
NCBI GI
                  q786129
BLAST score
                  46
E value
                  2.0e-16
Match length
                  118
% identity
NCBI Description Oryza sativa root-specific RCc2 mRNA, complete cds
                  417988
Seq. No.
Seq. ID
                  uC-osroM202025h05a1
Method
                  BLASTX
NCBI GI
                  g2342494
BLAST score
                  268
E value
                  2.0e-23
Match length
                  70
% identity
                  64
NCBI Description
                  (D14058) bromelain [Ananas comosus]
                  >gi_2463582_dbj_BAA22543_ (D38531) FB31 precursor (FB13
                  precursor) [Ananas comosus]
Seq. No.
                  417989
Seq. ID
                  uC-osroM202025h06b1
Method
                  BLASTX
NCBI GI
                  q4454039
BLAST score
                  287
E value
                  1.0e-25
Match length
                  92
% identity
                  62
NCBI Description (AL035394) putative Na+/H+-exchanging protein [Arabidopsis
                  thaliana]
                  417990
Seq. No.
Seq. ID
                  uC-osroM202025h07a1
                  BLASTN
Method
NCBI GI
                  q1743413
BLAST score
                  48
E value
                  9.0e-18
                  173
Match length
                  90
% identity
NCBI Description T.aestivum mRNA for transmembrane proton pump, partial
Seq. No.
                  417991
Seq. ID
                  uC-osroM202025h08a1
                  BLASTX
Method
NCBI GI
                  q6015059
BLAST score
                  235
                  1.0e-19
E value
Match length
                  58
% identity
                  81
```

(AF030517) translation elongation factor-1 alpha; EF-1

NCBI Description ELONGATION FACTOR 1-ALPHA (EF-1-ALPHA) >gi 2996096

alpha [Oryza sativa]

```
417992
Seq. No.
Seq. ID
                  uC-osroM202025h09b1
Method
                  BLASTX
NCBI GI
                  q82496
BLAST score
                  621
                  1.0e-64
E value
Match length
                  153
                  80
% identity
NCBI Description phenylalanine ammonia-lyase (EC 4.3.1.5) - rice
Seq. No.
                  417993
                  uC-osroM202025h10b1
Seq. ID
Method
                  BLASTN
NCBI GI
                  a20280
BLAST score
                  46
                  8.0e-17
E value
Match length
                  78
                  90
% identity
NCBI Description Rice gene for phenylalanine ammonia-lyase (EC 4.3.1.5)
                  417994
Seq. No.
                  uC-osroM202025h12b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3643594
BLAST score
                  657
E value
                  6.0e-69
Match length
                  161
% identity
                  73
NCBI Description (AC005395) unknown protein [Arabidopsis thaliana]
                  417995
Seq. No.
                  uC-osroM202026a08b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4235430
BLAST score
                  216
E value
                  4.0e-32
Match length
                  107
% identity
                  68
NCBI Description (AF098458) latex-abundant protein [Hevea brasiliensis]
                  417996
Seq. No.
Seq. ID
                  uC-osroM202026a11b1
Method
                  BLASTX
NCBI GI
                  g5262222
BLAST score
                  200
E value
                  2.0e-15
                  92
Match length
                  41
% identity
NCBI Description (AL080254) reticuline oxidase-like protein [Arabidopsis
                  thaliana]
```

Seq. No. 417997

Seq. ID uC-osroM202026b02b1

Method BLASTX
NCBI GI g4914402
BLAST score 466
E value 1.0e-46

```
Match length 150 % identity 59
```

NCBI Description (AL050352) hypothetical protein [Arabidopsis thaliana]

Seq. No. 417998

Seq. ID uC-osroM202026b03b1

Method BLASTX
NCBI GI g2829864
BLAST score 221
E value 2.0e-18
Match length 102
% identity 49

NCBI Description (AC002396) similar to zinc metalloproteinases [Arabidopsis

thaliana]

Seq. No. 417999

Seq. ID uC-osroM202026b06b1

Method BLASTX
NCBI GI g485517
BLAST score 757
E value 1.0e-80
Match length 148
% identity 99

NCBI Description ADP, ATP carrier protein - rice

Seq. No. 418000

Seq. ID uC-osroM202026b07b1

Method BLASTN
NCBI GI g6006355
BLAST score 337
E value 0.0e+00
Match length 341
% identity 100

NCBI Description Oryza sativa genomic DNA, chromosome 6, clone:P0493C11

Seq. No. 418001

Seq. ID uC-osroM202026b12b1

Method BLASTX
NCBI GI g2462832
BLAST score 298
E value 7.0e-27
Match length 154
% identity 42

NCBI Description (AF000657) similar to Bacillus CotA [Arabidopsis thaliana]

Seq. No. 418002

Seq. ID uC-osroM202026c11b1

Method BLASTX
NCBI GI g3023713
BLAST score 620
E value 1.0e-64
Match length 143
% identity 87

NCBI Description ENOLASE (2-PHOSPHOGLYCERATE DEHYDRATASE)

(2-PHOSPHO-D-GLYCERATE HYDRO-LYASE) (OSE1) >gi 780372

(U09450) enolase [Oryza sativa]

BLAST score

537

Seq. No. 418003 uC-osroM202026d01b1 Seq. ID Method BLASTX NCBI GI g21699 BLAST score 436 E value 6.0e-43Match length 126 66 % identity NCBI Description (X66013) cathepsin B [Triticum aestivum] Seq. No. 418004 Seq. ID uC-osroM202026d02b1 Method BLASTX NCBI GI q3334320 BLAST score 475 E value 4.0e-53 Match length 123 89 % identity NCBI Description 40S RIBOSOMAL PROTEIN SA (P40) >gi 2444420 (AF020553) ribosome-associated protein p40 [Glycine max] 418005 Seq. No. Seq. ID uC-osroM202026d05b1 Method BLASTX NCBI GI q2286153 BLAST score 690 E value 7.0e-73Match length 159 % identity NCBI Description (AF007581) cytoplasmic malate dehydrogenase [Zea mays] Seq. No. 418006 uC-osroM202026d09b1 Seq. ID Method BLASTN NCBI GI q6006355 BLAST score 59 4.0e-25 E value 59 Match length 100 % identity NCBI Description Oryza sativa genomic DNA, chromosome 6, clone:P0493C11 418007 Seq. No. Seq. ID uC-osroM202026d10b1 BLASTX Method NCBI GI g2130069 926 BLAST score 1.0e-100 E value 173 Match length 98 % identity NCBI Description catalase (EC 1.11.1.6) catA - rice >gi 1261858 dbj BAA06232_ (D29966) catalase [Oryza sativa] 418008 Seq. No. Seq. ID uC-osroM202026d11b1 Method BLASTX NCBI GI q2129753

54738



E value 8.0e-55
Match length 146
% identity 73

NCBI Description threonine synthase (EC 4.2.99.2) precursor - Arabidopsis thaliana (fragment) >gi_1448917 (L41666) threonine synthase

[Arabidopsis thaliana]

Seq. No. 418009

Seq. ID uC-osroM202026e02b1

Method BLASTX
NCBI GI g123620
BLAST score 604
E value 8.0e-63
Match length 123
% identity 93

NCBI Description HEAT SHOCK COGNATE 70 KD PROTEIN 2 >gi_100224_pir__S14950

heat shock cognate protein 70 - tomato

>gi 19258 emb CAA37971 (X54030) heat shock protein cognate

70 [Lycopersicon esculentum]

Seq. No. 418010

Seq. ID uC-osroM202026e03b1

Method BLASTX
NCBI GI g2980806
BLAST score 184
E value 2.0e-13
Match length 55
% identity 58

NCBI Description (AL022197) putative protein [Arabidopsis thaliana]

Seq. No. 418011

Seq. ID uC-osroM202026e05b1

Method BLASTX
NCBI GI g542176
BLAST score 247
E value 7.0e-21
Match length 123
% identity 47

NCBI Description probable finger protein WZF1 - wheat

>gi_485814_dbj_BAA03901_ (D16415) WZF1 [Triticum aestivum] >gi_485816_dbj_BAA03902_ (D16416) WZF1 [Triticum aestivum]

Seq. No. 418012

Seq. ID uC-osroM202026e08b1

Method BLASTX
NCBI GI g2980806
BLAST score 181
E value 4.0e-13
Match length 55
% identity 58

NCBI Description (AL022197) putative protein [Arabidopsis thaliana]

Seq. No. 418013

Seq. ID uC-osroM202026e09b1

Method BLASTX NCBI GI g21695 BLAST score 339 E value 1.0e-31 Match length 105% identity 63

NCBI Description (X66014) cathepsin B [Triticum aestivum]

Seq. No. 418014

Seq. ID uC-osroM202026e10b1

Method BLASTN
NCBI GI g5295936
BLAST score 60
E value 1.0e-25
Match length 100
% identity 100

NCBI Description Oryza sativa genomic DNA, chromosome 6, clone:P0681F10,

complete sequence

Seq. No. 418015

Seq. ID uC-osroM202026f01b1

Method BLASTN
NCBI GI g2058499
BLAST score 128
E value 1.0e-65
Match length 155
% identity 96

NCBI Description Oryza sativa hemoglobin 1 mRNA, complete cds

Seq. No. 418016

Seq. ID uC-osroM202026f06b1

Method BLASTX
NCBI GI g4455287
BLAST score 327
E value 3.0e-30
Match length 108
% identity 62

NCBI Description (AL035527) putative protein [Arabidopsis thaliana]

Seq. No. 418017

Seq. ID uC-osroM202026f07b1

Method BLASTX
NCBI GI 9733454
BLAST score 354
E value 1.0e-33
Match length 101
% identity 70

NCBI Description (U23188) chlorophyll a/b-binding apoprotein CP26 precursor

[Zea mays]

Seq. No. 418018

Seq. ID uC-osroM202026f08b1

Method BLASTX
NCBI GI g4512679
BLAST score 527
E value 1.0e-53
Match length 124
% identity 83

NCBI Description (AC006931) putative 60S ribosomal protein L11B [Arabidopsis

thalianal

```
Seq. No.
                  418019
Seq. ID
                  uC-osroM202026f10b1
Method
                  BLASTX
NCBI GI
                  q3892051
BLAST score
                  488
E value
                  1.0e-50
Match length
                  120
% identity
                  80
NCBI Description
                  (AC002330) predicted NADH dehydrogenase 24 kD subunit
                  [Arabidopsis thaliana]
                  418020
Seq. No.
Seq. ID
                  uC-osroM202026f12b1
Method
                  BLASTX
NCBI GI
                  q4490309
BLAST score
                  333
E value
                  4.0e-31
Match length
                  97
% identity
                  62
NCBI Description
                  (AL035678) peroxidase ATP17a-like protein [Arabidopsis
                  thaliana]
Seq. No.
                  418021
Seq. ID
                  uC-osroM202026q05b1
Method
                  BLASTX
NCBI GI
                  q4038034
BLAST score
                  315
E value
                  9.0e-29
Match length
                  92
% identity
                  67
NCBI Description (AC005936) unknown protein [Arabidopsis thaliana]
Seq. No.
                  418022
Seq. ID
                  uC-osroM202026q06b1
Method
                  BLASTX
NCBI GI
                  q1655536
BLAST score
                  269
E value
                  1.0e-23
Match length
                  126
% identity
                  44
NCBI Description
                  (Y09095) chloride channel [Arabidopsis thaliana]
                  >gi 1742957 emb CAA96059 (Z71447) CLC-c chloride channel
                  protein [Arabidopsis thaliana]
Seq. No.
                  418023
Seq. ID
                  uC-osroM202026g09b1
Method
                  BLASTX
NCBI GI
                  g3023751
BLAST score
                  221
E value
                  5.0e-18
Match length
                  52
% identity
                  81
NCBI Description
                  70 KD PEPTIDYLPROLYL ISOMERASE (PEPTIDYLPROLYL CIS-TRANS
                  ISOMERASE) (CYCLOPHILIN) (PPIASE) >gi_1076772_pir__S55383
                  peptidylprolyl isomerase (EC 5.2.1.8) - wheat
```

>gi_854626_emb_CAA60505_ (X86903) peptidylprolyl isomerase

[Triticum aestivum]

Seq. No. 418024

Seq. ID uC-osroM202026g10b1

Method BLASTX
NCBI GI g113622
BLAST score 735
E value 4.0e-78
Match length 152
% identity 96

NCBI Description FRUCTOSE-BISPHOSPHATE ALDOLASE, CYTOPLASMIC ISOZYME

>gi_68197_pir_ADRZY fructose-bisphosphate aldolase (EC
4.1.2.13), cytosolic - rice >gi_20204_emb_CAA37290_
(X53130) fructose-diphosphate aldolase (AA 1-358) [Oryza

sativa]

Seq. No. 418025

Seq. ID uC-osroM202026g12b1

Method BLASTX
NCBI GI g2062164
BLAST score 379
E value 2.0e-36
Match length 140
% identity 54

NCBI Description (AC001645) jasmonate inducible protein isolog [Arabidopsis

thaliana]

Seq. No. 418026

Seq. ID uC-osroM202026h01b1

Method BLASTX
NCBI GI g2055230
BLAST score 230
E value 5.0e-19
Match length 119
% identity 51

NCBI Description (AB000130) SRC2 [Glycine max]

Seq. No. 418027

Seq. ID uC-osroM202026h02b1

Method BLASTX
NCBI GI g2370232
BLAST score 549
E value 2.0e-56
Match length 134
% identity 84

NCBI Description (AJ001341) putative acyl-CoA oxidase [Hordeum vulgare]

Seq. No. 418028

Seq. ID uC-osroM202026h03b1

Method BLASTX
NCBI GI g2827143
BLAST score 393
E value 4.0e-38
Match length 115
% identity 65

NCBI Description (AF027174) cellulose synthase catalytic subunit

[Arabidopsis thaliana]

Seq. ID

```
418029
Seq. No.
Seq. ID
                  uC-osroM202026h04b1
Method
                  BLASTX
NCBI GI
                  g478740
BLAST score
                  462
E value
                  4.0e-46
Match length
                  110
% identity
                  85
NCBI Description phenylalanine ammonia-lyase (EC 4.1.3.5) - rice
Seq. No.
                  418030
Seq. ID
                  uC-osroM202026h08b1
Method
                  BLASTX
NCBI GI
                  q4803836
BLAST score
                  524
E value
                  3.0e-53
Match length
                  161
% identity
                  70
NCBI Description
                 (AB026987) a dynamin-like protein ADL3 [Arabidopsis
                  thaliana]
Seq. No.
                  418031
Seq. ID
                  uC-osroM202026h09b1
Method
                  BLASTX
NCBI GI
                  q5903092
BLAST score
                  432
E value
                  1.0e-42
Match length
                  125
% identity
                  73
NCBI Description (AC008017) Highly similar to developmental protein DG1118
                  [Arabidopsis thaliana]
                  418032
Seq. No.
Seq. ID
                  uC-osroM202026h10b1
Method
                  BLASTX
NCBI GI
                  q4538934
BLAST score
                  385
E value
                  5.0e-37
Match length
                  111
% identity
                  66
NCBI Description (AL049483) putative leucine-rich-repeat protein
                  [Arabidopsis thaliana]
Seq. No.
                  418033
Seq. ID
                  uC-osroM202026h12b1
                  BLASTX
Method
NCBI GI
                  q2497538
BLAST score
                  433
E value
                  1.0e-42
Match length
                  103
                  81
% identity
NCBI Description PYRUVATE KINASE, CYTOSOLIC ISOZYME >gi 466350 (L08632)
                  pyruvate kinase [Glycine max]
Seq. No.
                  418034
```

54743

uC-osroM202027a02a1

```
Method BLASTN
NCBI GI g5670155
BLAST score 47
E value 2.0e-17
Match length 130
```

% identity 85
NCBI Description Oryza sativa subsp. japonica BAC clone 34K24, complete

sequence

Seq. No. 418035

Seq. ID uC-osroM202027a03a1

Method BLASTX
NCBI GI g3641661
BLAST score 446
E value 3.0e-44
Match length 88
% identity 94

NCBI Description (AB008519) high affinity nitrate transporter [Oryza sativa]

Seq. No. 418036

Seq. ID uC-osroM202027a06a1

Method BLASTX
NCBI GI g5918310
BLAST score 158
E value 1.0e-10
Match length 58
% identity 48

NCBI Description (AL035708) putative protein [Arabidopsis thaliana]

Seq. No. 418037

Seq. ID uC-osroM202027b05a1

Method BLASTX
NCBI GI g4895238
BLAST score 182
E value 3.0e-13
Match length 64
% identity 58

NCBI Description (AC007659) unknown protein [Arabidopsis thaliana]

Seq. No. 418038

Seq. ID uC-osroM202027c02a1

Method BLASTX
NCBI GI g2462759
BLAST score 194
E value 6.0e-15
Match length 90
% identity 48

NCBI Description (AC002292) Putative Cytochrome B5 [Arabidopsis thaliana]

Seq. No. 418039

Seq. ID uC-osroM202027c04a1

Method BLASTX
NCBI GI g4454033
BLAST score 188
E value 4.0e-14
Match length 55
% identity 60

54744

NCBI Description

cholerae]

```
(AL035394) putative potassium transport protein
NCBI Description
                  [Arabidopsis thaliana]
                  418040
Seq. No.
                  uC-osroM202027c08a1
Seq. ID
                  BLASTN
Method
NCBI GI
                  g1132482
BLAST score
                  290
E value
                  1.0e-162
Match length
                  388
                  94
% identity
NCBI Description Rice mRNA for ADP-ribosylation factor, complete cds
Seq. No.
                  418041
                  uC-osroM202027c09a1
Seq. ID
                  BLASTN
Method
NCBI GI
                  g4680488
BLAST score
                  51
E value
                  1.0e-19
Match length
                  159
% identity
                  83
NCBI Description Oryza sativa BAC clone 1.H19, complete sequence
                  418042
Seq. No.
                  uC-osroM202027c11a1
Seq. ID
                  BLASTN
Method
NCBI GI
                  g1051257
BLAST score
                  34
E value
                  2.0e-09
Match length
                  46
                  93
% identity
NCBI Description Hordeum vulgare vacuolar ATPase catalytic subunit mRNA,
                  partial cds
                  418043
Seq. No.
Seq. ID
                  uC-osroM202027d01a1
                  BLASTX
Method
NCBI GI
                  g1076746
BLAST score
                  296
                  1.0e-26
E value
                  87
Match length
                  72
% identity
NCBI Description heat shock protein 70 - rice (fragment)
                  >gi_763160_emb_CAA47948 (X67711) heat shock protein 70
                  [Oryza sativa]
                  418044
Seq. No.
                  uC-osroM202027d02a1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g5880462
BLAST score
                  245
                  1.0e-20
E value
Match length
                  137
% identity
```

(AF090685) putative 2-hydroxy acid dehydrogenase [Vibrio

418045 Seq. No. Seq. ID uC-osroM202027d04a1 BLASTX Method g2760844 NCBI GI BLAST score 180 E value 4.0e-13 63 Match length % identity 51 NCBI Description (AC003105) hypothetical protein [Arabidopsis thaliana] 418046 Seq. No. Seq. ID uC-osroM202027d08a1 BLASTX Method NCBI GI q4580721 BLAST score 154 E value 4.0e-10 Match length 34 % identity 88 NCBI Description (AF136163) phosphoenolpyruvate carboxykinase 4 [Urochloa panicoides] 418047 Seq. No. uC-osroM202027d10a1 Seq. ID BLASTN Method NCBI GI g600766 BLAST score 291 E value 1.0e-163 315 Match length 98 % identity NCBI Description Oryza sativa cyclophilin 2 (Cyp2) gene, complete cds 418048 Seq. No. Seq. ID uC-osroM202027d11a1 Method BLASTN NCBI GI g1944204 BLAST score 125 E value 4.0e-64 Match length 177 % identity 93 NCBI Description Oryza sativa mRNA for RicMT, complete cds 418049 Seq. No. Seq. ID uC-osroM202027d12a1 Method BLASTX NCBI GI q3482971 BLAST score 142 E value 7.0e-09 Match length 33 % identity

Seq. No. 418050

Seq. ID uC-osroM202027e01a1

Method BLASTX
NCBI GI g3702317
BLAST score 172
E value 3.0e-12

NCBI Description (AL031369) putative protein [Arabidopsis thaliana]

Match length 38 % identity 87

NCBI Description (AC005397) unknown protein [Arabidopsis thaliana]

>qi 4559376 gb AAD23036.1 AC006526 1 (AC006526) unknown

protein [Arabidopsis thaliana]

Seq. No. 418051

Seq. ID uC-osroM202027e03a1

Method BLASTX
NCBI GI g1705677
BLAST score 177
E value 1.0e-12
Match length 37
% identity 95

NCBI Description CELL DIVISION CYCLE PROTEIN 48 HOMOLOG

>gi_2118115_pir__S60112 cell division control protein CDC48
homolog - Arabidopsis thaliana >gi_1019904 (U37587) cell

division cycle protein [Arabidopsis thaliana]

Seq. No. 418052

Seq. ID uC-osroM202027e09a1

Method BLASTX
NCBI GI g129591
BLAST score 313
E value 1.0e-28
Match length 59
% identity 97

NCBI Description PHENYLALANINE AMMONIA-LYASE >gi_295824_emb_CAA34226_

(X16099) phenylalanine ammonia-lyase [Oryza sativa]

Seq. No. 418053

Seq. ID uC-osroM202027f06a1

Method BLASTX
NCBI GI g3913426
BLAST score 330
E value 1.0e-30
Match length 62
% identity 100

NCBI Description S-ADENOSYLMETHIONINE DECARBOXYLASE PROENZYME (ADOMETDC)

(SAMDC) >gi 1532048 emb CAA69074 (Y07766)

S-adenosylmethionine decarboxylase [Oryza sativa]

Seq. No. 418054

Seq. ID uC-osroM202027f09a1

Method BLASTX
NCBI GI g2702268
BLAST score 257
E value 2.0e-22
Match length 93
% identity 53

NCBI Description (AC003033) putative cellulase [Arabidopsis thaliana]

Seq. No. 418055

Seq. ID uC-osroM202027f12a1

Method BLASTX
NCBI GI g3132310
BLAST score 340

```
E value
                  8.0e-32
Match length
                  77
                  87
% identity
NCBI Description (AB012228) phosphoenolpyruvate carboxylase [Zea mays]
                  418056
Seq. No.
Seq. ID
                  uC-osroM202027g01a1
Method
                  BLASTX
                  g129591
NCBI GI
BLAST score
                  211
                  1.0e-16
E value
Match length
                  39
                  97
% identity
NCBI Description PHENYLALANINE AMMONIA-LYASE >gi 295824 emb CAA34226
                  (X16099) phenylalanine ammonia-lyase [Oryza sativa]
                  418057
Seq. No.
Seq. ID
                  uC-osroM202027g03a1
Method
                  BLASTN
NCBI GI
                  g2894533
BLAST score
                  205
E value
                  1.0e-111
Match length
                  261
                  97
% identity
NCBI Description Oryza sativa mRNA for aquaporin, complete CDS
Seq. No.
                  418058
Seq. ID
                  uC-osroM202027g10a1
Method
                  BLASTN
NCBI GI
                  g4574138
BLAST score
                  202
E value
                  1.0e-110
Match length
                  202
                  100
% identity
NCBI Description Oryza sativa cysteine synthase (rcs3) mRNA, complete cds
                  418059
Seq. No.
Seq. ID
                  uC-osroM202027g11a1
Method
                  BLASTN
NCBI GI
                  q780371
BLAST score
                  210
E value
                  1.0e-114
Match length
                  254
% identity
                  96
NCBI Description Oryza sativa enolase mRNA, complete cds
Seq. No.
                  418060
```

Seq. ID uC-osroM202027h01a1

Method BLASTN
NCBI GI g460988
BLAST score 234
E value 1.0e-129
Match length 250
% identity 98

NCBI Description O.sativa (Arborio) Beta Tubulin mRNA, clone OSTB-34

Seq. No. 418061

NCBI GI

```
Seq. ID
                  uC-osroM202027h02a1
Method
                  BLASTX
NCBI GI
                  g3482918
BLAST score
                  178
E value
                  9.0e-13
Match length
                  38
% identity
                  87
NCBI Description (AC003970) Similar to ATP-citrate-lyase [Arabidopsis
                  thaliana]
Seq. No.
                  418062
Seq. ID
                  uC-osroM202027h03a1
Method
                  BLASTX
NCBI GI
                  q3252868
BLAST score
                  204
E value
                  7.0e-16
Match length
                  68
% identity
                  57
NCBI Description (AF033536) putative zinc transporter [Arabidopsis thaliana]
Seq. No.
                  418063
Seq. ID
                  uC-osroM202027h06a1
Method
                  BLASTN
NCBI GI
                  g685241
BLAST score
                  42
E value
                  3.0e-14
Match length
                  46
% identity
                  98
NCBI Description Oryza sativa cytosolic copper/zinc-superoxide dismutase
                  (SodCc1) gene, complete cds
                  418064
Seq. No.
Seq. ID
                  uC-osroM202027h09a1
Method
                  BLASTX
NCBI GI
                  q285741
BLAST score
                  252
E value
                  9.0e-22
Match length
                  89
% identity
                  54
NCBI Description (D14550) EDGP precursor [Daucus carota]
Seq. No.
                  418065
Seq. ID
                  uC-osroM202027h10a1
Method
                  BLASTX
NCBI GI
                  q1203832
BLAST score
                  507
E value
                  1.0e-51
Match length
                  121
% identity
                  80
NCBI Description
                  (U46003) beta-D-glucan exohydrolase, isoenzyme ExoII
                  [Hordeum vulgare] >gi_1588407_prf__2208395A beta-D-glucan
                  exohydrolase [Hordeum vulgare]
Seq. No.
                  418066
Seq. ID
                  uC-osroM202027h11a1
Method
                  BLASTN
```

54749

g6069643

```
BLAST score
                  38
E value
                  6.0e-12
                  86
Match length
                  86
% identity
NCBI Description Oryza sativa genomic DNA, chromosome 6, clone:P0514G12
Seq. No.
                  418067
Seq. ID
                  uC-osroM202028a01a1
                  BLASTX
Method
NCBI GI
                  q2982451
BLAST score
                  290
E value
                  6.0e-26
Match length
                  77
                  73
% identity
NCBI Description (AL022223) putative protein [Arabidopsis thaliana]
Seq. No.
                  418068
Seq. ID
                  uC-osroM202028a03b1
Method
                  BLASTX
NCBI GI
                  g3885882
BLAST score
                  411
E value
                  3.0e-40
                  92
Match length
% identity
                  86
NCBI Description (AF093629) inorganic pyrophosphatase [Oryza sativa]
                  418069
Seq. No.
Seq. ID
                  uC-osroM202028a04a1
Method
                  BLASTN
NCBI GI
                  q5734616
BLAST score
                  346
E value
                  0.0e+00
Match length
                  414
% identity
                  100
NCBI Description Oryza sativa genomic DNA, chromosome 6, clone:P0538C01
Seq. No.
                  418070
Seq. ID
                  uC-osroM202028a04b1
Method
                  BLASTN
NCBI GI
                  q5734616
BLAST score
                  427
E value
                  0.0e + 00
Match length
                  435
% identity
                  100
NCBI Description Oryza sativa genomic DNA, chromosome 6, clone:P0538C01
Seq. No.
                  418071
Seq. ID
                  uC-osroM202028a05a1
Method
                  BLASTX
NCBI GI
                  g5915857
BLAST score
                  188
E value
                  5.0e-14
Match length
                  48
% identity
                  75
```

NCBI Description CYTOCHROME P450 98A1 >gi 2766448 (AF029856) cytochrome P450

CYP98A1 [Sorghum bicolor]

418072 Seq. No. Seq. ID uC-osroM202028a05b1 Method BLASTX NCBI GI g5915857 BLAST score 341 E value 2.0e-56 Match length 132 % identity 75 NCBI Description CYTOCHROME P450 98A1 >gi 2766448 (AF029856) cytochrome P450 CYP98A1 [Sorghum bicolor] 418073 Seq. No. Seq. ID uC-osroM202028a06a1 Method BLASTX NCBI GI q2662343 BLAST score 239 E value 4.0e-20 Match length 57 % identity 84 NCBI Description (D63581) EF-1 alpha [Oryza sativa] Seq. No. 418074 Seq. ID uC-osroM202028a07a1 Method BLASTX NCBI GI q1362060 BLAST score 469 E value 6.0e-47Match length 157 % identity 62 NCBI Description dehydroquinase-shikimate dehydrogenase - garden pea Seq. No. 418075 Seq. ID uC-osroM202028a08b1 Method BLASTX NCBI GI q4490738 BLAST score 219 E value 1.0e-17 Match length 139 % identity 37 NCBI Description (AL035708) putative protein [Arabidopsis thaliana] 418076 Seq. No. Seq. ID uC-osroM202028a10a1 Method BLASTX NCBI GI g913445 BLAST score 165 E value 2.0e-11 Match length 39 % identity 77 NCBI Description (S75487) alcohol dehydrogenase ADH=alcohol dehydrogenase homolog {EC 1.1.1.1} [Lycopersicon esculentum=tomatoes, cv. red cherry, Peptide, 389 aa] [Lycopersicon esculentum]

Seq. No. 418077

Seq. ID uC-osroM202028a10b1

Method BLASTX NCBI GI g1076580

NCBI GI

E value

BLAST score

q4938477

1.0e-13

185

BLAST score 381 E value 9.0e-37 Match length 100 % identity 66 NCBI Description alcohol dehydrogenase homolog ADH3b - tomato >gi_913446_bbs_160508 (S75487) alcohol dehydrogenase ADH {EC 1.1.1.1} [Lycopersicon esculentum=tomatoes, cv. red cherry, Peptide, 390 aa] [Lycopersicon esculentum] Seq. No. 418078 Seq. ID uC-osroM202028a11b1 Method BLASTX NCBI GI q4835761 BLAST score 208 E value 2.0e-16 Match length 78 % identity 45 NCBI Description (AC007202) T8K14.10 [Arabidopsis thaliana] Seq. No. 418079 Seq. ID uC-osroM202028b05b1 Method BLASTX NCBI GI q2493318 BLAST score 272 E value 5.0e - 24Match length 89 % identity 60 NCBI Description BLUE COPPER PROTEIN PRECURSOR >gi 562779 emb CAA80963 (Z25471) blue copper protein [Pisum sativum] >gi_1098264_prf 2115352A blue Cu protein [Pisum sativum] Seq. No. 418080 Seq. ID uC-osroM202028b06a1 Method BLASTX NCBI GI q3445397 BLAST score 312 E value 1.0e-28 Match length 67 % identity 85 NCBI Description (AJ010166) S-domain receptor-like protein kinase [Zea mays] Seq. No. 418081 Seq. ID uC-osroM202028b06b1 Method BLASTX NCBI GI g3445397 BLAST score 454 E value 3.0e-45Match length 109 % identity NCBI Description (AJ010166) S-domain receptor-like protein kinase [Zea mays] Seq. No. 418082 Seq. ID uC-osroM202028b08b1 Method BLASTX

```
Match length
                  72
% identity
NCBI Description (AL078464) putative protein [Arabidopsis thaliana]
                  418083
Seq. No.
                  uC-osroM202028b09b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2182267
BLAST score
                  566
E value
                  2.0e-58
Match length
                  137
% identity
                  80
NCBI Description (L37359) lipoxygenase [Hordeum vulgare]
Seq. No.
                  418084
                  uC-osroM202028b12a1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g780371
BLAST score
                  109
E value
                  2.0e-54
                  221
Match length
% identity
                  87
NCBI Description Oryza sativa enolase mRNA, complete cds
Seq. No.
                  418085
Seq. ID
                  uC-osroM202028b12b1
Method
                  BLASTX
NCBI GI
                  g3023713
BLAST score
                  751
E value
                  4.0e-80
                  147
Match length
                  98
% identity
NCBI Description ENOLASE (2-PHOSPHOGLYCERATE DEHYDRATASE)
                  (2-PHOSPHO-D-GLYCERATE HYDRO-LYASE) (OSE1) >gi 780372
                  (U09450) enolase [Oryza sativa]
Seq. No.
                  418086
                  uC-osroM202028c01a1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g20280
BLAST score
                  96
E value
                  2.0e-46
Match length
                  256
% identity
                  85
NCBI Description Rice gene for phenylalanine ammonia-lyase (EC 4.3.1.5)
Seq. No.
                  418087
Seq. ID
                  uC-osroM202028c01b1
Method
                  BLASTX
NCBI GI
                  q4586449
```

Method BLASTX
NCBI GI g4586449
BLAST score 324
E value 5.0e-30
Match length 78
% identity 68

NCBI Description (AB025187) cytochrome c oxidase subunit 6b-1 [Oryza sativa]

Seq. No. 418088

```
uC-osroM202028c03a1
Seq. ID
Method
                  BLASTN
NCBI GI
                  q790969
BLAST score
                  227
E value
                  1.0e-124
Match length
                  249
% identity
                  98
NCBI Description Rice mRNA for aldolase C-1, complete cds
Seq. No.
                  418089
                  uC-osroM202028c03b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2130073
BLAST score
                  493
E value
                  3.0e-64
Match length
                  130
% identity
                  92
                  fructose-bisphosphate aldolase (EC 4.1.2.13) isoenzyme C-1,
NCBI Description
                  cytosolic - rice >gi_786178_dbj_BAA08845_ (D50307) aldolase
                  C-1 [Oryza sativa] >gi_790970_dbj_BAA08830_ (D50301)
                  aldolase C-1 [Oryza sativa]
                  418090
Seq. No.
Seq. ID
                  uC-osroM202028c04a1
Method
                  BLASTX
NCBI GI
                  q2078350
BLAST score
                  205
                  4.0e-16
E value
Match length
                  53
                  75
% identity
NCBI Description (U95923) transaldolase [Solanum tuberosum]
Seq. No.
                  418091
Seq. ID
                  uC-osroM202028c04b1
Method
                  BLASTX
                  g2078350
NCBI GI
BLAST score
                  291
                  4.0e-26
E value
Match length
                  76
% identity
                  71
NCBI Description (U95923) transaldolase [Solanum tuberosum]
                  418092
Seq. No.
                  uC-osroM202028c05a1
Seq. ID
Method
                  BLASTN
NCBI GI
                  q786131
BLAST score
                  42
E value
                  3.0e-14
Match length
                  58
% identity
                  93
NCBI Description Oryza sativa root-specific RCc3 mRNA, complete cds
```

Seq. No. 418093

Seq. ID uC-osroM202028c05b1

Method BLASTX
NCBI GI g1084461
BLAST score 493



E value 1.0e-49
Match length 130
% identity 77
NCBI Description RCc3 pro

NCBI Description RCc3 protein - rice >gi_786132 (L27208) RCc3 [Oryza sativa]

Seq. No. 418094

Seq. ID uC-osroM202028c07a1

Method BLASTX
NCBI GI g129591
BLAST score 284
E value 3.0e-25
Match length 52
% identity 100

NCBI Description PHENYLALANINE AMMONIA-LYASE >gi_295824_emb_CAA34226_ (X16099) phenylalanine ammonia-lyase [Oryza sativa]

Seq. No. 418095

Seq. ID uC-osroM202028c07b1

Method BLASTX
NCBI GI g129591
BLAST score 397
E value 1.0e-38
Match length 102
% identity 76

NCBI Description PHENYLALANINE AMMONIA-LYASE >gi 295824 emb CAA34226_

(X16099) phenylalanine ammonia-lyase [Oryza sativa]

Seq. No. 418096

Seq. ID uC-osroM202028c08a1

Method BLASTX
NCBI GI g4455225
BLAST score 204
E value 5.0e-16
Match length 40
% identity 80

NCBI Description (AL035440) putative protein [Arabidopsis thaliana]

Seq. No. 418097

Seq. ID uC-osroM202028c11b1

Method BLASTX
NCBI GI g2492636
BLAST score 591
E value 3.0e-61
Match length 142
% identity 82

NCBI Description ACONITASE (ACONITATE HYDRATASE) (CITRATE HYDRO-LYASE)

>gi_1084317_pir__S49849 aconitate hydratase (EC 4.2.1.3) -

muskmelon (fragment) >gi 599723 emb CAA58047 (X82840)

aconitase [Cucumis melo]

Seq. No. 418098

Seq. ID uC-osroM202028c12b1

Method BLASTX
NCBI GI g4587571
BLAST score 640
E value 5.0e-67
Match length 150

% identity (AC006550) Belongs to the PF 01027 Uncharacterized protein NCBI Description family UPF0005 with 7 transmembrane domains. [Arabidopsis thaliana] 418099 Seq. No. Seq. ID uC-osroM202028d01b1 Method BLASTX NCBI GI q3152605 BLAST score 423 E value 1.0e-41 Match length 111 % identity 70 NCBI Description (AC004482) hypothetical protein [Arabidopsis thaliana] 418100 Seq. No. Seq. ID uC-osroM202028d02a1 BLASTX Method NCBI GI g1747296 BLAST score 198 E value 3.0e-15 Match length 39 97 % identity NCBI Description (D45384) vacuolar H+-pyrophosphatase [Oryza sativa] >qi 3298476 dbj BAA31524 (AB012766) ovp2 [Oryza sativa] Seq. No. 418101 Seq. ID uC-osroM202028d02b1 BLASTX Method NCBI GI g1747296 BLAST score 413 2.0e-40 E value 103 Match length % identity 79 NCBI Description (D45384) vacuolar H+-pyrophosphatase [Oryza sativa] >gi 3298476 dbj BAA31524 (AB012766) ovp2 [Oryza sativa] 418102 Seq. No. uC-osroM202028d04b1 Seq. ID Method BLASTN NCBI GI g444046 BLAST score 40 E value 5.0e-13 Match length 100 % identity 85 NCBI Description Z.mays OBF1 mRNA for ocs-element binding factor 418103 Seq. No. Seq. ID uC-osroM202028d05a1 Method BLASTX NCBI GI g3789942 BLAST score 370 E value 2.0e-35 Match length 75 % identity 20 NCBI Description (AF093505) polyubiquitin [Saccharum hybrid cultivar H32-8560]

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418104
Seq. No.
Seq. ID
                  uC-osroM202028d05b1
Method
                  BLASTX
NCBI GI
                  g625509
BLAST score
                  663
E value
                  1.0e-69
Match length
                  135
                  28
% identity
NCBI Description ubiquitin precursor - Arabidopsis thaliana (fragment)
Seq. No.
                  418105
                  uC-osroM202028d07a1
Seq. ID
                  BLASTX
Method
NCBI GI
                  g3395432
BLAST score
                  217
E value
                  2.0e-17
                  60
Match length
% identity
                  65
                  (AC004683) unknown protein [Arabidopsis thaliana]
NCBI Description
                  >gi 5731261 gb AAD48838.1 AF166352 1 (AF166352)
                  alanine:glyoxylate aminotransferase 2 homolog [Arabidopsis
                  thaliana]
                  418106
Seq. No.
Seq. ID
                  uC-osroM202028d07b1
Method
                  BLASTX
NCBI GI
                  g3152605
BLAST score
                  202
E value
                  1.0e-15
Match length
                  89
% identity
                  49
NCBI Description (AC004482) hypothetical protein [Arabidopsis thaliana]
                  418107
Seq. No.
Seq. ID
                  uC-osroM202028d08a1
Method
                  BLASTX
NCBI GI
                  q584892
BLAST score
                  308
E value
                  3.0e-28
Match length
                  92
                  54
% identity
NCBI Description
                  SERINE CARBOXYPEPTIDASE I PRECURSOR (CARBOXYPEPTIDASE C)
                  >qi 629805 pir S43516 serine carboxypeptidase I - rice
                  >gi 409580 dbj BAA04510 (D17586) serine carboxypeptidase I
                  [Oryza sativa]
Seq. No.
                  418108
                  uC-osroM202028d08b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4101703
BLAST score
                  297
E value
                  8.0e-27
Match length
                  142
% identity
                  44
NCBI Description
                 (AF006078) glucose acyltransferase [Solanum berthaultii]
```

Method

NCBI GI

BLAST score

BLASTN

g20367

195

```
Seq. No.
                   418109
Seq. ID
                  uC-osroM202028d09b1
Method
                  BLASTX
NCBI GI
                   g2464938
BLAST score
                  218
E value
                   1.0e-17
Match length
                  43
% identity
                  88
NCBI Description (Z99708) MAP kinase like protein [Arabidopsis thaliana]
Seq. No.
                   418110
Seq. ID
                  uC-osroM202028d10a1
Method
                  BLASTX
NCBI GI
                  g1362060
BLAST score
                  149
E value
                   4.0e-10
Match length
                  50
                  54
% identity
NCBI Description dehydroquinase-shikimate dehydrogenase - garden pea
Seq. No.
                   418111
Seq. ID
                  uC-osroM202028d11b1
Method
                  BLASTX
NCBI GI
                  q5734634
BLAST score
                  270
E value
                  1.0e-23
Match length
                  112
                  54
% identity
NCBI Description (AP000391) Similar to putative lipase (AC006232) [Oryza
                  sativa]
Seq. No.
                  418112
Seq. ID
                  uC-osroM202028d12b1
Method
                  BLASTX
NCBI GI
                  g4559381
BLAST score
                  144
E value
                  6.0e-09
Match length
                  104
% identity
                  37
NCBI Description (AC006526) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  418113
Seq. ID
                  uC-osroM202028e02b1
Method
                  BLASTX
NCBI GI
                  q5702231
BLAST score
                  189
E value
                  3.0e-17
Match length
                  94
% identity
                  54
NCBI Description (AF145386) hypersensitive reaction associated Ca2+-binding
                  protein [Phaseolus vulgaris]
Seq. No.
                  418114
Seq. ID
                  uC-osroM202028e03a1
```

```
1.0e-105
E value
Match length
                  271
                  94
% identity
NCBI Description
                  Oryza sativa shoot GS1 mRNA for cytosolic glutamine
                  synthetase (EC 6.3.1.2) (clone lambda-GS28)
Seq. No.
                  418115
Seq. ID
                  uC-osroM202028e03b1
Method
                  BLASTX
NCBI GI
                  g121349
BLAST score
                  670
E value
                  1.0e-70
Match length
                  126
% identity
                  100
NCBI Description GLUTAMINE SYNTHETASE SHOOT ISOZYME (GLUTAMATE--AMMONIA
                  LIGASE) (CLONE LAMBDA-GS28) >gi 20368 emb CAA32461
                  (X14245) cytosolic glutamine synthetase (AA 1-356) [Oryza
                  sativa]
Seq. No.
                  418116
Seq. ID
                  uC-osroM202028e04a1
Method
                  BLASTX
NCBI GI
                  q3935181
BLAST score
                  198
E value
                  3.0e-15
                  43
Match length
                  79
% identity
NCBI Description (AC004557) F17L21.24 [Arabidopsis thaliana]
                  418117
Seq. No.
                  uC-osroM202028e04b1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g2760165
BLAST score
                  62
                  4.0e-26
E value
Match length
                  202
% identity
                  83
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MAC9, complete sequence
Seq. No.
                  418118
Seq. ID
                  uC-osroM202028e06b1
Method
                  BLASTX
NCBI GI
                  g121332
BLAST score
                  556
                  2.0e-57
E value
Match length
                  106
% identity
                  98
NCBI Description GLUTAMINE SYNTHETASE ROOT ISOZYME (GLUTAMATE--AMMONIA
                  LIGASE) (CLONE LAMBDA-GS8) >gi 68590 pir AJRZQB
                  glutamate--ammonia ligase (EC 6.3.1.2) beta, cytosolic -
                  rice >gi_20358_emb_CAA32460_ (X14244) cytosolic glutamine
```

Seq. No. 418119

Seq. ID uC-osroM202028e08b1

Method BLASTX

syntethase (AA 1-357) [Oryza sativa]

Match length

```
NCBI GI
                   q5565981
BLAST score
                   433
E value
                   1.0e-42
Match length
                  120
% identity
                   77
NCBI Description (AF152600) unknown [Zea mays]
Seq. No.
                   418120
Seq. ID
                  uC-osroM202028e09b1
Method
                  BLASTX
NCBI GI
                   g1184776
BLAST score
                  547
E value
                   3.0e-56
Match length
                  113
% identity
                  89
                  (U45857) cytosolic glyceroldehyde-3-phosphate dehydrogenase
NCBI Description
                  GAPC4 [Zea mays]
Seq. No.
Seq. ID
                   418121
                   uC-osroM202028e10b1
Method
                  BLASTX
NCBI GI
                   g1619602
BLAST score
                  206
E value
                   4.0e-16
Match length
                  129
% identity
                   39
NCBI Description (Y08726) MtN3 [Medicago truncatula]
Seq. No.
                   418122
Seq. ID
                  uC-osroM202028e11b1
Method
                  BLASTX
NCBI GI
                  g4406756
BLAST score
                  490
E value
                  2.0e-49
Match length
                  119
                   77
% identity
NCBI Description (AC006836) putative integral membrane protein A3
                   [Arabidopsis thaliana]
Seq. No.
                   418123
Seq. ID
                  uC-osroM202028e12a1
Method
                  BLASTN
NCBI GI
                  g6041757
BLAST score
                  91
E value
                  1.0e-43
                  131
Match length
% identity
                  93
NCBI Description Genomic Sequence For Oryza sativa Clone 10P20, Lemont
                  Strain, Complete Sequence, complete sequence
Seq. No.
                   418124
                  uC-osroM202028e12b1
Seq. ID
Method
                  BLASTN
NCBI GI
                  q6041757
BLAST score
                  53
                  7.0e-21
E value
```

% identity 94

NCBI Description Genomic Sequence For Oryza sativa Clone 10P20, Lemont

Strain, Complete Sequence, complete sequence

Seq. No. 418125

Seq. ID uC-osroM202028f01a1

Method BLASTX
NCBI GI g4836452
BLAST score 160
E value 8.0e-11
Match length 90
% identity 40

NCBI Description (AF121878) cytidine deaminase [Arabidopsis thaliana]

Seq. No. 418126

Seq. ID uC-osroM202028f03a1

Method BLASTN
NCBI GI g425794
BLAST score 241
E value 1.0e-133
Match length 252
% identity 99

NCBI Description Rice mRNA for heat shock protein 82 (gene name AD167),

partial cds

Seq. No. 418127

Seq. ID uC-osroM202028f03b1

Method BLASTX
NCBI GI g417154
BLAST score 446
E value 7.0e-53
Match length 118
% identity 98

NCBI Description HEAT SHOCK PROTEIN 82 >gi_100685_pir__S25541 heat shock

protein 82 - rice (strain Taichung Native One)

>gi_20256_emb_CAA77978_ (Z11920) heat shock protein 82

(HSP82) [Oryza sativa]

Seq. No. 418128

Seq. ID uC-osroM202028f04a1

Method BLASTX
NCBI GI g2342494
BLAST score 296
E value 1.0e-26
Match length 88
% identity 59

NCBI Description (D14058) bromelain [Ananas comosus]

>gi 2463582 dbj BAA22543 (D38531) FB31 precursor (FB13

precursor) [Ananas comosus]

Seq. No. 418129

Seq. ID uC-osroM202028f04b1

Method BLASTX
NCBI GI g1323748
BLAST score 219
E value 9.0e-18
Match length 84



```
% identity
NCBI Description (U32430) thiol protease [Triticum aestivum]
                  418130
Seq. No.
Seq. ID
                  uC-osroM202028f09a1
Method
                  BLASTX
                  g4887741
NCBI GI
BLAST score
                  266
E value
                  2.0e-23
Match length
                  71
                  73
% identity
NCBI Description (AC006533) molybdopterin biosynthesis cnx2 protein
                  [Arabidopsis thaliana]
                  418131
Seq. No.
Seq. ID
                  uC-osroM202028f09b1
Method
                  BLASTX
NCBI GI
                  g4887741
BLAST score
                  301
E value
                  1.0e-27
Match length
                  68
% identity
                  85
NCBI Description (AC006533) molybdopterin biosynthesis cnx2 protein
                  [Arabidopsis thaliana]
Seq. No.
                  418132
Seq. ID
                  uC-osroM202028f10a1
Method
                  BLASTX
NCBI GI
                  g4584345
BLAST score
                  156
E value
                  3.0e-10
Match length
                  68
% identity
                  53
NCBI Description (AC007127) putative serine/threonine protein kinase
                  [Arabidopsis thaliana]
Seq. No.
                  418133
Seq. ID
                  uC-osroM202028q01b1
Method
                  BLASTX
NCBI GI
                  q266346
BLAST score
                  238
E value
                  6.0e-20
Match length
                  60
% identity
                  73
NCBI Description
                  KETOL-ACID REDUCTOISOMERASE PRECURSOR (ACETOHYDROXY-ACID
                  REDUCTOISOMERASE) (ALPHA-KETO-BETA-HYDROXYLACIL
                  REDUCTOISOMERASE) >gi 81509 pir S17180 ketol-acid
                  reductoisomerase (EC 1.1.1.86) precursor - spinach
                  >gi 21234 emb CAA40356 (X57073) ketol-acid
                  reductoisomerase [Spinacia oleracea]
```

Seq. No. 418134

Seq. ID uC-osroM202028g02a1

Method BLASTX NCBI GI q1931643 BLAST score 153 E value 6.0e-10

```
56
Match length
% identity
                   48
NCBI Description (U95973) DnaJ isolog [Arabidopsis thaliana]
                  418135
Seq. No.
Seq. ID
                  uC-osroM202028g02b1
Method
                  BLASTX
NCBI GI
                  g4981382
BLAST score
                  178
                  7.0e-13
E value
                  64
Match length
                  55
% identity
NCBI Description (AE001751) dnaJ protein [Thermotoga maritima]
                  418136
Seq. No.
Seq. ID
                  uC-osroM202028g03b1
Method
                  BLASTX
NCBI GI
                  g2292907
BLAST score
                  671
E value
                  1.0e-70
                  142
Match length
                  91
% identity
NCBI Description (Y10099) P-glycoprotein homologue [Hordeum vulgare]
Seq. No.
                  418137
Seq. ID
                  uC-osroM202028g04a1
Method
                  BLASTX
NCBI GI
                  g3757522
BLAST score
                  180
E value
                  4.0e-13
Match length
                  48
% identity
                  67
NCBI Description (AC005167) putative splicing factor [Arabidopsis thaliana]
Seq. No.
                  418138
Seq. ID
                  uC-osroM202028g05b1
Method
                  BLASTX
NCBI GI
                  g4836452
BLAST score
                  191
E value
                  2.0e-14
Match length
                  81
% identity
NCBI Description (AF121878) cytidine deaminase [Arabidopsis thaliana]
                  418139
Seq. No.
Seq. ID
                  uC-osroM202028q07b1
Method
                  BLASTX
NCBI GI
                  g322871
BLAST score
                  325
E value
                  3.0e-35
Match length
                  153
% identity
                  47
NCBI Description hypothetical protein 1 - maize transposon En-1
                  >gi_225005_prf__1206239A ORF 1 [Zea mays]
Seq. No.
                  418140
Seq. ID
                  uC-osroM202028q08a1
```

```
Method
                  BLASTX
NCBI GI
                  g4490301
BLAST score
                  309
E value
                  3.0e-28
                  122
Match length
                  46
% identity
NCBI Description (AL035678) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  418141
Seq. ID
                  uC-osroM202028g11a1
Method
                  BLASTX
NCBI GI
                  g4314378
BLAST score
                  153
E value
                  6.0e-10
Match length
                  52
                  52
% identity
NCBI Description
                  (AC006232) putative lipase [Arabidopsis thaliana]
                  >gi_5306262_gb AAD41994.1 AC006233_5 (AC006233) putative
                  lipase [Arabidopsis thaliana]
Seq. No.
                  418142
Seq. ID
                  uC-osroM202028q11b1
Method
                  BLASTX
NCBI GI
                  g5734634
BLAST score
                  173
E value
                  2.0e-12
                  70
Match length
% identity
                  56
NCBI Description (AP000391) Similar to putative lipase (AC006232) [Oryza
                  sativa]
Seq. No.
                  418143
Seq. ID
                  uC-osroM202028g12b1
Method
                  BLASTX
NCBI GI
                  q2980766
BLAST score
                  159
E value
                  1.0e-10
```

Match length 131 % identity 33

NCBI Description (AL022198) putative calmodulin-binding protein [Arabidopsis

thaliana]

Seq. No. 418144

Seq. ID uC-osroM202028h04a1

Method BLASTX NCBI GI q112785 BLAST score 178 E value 6.0e-13 Match length 105 % identity 37

NCBI Description DNA-3-METHYLADENINE GLYCOSYLASE I (3-METHYLADENINE-DNA

GLYCOSYLASE I, CONSTITUTIVE) (TAG I) (DNA-3-METHYLADENINE GLYCOSIDASE I) >gi 67508 pir DGECM1 3-methyladenine DNA

glycosylase (EC 3.2.2.-) I - Escherichia coli >gi_43030_emb_CAA27472_ (X03845) TAGI (aa 1-187)

[Escherichia coli] >gi 147920 (J02606) 3-methyladenine-DNA glycosylase I (tag) [Escherichia coli] >qi 466687 (U00039)

3-methyladenine DNA glycosylase I, constitutive [Escherichia coli] >gi_1789971 (AE000432) 3-methyl-adenine DNA glycosylase I, constitutive [Escherichia coli]

 Seq. No.
 418145

 Seq. ID
 uC-osroM202028h06a1

 Method
 BLASTX

 NCBI GI
 g4158221

BLAST score 171
E value 1.0e-24
Match length 61
% identity 92

NCBI Description (Y18624) reversibly glycosylated polypeptide [Oryza sativa]

Seq. No. 418146

Seq. ID uC-osroM202028h06b1

Method BLASTX
NCBI GI g3646373
BLAST score 608
E value 8.0e-65
Match length 127
% identity 96

NCBI Description (AJ011078) RGP1 protein [Oryza sativa]

Seq. No. 418147

Seq. ID uC-osroM202028h10b1

Method BLASTX
NCBI GI g2288999
BLAST score 309
E value 3.0e-28
Match length 102
% identity 55

NCBI Description (AC002335) electron transfer flavoprotein ubiquinone

oxidoreductase isolog [Arabidopsis thaliana]

Seq. No. 418148

Seq. ID uC-osroM202029a03a1

Method BLASTX
NCBI GI g3193287
BLAST score 209
E value 2.0e-16
Match length 152
% identity 35

NCBI Description (AF069298) Arabidopsis predicted protein of unknown function T10P11.19 (GB:AC002330) [Arabidopsis thaliana]

Seq. No. 418149

Seq. ID uC-osroM202029a03b1

Method BLASTX
NCBI GI g3892054
BLAST score 205
E value 5.0e-16
Match length 56
% identity 64

NCBI Description (AC002330) putative glycosyltransferase [Arabidopsis

thaliana]

```
Seq. No.
                  418150
Seq. ID
                  uC-osroM202029a05b1
                  BLASTX
Method
NCBI GI
                  g4538967
BLAST score
                  521
E value
                  4.0e-53
Match length
                  151
                  72
% identity
NCBI Description (AL049488) major intrinsic protein (MIP)-like [Arabidopsis
                  thaliana]
                  418151
Seq. No.
Seq. ID
                  uC-osroM202029a06a1
                  BLASTX
Method
NCBI GI
                  g2244797
BLAST score
                  286
E value
                  2.0e-25
Match length
                  118
                  51
% identity
NCBI Description (Z97336) hypothetical protein [Arabidopsis thaliana]
                  418152
Seq. No.
Seq. ID
                  uC-osroM202029a08a1
Method
                  BLASTX
NCBI GI
                  g4191782
                  293
BLAST score
E value
                  3.0e-26
                  78
Match length
% identity
                  67
NCBI Description (AC005917) WD-40 repeat protein [Arabidopsis thaliana]
Seq. No.
                  418153
Seq. ID
                  uC-osroM202029a08b1
Method
                  BLASTX
NCBI GI
                  g5123567
BLAST score
                  621
E value
                  1.0e-64
Match length
                  173
% identity
                  69
NCBI Description (AL079344) WD-40 repeat-like protein [Arabidopsis thaliana]
Seq. No.
                  418154
Seq. ID
                  uC-osroM202029a09b1
Method
                  BLASTX
NCBI GI
                  q4689473
BLAST score
                  230
E value
                  7.0e-19
Match length
                  119
% identity
NCBI Description
                  (AC007213) putative receptor protein kinase [Arabidopsis
                  thaliana]
Seq. No.
                  418155
Seq. ID
                  uC-osroM202029a10b1
Method
                  BLASTX
NCBI GI
                  g1352830
BLAST score
                  799
```



1.0e-85 E value Match length 171 % identity 89

VACUOLAR ATP SYNTHASE CATALYTIC SUBUNIT A (V-ATPASE 69 KD NCBI Description

SUBUNIT) >gi 1049253 (U36436) vacuolar ATPase 69 kDa

subunit [Zea mays]

418156 Seq. No.

uC-osroM202029a11a1 Seq. ID

BLASTN Method NCBI GI q2773153 BLAST score 310 1.0e-174 E value 314 Match length 100 % identity

NCBI Description Oryza sativa abscisic acid- and stress-inducible protein

(Asr1) mRNA, complete cds

Seq. No. 418157

Seq. ID uC-osroM202029a11b1

BLASTX Method NCBI GI g2773154 BLAST score 317 E value 4.0e-29 Match length 133 50 % identity

NCBI Description (AF039573) abscisic acid- and stress-inducible protein

[Oryza sativa]

418158 Seq. No.

Seq. ID uC-osroM202029b01a1

Method BLASTX NCBI GI q1203832 BLAST score 309 3.0e-28 E value 69 Match length

% identity

NCBI Description (U46003) beta-D-glucan exohydrolase, isoenzyme ExoII

[Hordeum vulgare] >gi 1588407 prf 2208395A beta-D-glucan

ر پيم سير

exohydrolase [Hordeum vulgare]

Seq. No. 418159

Seq. ID uC-osroM202029b01b1

Method BLASTX NCBI GI q1203832 BLAST score 286 E value 1.0e-25 Match length 79 % identity 80

NCBI Description (U46003) beta-D-glucan exohydrolase, isoenzyme ExoII

[Hordeum vulgare] >gi 1588407 prf 2208395A beta-D-glucan

exohydrolase [Hordeum vulgare]

Seq. No. 418160

Seq. ID uC-osroM202029b03a1

Method BLASTX NCBI GI g480618

NCBI GI

BLAST score

```
BLAST score
                  4.0e-15
E value
Match length
                  106
% identity
                  48
NCBI Description ATAF1 protein - Arabidopsis thaliana (fragment)
                  >gi_1345506_emb_CAA52771 (X74755) ATAF1 [Arabidopsis
                  thaliana]
                  418161
Seq. No.
Seq. ID
                  uC-osroM202029b03b1
Method
                  BLASTX
NCBI GI
                  q480618
BLAST score
                  526
E value
                  1.0e-53
                  105
Match length
                  93
% identity
NCBI Description ATAF1 protein - Arabidopsis thaliana (fragment)
                  >gi 1345506 emb CAA52771 (X74755) ATAF1 [Arabidopsis
                  thaliana]
Seq. No.
                  418162
Seq. ID
                  uC-osroM202029b04a1
Method
                  BLASTX
NCBI GI
                  g3047096
BLAST score
                  156
E value
                  3.0e-10
Match length
                  102
% identity
                  34
NCBI Description (AF058826) similar to eukaryotic protein kinase domains
                  (Pfam: pkinase.hmm, score: 189.74) [Arabidopsis thaliana]
                  418163
Seq. No.
Seq. ID
                  uC-osroM202029b04b1
Method
                  BLASTX
NCBI GI
                  g3047096
BLAST score
                  193
E value
                  1.0e-14
Match length
                  113
% identity
                  43
NCBI Description (AF058826) similar to eukaryotic protein kinase domains
                  (Pfam: pkinase.hmm, score: 189.74) [Arabidopsis thaliana]
Seq. No.
                  418164
                  uC-osroM202029b05a1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4874306
BLAST score
                  236
E value
                  1.0e-19
Match length
                  78
                  59
% identity
NCBI Description (AC006053) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  418165
                  uC-osroM202029b05b1
Seq. ID
Method
                  BLASTX
```

54768

q4874306

```
E value
                  2.0e-29
Match length
                  113
% identity
                  60
NCBI Description (AC006053) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  418166
                  uC-osroM202029b06a1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4874306
BLAST score
                  236
                  1.0e-19
E value
                  78
Match length
% identity
                  59
NCBI Description (AC006053) hypothetical protein [Arabidopsis thaliana]
                  418167
Seq. No.
Seq. ID
                  uC-osroM202029b06b1
Method
                  BLASTX
NCBI GI
                  g4874306
BLAST score
                  317
E value
                  4.0e-29
Match length
                  109
% identity
                  62
NCBI Description (AC006053) hypothetical protein [Arabidopsis thaliana]
                  418168
Seq. No.
Seq. ID
                  uC-osroM202029b07a1
Method
                  BLASTX
                  q3377841
NCBI GI
BLAST score
                  356
                  1.0e-33
E value
                  78
Match length
% identity
NCBI Description (AF075598) contains similarity to phosphofructokinases
                  (Pfam; PFK.hmm, score; 36.60) [Arabidopsis thaliana]
Seq. No.
                  418169
Seq. ID
                  uC-osroM202029b07b1
Method
                  BLASTX
NCBI GI
                  g3790100
BLAST score
                  390
E value
                  2.0e-49
Match length
                  130
% identity
                  77
NCBI Description (AF095520) pyrophosphate-dependent phosphofructokinase beta
                  subunit [Citrus X paradisi]
Seq. No.
                  418170
                  uC-osroM202029b08b1
Seq. ID
                  BLASTX
Method
NCBI GI
                  g445612
BLAST score
                  485
E value
                  9.0e-49
Match length
                  125
% identity
                  74
NCBI Description ribosomal protein S19 [Solanum tuberosum]
```



```
418171
Seq. No.
Seq. ID
                   uC-osroM202029b09a1
Method
                  BLASTX
NCBI GI
                  g861170
BLAST score
                   311
                   2.0e-28
E value
Match length
                  64
% identity
                   92
NCBI Description (X03697) heat shock protein 70 [Zea mays]
Seq. No.
                   418172
                   uC-osroM202029b09b1
Seq. ID
Method
                  BLASTX
NCBI GI
                   g123620
```

BLAST score 610 E value 2.0e-63 Match length 124 % identity 94

NCBI Description HEAT SHOCK COGNATE 70 KD PROTEIN 2 >gi 100224 pir S14950

heat shock cognate protein 70 - tomato

>qi 19258 emb CAA37971 (X54030) heat shock protein cognate

70 [Lycopersicon esculentum]

Seq. No. 418173

Seq. ID uC-osroM202029b11a1

Method BLASTX NCBI GI q3377841 BLAST score 323 8.0e-30 E value Match length 75 83 % identity

NCBI Description (AF075598) contains similarity to phosphofructokinases (Pfam; PFK.hmm, score; 36.60) [Arabidopsis thaliana]

Seq. No. 418174

Seq. ID uC-osroM202029b11b1

BLASTX Method NCBI GI g3790100 BLAST score 430 E value 4.0e-52 Match length 134 % identity

NCBI Description (AF095520) pyrophosphate-dependent phosphofructokinase beta

subunit [Citrus X paradisi]

418175 Seq. No.

uC-osroM202029b12a1 Seq. ID

BLASTX Method NCBI GI q464986 BLAST score 464 2.0e-46 E value Match length 96 89 % identity

NCBI Description UBIQUITIN-CONJUGATING ENZYME E2-17 KD 9 (UBIQUITIN-PROTEIN

LIGASE 9) (UBIQUITIN CARRIER PROTEIN 9) (UBCAT4B) >gi 421857 pir S32674 ubiquitin--protein ligase (EC

6.3.2.19) UBC9 - Arabidopsis thaliana



>qi 297884 emb CAA78714 (Z14990) ubiquitin conjugating enzyme homolog [Arabidopsis thaliana] >gi 349211 (L00639) ubiquitin conjugating enzyme [Arabidopsis thaliana] >gi 600391_emb_CAA51201_ (X72626) ubiquitin conjugating enzyme E2 [Arabidopsis thaliana] >gi_4455355_emb_CAB36765.1 (AL035524) ubiquitin-protein ligase UBC9 [Arabidopsis thaliana]

Seq. No. 418176

Seq. ID uC-osroM202029b12b1

BLASTX Method NCBI GI q464986 BLAST score 744 E value 4.0e-79 147 Match length 93 % identity

UBIQUITIN-CONJUGATING ENZYME E2-17 KD 9 (UBIQUITIN-PROTEIN NCBI Description

LIGASE 9) (UBIQUITIN CARRIER PROTEIN 9) (UBCAT4B) >gi_421857_pir__S32674 ubiquitin--protein ligase (EC 6.3.2.19) UBC9 - Arabidopsis thaliana

>gi_297884_emb_CAA78714_ (Z14990) ubiquitin conjugating enzyme homolog [Arabidopsis thaliana] >gi 349211 (L00639) ubiquitin conjugating enzyme [Arabidopsis thaliana] >gi 600391 emb CAA51201 (X72626) ubiquitin conjugating

enzyme E2 [Arabidopsis thaliana]

>qi 4455355 emb CAB36765.1 (AL035524) ubiquitin-protein

ligase UBC9 [Arabidopsis thaliana]

Seq. No. 418177

Seq. ID uC-osroM202029c03a1

Method BLASTX NCBI GI g2146774 BLAST score 303 E value 2.0e-27 87 Match length 70 % identity

NCBI Description serine acetyltransferase (EC 2.3.1.30) Sat-52 - Arabidopsis

thaliana >gi 905391 (U30298) serine acetyltransferase

[Arabidopsis thaliana]

Seq. No. 418178

Seq. ID uC-osroM202029c04a1

Method BLASTX NCBI GI q4587989 BLAST score 245 1.0e-20 E value 123 Match length % identity 49

NCBI Description (AF085279) hypothetical Cys-3-His zinc finger protein

[Arabidopsis thaliana]

Seq. No. 418179

Seq. ID uC-osroM202029c04b1

Method BLASTX NCBI GI g1871192 BLAST score 502 7.0e-51 E value

Match length 107 % identity 79

NCBI Description (U90439) Cys3His zinc finger protein isolog [Arabidopsis

thaliana]

Seq. No. 418180

Seq. ID uC-osroM202029c05a1

Method BLASTX
NCBI GI g2642448
BLAST score 285
E value 2.0e-25
Match length 71
% identity 83

NCBI Description (AC002391) hypothetical protein [Arabidopsis thaliana]

>gi 3169187 gb_AAC17830.1_ (AC004401) hypothetical protein

[Arabidopsis thaliana]

Seq. No. 418181

Seq. ID uC-osroM202029c05b1

Method BLASTX
NCBI GI g2642448
BLAST score 171
E value 6.0e-12
Match length 124
% identity 39

NCBI Description (AC002391) hypothetical protein [Arabidopsis thaliana]

>gi 3169187 gb AAC17830.1 (AC004401) hypothetical protein

[Arabidopsis thaliana]

Seq. No. 418182

Seq. ID uC-osroM202029c06a1

Method BLASTX
NCBI GI g584861
BLAST score 198
E value 3.0e-15
Match length 72
% identity 54

NCBI Description CYTOCHROME P450 71A2 (CYPLXXIA2) (P-450EG4)

>gi_480396_pir__S36806 cytochrome P450 71A2 - eggplant
>gi_408140_emb_CAA50645_ (X71654) P450 hydroxylase [Solanum melongena] >gi_441185_dbj_BAA03635_ (D14990) Cytochrome

P-450EG4 [Solanum melongena]

Seq. No. 418183

Seq. ID uC-osroM202029c06b1

Method BLASTX
NCBI GI g5915838
BLAST score 184
E value 2.0e-13
Match length 112
% identity 30

NCBI Description CYTOCHROME P450 71D9 (P450 CP3) >gi 3334661 emb CAA71514

(Y10490) putative cytochrome P450 [Glycine max]

Seq. No. 418184

Seq. ID uC-osroM202029c07b1

Method BLASTX

```
q6006373
NCBI GI
BLAST score
                  421
E value
                  3.0e-41
Match length
                  133
% identity
                  (AP000559) Similar to NAM like protein (AC005310) [Oryza
NCBI Description
                  sativa]
Seq. No.
                  418185
Seq. ID
                  uC-osroM202029c08b1
Method
                  BLASTX
NCBI GI
                  q1084461
BLAST score
                  437
E value
                  4.0e-43
Match length
                  129
% identity
                  69
NCBI Description RCc3 protein - rice >gi 786132 (L27208) RCc3 [Oryza sativa]
Seq. No.
                  418186
                  uC-osroM202029c09a1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g129591
BLAST score
                  345
E value
                  2.0e-32
Match length
                  64
% identity
                  100
NCBI Description PHENYLALANINE AMMONIA-LYASE >qi 295824 emb CAA34226
                  (X16099) phenylalanine ammonia-lyase [Oryza sativa]
Seq. No.
                  418187
                  uC-osroM202029c09b1
Seq. ID
                  BLASTX
Method
NCBI GI
                  g82496
BLAST score
                  674
E value
                  6.0e-71
Match length
                  152
                  87
% identity
NCBI Description phenylalanine ammonia-lyase (EC 4.3.1.5) - rice
Seq. No.
                  418188
Seq. ID
                  uC-osroM202029c10a1
                  BLASTX
Method
NCBI GI
                  g4262167
BLAST score
                  288
                  1.0e-25
E value
Match length
                  158
% identity
                  44
NCBI Description (AC005275) putative LRR receptor-linked protein kinase
                  [Arabidopsis thaliana]
Seq. No.
                  418189
                  uC-osroM202029c10b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q5734735
BLAST score
                  258
E value
                  3.0e-22
Match length
                  103
```

Seq. No.

418195

```
% identity
NCBI Description (AC007259) Similar to protein kinases [Arabidopsis
                  thaliana]
                  418190
Seq. No.
Seq. ID
                  uC-osroM202029c11a1
Method
                  BLASTX
NCBI GI
                  q3746431
BLAST score
                  396
E value
                  2.0e-38
                  76
Match length
% identity
                  99
NCBI Description (AF038585) pyruvate dehydrogenase kinase isoform 1; PDK1
                  [Zea mays]
                  418191
Seq. No.
Seq. ID
                  uC-osroM202029c12a1
Method
                  BLASTX
NCBI GI
                  q4914332
BLAST score
                  149
E value
                  2.0e-09
Match length
                  39
% identity
                  77
NCBI Description (AC005489) F14N23.18 [Arabidopsis thaliana]
                  418192
Seq. No.
Seq. ID
                  uC-osroM202029c12b1
Method
                  BLASTX
NCBI GI
                  g4914332
BLAST score
                  390
                  1.0e-37
E value
                  176
Match length
% identity
                  49
NCBI Description (AC005489) F14N23.18 [Arabidopsis thaliana]
Seq. No.
                  418193
Seq. ID
                  uC-osroM202029d02b1
Method
                  BLASTX
NCBI GI
                  g3236250
BLAST score
                  238
E value
                  9.0e-20
Match length
                  43
% identity
NCBI Description (AC004684) hypothetical protein [Arabidopsis thaliana]
                  418194
Seq. No.
                  uC-osroM202029d06a1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1703447
BLAST score
                  466
E value
                  1.0e-46
Match length
                  158
% identity
                  69
NCBI Description L-ASPARAGINASE (L-ASPARAGINE AMIDOHYDROLASE) >gi 496102
                  (L19141) L-asparaginase [Lupinus albus]
```



Seq. ID uC-osroM202029d06b1

Method BLASTX
NCBI GI g1703446
BLAST score 550
E value 2.0e-56
Match length 169
% identity 69

NCBI Description L-ASPARAGINASE (L-ASPARAGINE AMIDOHYDROLASE)

>gi_1076292_pir__S53127 asparaginase - Arabidopsis thaliana >gi_735918 emb_CAA84367 (Z34884) asparaginase [Arabidopsis

thaliana]

Seq. No. 418196

Seq. ID uC-osroM202029d07b1

Method BLASTX
NCBI GI g1084461
BLAST score 452
E value 7.0e-45
Match length 133
% identity 69

NCBI Description RCc3 protein - rice >gi_786132 (L27208) RCc3 [Oryza sativa]

Seq. No. 418197

Seq. ID uC-osroM202029d10a1

Method BLASTX
NCBI GI g4158219
BLAST score 406
E value 1.0e-39
Match length 101
% identity 79

NCBI Description (Y18623) amylogenin [Oryza sativa]

Seq. No. 418198

Seq. ID uC-osroM202029d10b1

Method BLASTX
NCBI GI g4158219
BLAST score 799
E value 1.0e-85
Match length 158
% identity 98

NCBI Description (Y18623) amylogenin [Oryza sativa]

Seq. No. 418199

Seq. ID uC-osroM202029d11a1

Method BLASTN
NCBI GI g5922603
BLAST score 296
E value 1.0e-165
Match length 406
% identity 100

NCBI Description Oryza sativa genomic DNA, chromosome 1, clone:P0705D01

Seq. No. 418200

Seq. ID uC-osroM202029d11b1

Method BLASTN
NCBI GI g5922603
BLAST score 369

BLAST score

339

```
E value
                  0.0e + 00
                  481
Match length
                  100
% identity
NCBI Description Oryza sativa genomic DNA, chromosome 1, clone:P0705D01
                  418201
Seq. No.
Seq. ID
                  uC-osroM202029d12a1
                  BLASTX
Method
                  g5441892
NCBI GI
                  227
BLAST score
                  1.0e-18
E value
                  43
Match length
                  100
% identity
                  (AP000367) ESTs
NCBI Description
                  C96653(C10531), C96654(C10531), C28571(C61641) correspond to
                  a region of the predicted gene.; Similar to citrate
                  synthetase. (AC004521) [Oryza sativa]
                  418202
Seq. No.
                  uC-osroM202029d12b1
Seq. ID
Method .
                  BLASTX
NCBI GI
                  q5441892
BLAST score
                  754
E value
                  2.0e-80
Match length
                  145
                  99
% identity
                  (AP000367) ESTs
NCBI Description
                  C96653(C10531), C96654(C10531), C28571(C61641) correspond to
                  a region of the predicted gene.; Similar to citrate
                  synthetase. (AC004521) [Oryza sativa]
                  418203
Seq. No.
Seq. ID
                  uC-osroM202029e04b1
                  BLASTX
Method
NCBI GI
                  g4490331
BLAST score
                  422
E value
                  2.0e-41
                  103
Match length
% identity
                  81
NCBI Description (AL035656) hypothetical protein [Arabidopsis thaliana]
                  418204
Seq. No.
Seq. ID
                  uC-osroM202029e05a1
Method
                  BLASTX
NCBI GI
                  q4204278
BLAST score
                  177
                  1.0e-12
E value
                  47
Match length
% identity
                  (AC004146) putative Cytochrome P450 protein [Arabidopsis
NCBI Description
                  thaliana]
                  418205
Seq. No.
Seq. ID
                  uC-osroM202029e06a1
Method
                  BLASTX
NCBI GI
                  q1173137
```



E value 1.0e-31 Match length 71 % identity 93

NCBI Description DNA-DIRECTED RNA POLYMERASE II 19 KD POLYPEPTIDE (RNA POLYMERASE II SUBUNIT 5) >gi_322700_pir__B44457 RNA

polymerase II fifth largest subunit - Glycine max=soybeans

>gi_170052 (M90504) RNA polymerase II [Glycine max]

Seq. No. 418206

Seq. ID uC-osroM202029e06b1

Method BLASTX
NCBI GI g1173137
BLAST score 783
E value 1.0e-83
Match length 164
% identity 90

NCBI Description DNA-DIRECTED RNA POLYMERASE II 19 KD POLYPEPTIDE (RNA POLYMERASE II SUBUNIT 5) >gi 322700_pir__B44457 RNA

polymerase II fifth largest subunit - Glycine max=soybeans

>gi_170052 (M90504) RNA polymerase II [Glycine max]

Seq. No. 418207

Seq. ID uC-osroM202029e07a1

Method BLASTX
NCBI GI g4580515
BLAST score 446
E value 3.0e-44
Match length 155
% identity 55

NCBI Description (AF036301) scarecrow-like 3 [Arabidopsis thaliana]

Seq. No. 418208

Seq. ID uC-osroM202029e08a1

Method BLASTX
NCBI GI g2351107
BLAST score 221
E value 7.0e-18
Match length 79
% identity 52

NCBI Description (D14057) bromelain [Ananas comosus]

Seq. No. 418209

Seq. ID uC-osroM202029e08b1

Method BLASTX
NCBI GI g1323748
BLAST score 245
E value 1.0e-20
Match length 133
% identity 44

NCBI Description (U32430) thiol protease [Triticum aestivum]

Seq. No. 418210

Seq. ID uC-osroM202029e11a1

Method BLASTX
NCBI GI g4008006
BLAST score 262
E value 1.0e-22



Match length 129 % identity 43

NCBI Description (AF084034) receptor-like protein kinase [Arabidopsis

thaliana]

Seq. No. 418211

Seq. ID uC-osroM202029e12a1

Method BLASTN
NCBI GI g6016845
BLAST score 380
E value 0.0e+00
Match length 408
% identity 98

NCBI Description Oryza sativa genomic DNA, chromosome 1, clone:P0711E10

Seq. No. 418212

Seq. ID uC-osroM202029e12b1

Method BLASTX
NCBI GI g5922624
BLAST score 429
E value 4.0e-42
Match length 124
% identity 75

NCBI Description (AP000492) ESTs C97742(C62458), AU078102(C62458) correspond

to a region of the predicted gene.; similar to syntaxin

related protein AtVam3p (U88045) [Oryza sativa]

>gi_6016857_dbj_BAA85200.1_ (AP000570) ESTs C97742(C62458),AU078102(C62458) correspond to a region of

the predicted gene.; Similar to syntaxin related protein

AtVam3p (U88045) [Oryza sativa]

Seq. No. 418213

Seq. ID uC-osroM202029f04a1

Method BLASTX
NCBI GI g1172553
BLAST score 225
E value 2.0e-18
Match length 82
% identity 54

NCBI Description OUTER MITOCHONDRIAL MEMBRANE PROTEIN PORIN

(VOLTAGE-DEPENDENT ANION-SELECTIVE CHANNEL PROTEIN) (VDAC) >gi_456672_emb_CAA54788_ (X77733) voltage dependent anion

channel (VDAC) [Triticum aestivum]

Seq. No. 418214

Seq. ID uC-osroM202029f04b1

Method BLASTX
NCBI GI g1172556
BLAST score 396
E value 2.0e-38
Match length 166
% identity 49

NCBI Description 36 KD OUTER MITOCHONDRIAL MEMBRANE PROTEIN PORIN

(VOLTAGE-DEPENDENT ANION-SELECTIVE CHANNEL PROTEIN) (VDAC) (POM 36) >gi_629729_pir__S46925 porin II, 36K - potato >gi_1076681_pir_B55364 porin (clone pPOM 36.2) - potato mitochondrion >gi_515360_emb_CAA56600_ (X80387) 36kDA porin

II [Solanum tuberosum]

Seq. No. 418215

Seq. ID uC-osroM202029f05b1

Method BLASTX
NCBI GI g5031275
BLAST score 567
E value 4.0e-59
Match length 161
% identity 68

NCBI Description (AF139496) unknown [Prunus armeniaca]

Seq. No. 418216

Seq. ID uC-osroM202029f06a1

Method BLASTX
NCBI GI g4314378
BLAST score 175
E value 2.0e-12
Match length 75
% identity 47

NCBI Description (AC006232) putative lipase [Arabidopsis thaliana]

>gi_5306262_gb_AAD41994.1_AC006233 5 (AC006233) putative

lipase [Arabidopsis thaliana]

Seq. No. 418217

Seq. ID uC-osroM202029f06b1

Method BLASTX
NCBI GI g5734634
BLAST score 188
E value 4.0e-14
Match length 72
% identity 57

NCBI Description (AP000391) Similar to putative lipase (AC006232) [Oryza

satival

Seq. No. 418218

Seq. ID uC-osroM202029f07b1

Method BLASTX
NCBI GI g4522009
BLAST score 374
E value 1.0e-35
Match length 131
% identity 58

NCBI Description (AC007069) unknown protein [Arabidopsis thaliana]

Seq. No. 418219

Seq. ID uC-osroM202029f08b1

Method BLASTX
NCBI GI g2244797
BLAST score 258
E value 4.0e-22
Match length 156
% identity 40

NCBI Description (Z97336) hypothetical protein [Arabidopsis thaliana]

Seq. No. 418220

Seq. ID uC-osroM202029f10a1

```
Method
                  BLASTX
NCBI GI
                  g3980396
BLAST score
                  254
E value
                  1.0e-21
                  50
Match length
                  86
% identity
NCBI Description (AC004561) putative C-4 sterol methyl oxidase [Arabidopsis
                  thaliana]
Seq. No.
                  418221
Seq. ID
                  uC-osroM202029f10b1
                  BLASTX
Method
NCBI GI
                  g3980396
BLAST score
                  538
E value
                  6.0e-55
Match length
                  139
                  65
% identity
NCBI Description (AC004561) putative C-4 sterol methyl oxidase [Arabidopsis
                  thaliana]
Seq. No.
                  418222
Seq. ID
                  uC-osroM202029f11a1
Method
                  BLASTX
NCBI GI
                  g3935181
BLAST score
                  452
E value
                  6.0e-45
Match length
                  97
                  86
% identity
NCBI Description (AC004557) F17L21.24 [Arabidopsis thaliana]
Seq. No.
                  418223
                  uC-osroM202029f11b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3935181
BLAST score
                  370
E value
                  3.0e-35
Match length
                  78
% identity
                  83
NCBI Description (AC004557) F17L21.24 [Arabidopsis thaliana]
Seq. No.
                  418224
Seq. ID
                  uC-osroM202029f12a1
Method
                  BLASTN
NCBI GI
                  g2773153
BLAST score
                  341
E value
                  0.0e + 00
Match length
                  469
% identity
                  93
NCBI Description Oryza sativa abscisic acid- and stress-inducible protein
                  (Asr1) mRNA, complete cds
```

Seq. No. 418225

Seq. ID uC-osroM202029f12b1

Method BLASTX
NCBI GI g2773154
BLAST score 364
E value 1.0e-34



```
Match length
                  138
% identity
NCBI Description (AF039573) abscisic acid- and stress-inducible protein
                  [Oryza sativa]
Seq. No.
                  418226
Seq. ID
                  uC-osroM202029g01a1
                  BLASTX
Method
NCBI GI
                  g585338
BLAST score
                  529
E value
                  6.0e-54
Match length
                  103
% identity
                  99
NCBI Description ADENYLATE KINASE B (ATP-AMP TRANSPHOSPHORYLASE)
                  >gi 391879 dbj BAA01181 (D10335) adenylate kinase-b [Oryza
                  sativa]
                  418227
Seq. No.
Seq. ID
                  uC-osroM202029g01b1
Method
                  BLASTX
NCBI GI
                  g585338
BLAST score
                  664
E value
                  8.0e-70
Match length
                  142
                  93
% identity
NCBI Description ADENYLATE KINASE B (ATP-AMP TRANSPHOSPHORYLASE)
                  >gi_391879_dbj_BAA01181_ (D10335) adenylate kinase-b [Oryza
                  satīva]
                  418228
Seq. No.
Seq. ID
                  uC-osroM202029g02a1
Method
                  BLASTX
NCBI GI
                  q123593
BLAST score
                  486
                  8.0e-53
E value
                  124
Match length
% identity
                  81
NCBI Description HEAT SHOCK 70 KD PROTEIN >gi 82697 pir A25089 heat shock
                  protein 70 - maize
Seq. No.
                  418229
Seq. ID
                  uC-osroM202029q02b1
Method
                  BLASTX
NCBI GI
                  g123620
BLAST score
                  592
E value
                  3.0e-61
Match length
                  120
% identity
                  93
NCBI Description HEAT SHOCK COGNATE 70 KD PROTEIN 2 >gi 100224 pir S14950
```

heat shock cognate protein 70 - tomato

>gi 19258 emb CAA37971 (X54030) heat shock protein cognate

70 [Lycopersicon esculentum]

Seq. No. 418230

uC-osroM202029g03a1 Seq. ID

Method BLASTX NCBI GI g4574139

NCBI Description

```
BLAST score
                  386
E value
                  3.0e-37
                  94
Match length
                  87
% identity
NCBI Description (AF073697) cysteine synthase [Oryza sativa]
Seq. No.
                  418231
Seq. ID
                  uC-osroM202029g03b1
Method
                  BLASTX
NCBI GI
                  g4574139
BLAST score
                  464
E value
                  2.0e-46
Match length
                  121
                  81
% identity
NCBI Description (AF073697) cysteine synthase [Oryza sativa]
Seq. No.
                  418232
Seq. ID
                  uC-osroM202029g05a1
Method
                  BLASTX
NCBI GI
                  g2182267
BLAST score
                  314
E value
                  9.0e-29
                  74
Match length
% identity
                  82
NCBI Description (L37359) lipoxygenase [Hordeum vulgare]
                  418233
Seq. No.
Seq. ID
                  uC-osroM202029g05b1
Method
                  BLASTX
NCBI GI
                  g126401
BLAST score
                  598
E value
                  1.0e-65
Match length
                  177
% identity
                  72
NCBI Description LIPOXYGENASE L-2 >gi 100690 pir S23454 lipoxygenase (EC
                  1.13.11.12) L-2 - rice >gi 20267 emb CAA45738 (X64396)
                  lipoxygenase [Oryza sativa]
                  418234
Seq. No.
Seq. ID
                  uC-osroM202029g06b1
Method
                  BLASTX
NCBI GI
                  g2832660
BLAST score
                  331
                  8.0e-31
E value
Match length
                  118
% identity
                  51
NCBI Description (AL021710) lipase-like protein [Arabidopsis thaliana]
Seq. No.
                  418235
Seq. ID
                  uC-osroM202029g08b1
Method
                  BLASTX
NCBI GI
                  g2292907
BLAST score
                  328
E value
                  2.0e-30
Match length
                  109
% identity
```

54782

(Y10099) P-glycoprotein homologue [Hordeum vulgare]

```
Seq. No.
                  418236
Seq. ID
                  uC-osroM202029g09a1
Method
                  BLASTX
NCBI GI
                  g3641252
BLAST score
                  188
E value
                  5.0e-14
Match length
                  91
% identity
                  43
NCBI Description
                 (AF053127) leucine-rich receptor-like protein kinase [Malus
                  domestica]
Seq. No.
                  418237
Seq. ID
                  uC-osroM202029q09b1
Method
                  BLASTX
NCBI GI
                  g2160189
BLAST score
                  242
E value
                  3.0e-35
Match length
                  179
% identity
                  (AC000132) Similar to A. thaliana receptor-like protein
NCBI Description
                  kinase (gb_RLK5_ARATH). ESTs gb_ATTS0475,gb_ATTS4362 come
                  from this gene. [Arabidopsis thaliana]
Seq. No.
                  418238
                  uC-osroM202029q10a1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3023713
BLAST score
                  361
E value
                  3.0e-34
                  71
Match length
                  99
% identity
NCBI Description ENOLASE (2-PHOSPHOGLYCERATE DEHYDRATASE)
                  (2-PHOSPHO-D-GLYCERATE HYDRO-LYASE) (OSE1) >gi 780372
                  (U09450) enolase [Oryza sativa]
Seq. No.
                  418239
Seq. ID
                  uC-osroM202029g10b1
Method
                  BLASTX
NCBI GI
                  g3023713
BLAST score
                  785
E value
                  7.0e-84
                  161
Match length
% identity
                  96
NCBI Description ENOLASE (2-PHOSPHOGLYCERATE DEHYDRATASE)
                   (2-PHOSPHO-D-GLYCERATE HYDRO-LYASE) (OSE1) >gi 780372
                   (U09450) enolase [Oryza sativa]
                  418240
Seq. No.
                  uC-osroM202029g11b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3128208
BLAST score
                  269
E value
                  2.0e-23
Match length
                  102
% identity
NCBI Description (AC004077) hypothetical protein [Arabidopsis thaliana]
```

```
Seq. No.
                   418241
Seq. ID
                   uC-osroM202029g12b1
Method
                   BLASTX
NCBI GI
                   g2493809
BLAST score
                   147
E value
                   2.0e-09
Match length
                   98
% identity
                   42
NCBI Description COPROPORPHYRINOGEN III OXIDASE PRECURSOR
                   (COPROPORPHYRINOGENASE) (COPROGEN OXIDASE) >gi_1212994_emb_CAA58037_ (X82830) coproporphyrinogen
                   oxidase [Hordeum vulgare]
                   418242
Seq. No.
Seq. ID
                   uC-osroM202029h01a1
Method
                   BLASTX
NCBI GI
                   g123593
BLAST score
                   380
                   7.0e-37
E value
Match length
                   78
% identity
                   92
NCBI Description HEAT SHOCK 70 KD PROTEIN >gi 82697 pir A25089 heat shock
                   protein 70 - maize
                   418243
Seq. No.
Seq. ID
                   uC-osroM202029h01b1
                   BLASTX
Method
NCBI GI
                   g123620
                   573
BLAST score
E value
                   3.0e-59
Match length
                   116
                   93
% identity
NCBI Description HEAT SHOCK COGNATE 70 KD PROTEIN 2 >gi 100224 pir S14950
                   heat shock cognate protein 70 - tomato
                   >gi 19258 emb CAA37971 (X54030) heat shock protein cognate
                   70 [Lycopersicon esculentum]
                   418244
Seq. No.
Seq. ID
                   uC-osroM202029h04b1
                   BLASTX
Method
NCBI GI
                   q5081612
BLAST score
                   594
                   2.0e-61
E value
Match length
                   178
% identity
                   67
NCBI Description (AF136152) PUR alpha-1 [Arabidopsis thaliana]
Seq. No.
                   418245
Seq. ID
                   uC-osroM202029h05a1
Method
                   BLASTX
NCBI GI
                   q2832660
BLAST score
                   231
E value
                   5.0e-19
Match length
                   86
% identity
                   52
NCBI Description (AL021710) lipase-like protein [Arabidopsis thaliana]
```

Method

BLASTX

```
Seq. No.
                  418246
Seq. ID
                  uC-osroM202029h05b1
                  BLASTX
Method
NCBI GI
                  g2832660
BLAST score
                  376
E value
                  5.0e-36
Match length
                  141
                  51
% identity
NCBI Description (AL021710) lipase-like protein [Arabidopsis thaliana]
Seq. No.
                  418247
Seq. ID
                  uC-osroM202029h10a1
                  BLASTX
Method
NCBI GI
                  g3913181
BLAST score
                  384
E value
                  6.0e-37
Match length
                  97
                  80
% identity
NCBI Description CINNAMYL-ALCOHOL DEHYDROGENASE (CAD) >gi 2388662 (AF010290)
                  cinnamyl alcohol dehydrogenase [Lolium perenne]
Seq. No.
                  418248
Seq. ID
                  uC-osroM202029h10b1
Method
                  BLASTX
NCBI GI
                  q3341513
BLAST score
                  463
E value
                  3.0e-46
Match length
                  126
                  67
% identity
NCBI Description (AJ231135) cinnamyl alcohol dehydrogenase [Saccharum
                  officinarum]
Seq. No.
                  418249
Seq. ID
                  uC-osroM202029h11b1
Method
                  BLASTX
NCBI GI
                  q5107819
BLAST score
                  487
E value
                  5.0e-49
Match length
                  164
% identity
                  54
NCBI Description (AF149413) contains similarity to arabinosidase
                  [Arabidopsis thaliana]
Seq. No.
                  418250
Seq. ID
                  uC-osroM202030a02a1
Method
                  BLASTX
NCBI GI
                  q2459425
BLAST score
                  264
E value
                  7.0e-23
Match length
                  72
                  76
% identity
NCBI Description (AC002332) plastid protein [Arabidopsis thaliana]
Seq. No.
                  418251
                  uC-osroM202030a02b1
Seq. ID
```

Match length

106

```
q2459425
NCBI GI
BLAST score
                  219
E value
                  9.0e-18
                  56
Match length
                  73
% identity
NCBI Description (AC002332) plastid protein [Arabidopsis thaliana]
Seq. No.
                  418252
                  uC-osroM202030a06a1
Seq. ID
                  BLASTX
Method
NCBI GI
                  g82734
BLAST score
                  325
E value
                  4.0e-30
Match length
                  69
                  28
% identity
NCBI Description ubiquitin precursor - maize (fragment)
                  >gi_226763_prf__1604470A poly-ubiquitin [Zea mays]
Seq. No.
                  418253
Seq. ID
                  uC-osroM202030a06b1
Method
                  BLASTX
NCBI GI
                  g3126967
BLAST score
                  585
E value
                  1.0e-60
Match length
                  124
                  17
% identity
NCBI Description (AF061807) polyubiquitin [Elaeagnus umbellata]
Seq. No.
                  418254
Seq. ID
                  uC-osroM202030a07a1
Method
                  BLASTX
NCBI GI
                  g2832623
BLAST score
                  147
E value
                  4.0e-09
Match length
                  51
% identity
                  47
NCBI Description (AL021711) protein kinase-like protein [Arabidopsis
                  thaliana]
                  418255
Seq. No.
Seq. ID
                  uC-osroM202030a07b1
Method
                  BLASTX
NCBI GI
                  g2832623
BLAST score
                  214
E value
                  4.0e-17
Match length
                  68
                  57
% identity
NCBI Description (AL021711) protein kinase-like protein [Arabidopsis
                  thaliana]
Seq. No.
                  418256
                  uC-osroM202030a09a1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4336436
BLAST score
                  381
E value
                  1.0e-36
```

```
% identity
NCBI Description (AF092432) protein phosphatase type 2C [Lotus japonicus]
                  418257
Seq. No.
Seq. ID
                  uC-osroM202030a09b1
Method
                  BLASTX
                  g4336436
NCBI GI
BLAST score
                  297
E value
                  7.0e-27
Match length
                  94
% identity
NCBI Description (AF092432) protein phosphatase type 2C [Lotus japonicus]
Seq. No.
                  418258
Seq. ID
                  uC-osroM202030a10a1
Method
                  BLASTX
NCBI GI
                  g2130073
BLAST score
                  248
                  4.0e-30
E value
Match length
                  74
                  99
% identity
NCBI Description fructose-bisphosphate aldolase (EC 4.1.2.13) isoenzyme C-1,
                  cytosolic - rice >gi_786178_dbj_BAA08845_ (D50307) aldolase
                  C-1 [Oryza sativa] >gi_790970_dbj_BAA08830_ (D50301)
                  aldolase C-1 [Oryza sativa]
Seq. No.
                  418259
Seq. ID
                  uC-osroM202030a10b1
Method
                  BLASTX
NCBI GI
                  g2130073
BLAST score
                  687
E value
                  1.0e-72
Match length
                  133
% identity
                  100
NCBI Description fructose-bisphosphate aldolase (EC 4.1.2.13) isoenzyme C-1,
                  cytosolic - rice >gi_786178_dbj_BAA08845_ (D50307) aldolase
                  C-1 [Oryza sativa] >gi_790970_dbj_BAA08830_ (D50301)
                  aldolase C-1 [Oryza sativa]
Seq. No.
                  418260
Seq. ID
                  uC-osroM202030a11a1
                  BLASTX
Method
NCBI GI
                  q5032258
BLAST score
                  160
E value
                  9.0e-11
Match length
                  52
% identity
NCBI Description
                  (AF126057) microtubule-associated protein [Arabidopsis
                  thaliana]
Seq. No.
                  418261
Seq. ID
                  uC-osroM202030a11b1
```

Method BLASTN

NCBI GI g425793 BLAST score 56 E value 1.0e-22 Match length 96

% identity 90

NCBI Description Rice mRNA for fructose-diphosphate aldolase (gene name

AD130), partial cds

Seq. No. 418262

Seq. ID uC-osroM202030a12a1

Method BLASTX
NCBI GI g2622714
BLAST score 201
E value 1.0e-15
Match length 123
% identity 37

NCBI Description (AE000918) phosphonopyruvate decarboxylase

[Methanobacterium thermoautotrophicum]

Seq. No. 418263

Seq. ID uC-osroM202030b03a1

Method BLASTX
NCBI GI g113178
BLAST score 174
E value 2.0e-12
Match length 77
% identity 38

NCBI Description ACYLAMINO-ACID-RELEASING ENZYME (ACYL-PEPTIDE HYDROLASE)

(APH) (ACYLAMINOACYL-PEPTIDASE) >gi_91923_pir__S07624 acylaminoacyl-peptidase (EC 3.4.19.1) - rat >gi_202932 (J04733) acyl-peptide hydrolase [Rattus norvegicus]

Seq. No. 418264

Seq. ID uC-osroM202030b03b1

Method BLASTX
NCBI GI g2244813
BLAST score 419
E value 4.0e-41
Match length 132
% identity 61

NCBI Description (Z97336) acylaminoacyl-peptidase like protein [Arabidopsis

thaliana]

Seq. No. 418265

Seq. ID uC-osroM202030b04b1

Method BLASTX
NCBI GI g2980802
BLAST score 221
E value 5.0e-18
Match length 106
% identity 47

NCBI Description (AL022197) transcriptional activator CBF1-like protein

[Arabidopsis thaliana]

Seq. No. 418266

Seq. ID uC-osroM202030b05a1

Method BLASTX
NCBI GI g1170937
BLAST score 255
E value 6.0e-22
Match length 46

NCBI GI

q584998

```
% identity
NCBI Description S-ADENOSYLMETHIONINE SYNTHETASE 1 (METHIONINE
                  ADENOSYLTRANSFERASE 1) (ADOMET SYNTHETASE 1)
                  >gi_450549_emb_CAA81481_ (Z26867) S-adenosyl methionine
                  synthetase [Oryza sativa]
Seq. No.
                  418267
Seq. ID
                  uC-osroM202030b05b1
Method
                  BLASTX
NCBI GI
                  g1170937
BLAST score
                  587
E value
                  8.0e-61
Match length
                  112
% identity
                  100
NCBI Description S-ADENOSYLMETHIONINE SYNTHETASE 1 (METHIONINE
                  ADENOSYLTRANSFERASE 1) (ADOMET SYNTHETASE 1)
                  >gi_450549 emb CAA81481 (Z26867) S-adenosyl methionine
                  synthetase [Oryza sativa]
Seq. No.
                  418268
Seq. ID
                  uC-osroM202030b06a1
Method
                  BLASTX
NCBI GI
                  g1723239
BLAST score
                  201
E value
                  2.0e-15
Match length
                  76
                  50
% identity
NCBI Description HYPOTHETICAL 35.7 KD PROTEIN C26A3.11 IN CHROMOSOME I
                  >gi_1177358_emb_CAA93234_ (Z69240) putative amidohydrolase
                  [Schizosaccharomyces pombe]
Seq. No.
                  418269
Seq. ID
                  uC-osroM202030b06b1
Method
                  BLASTX
NCBI GI
                  q1723239
BLAST score
                  241
E value
                  3.0e-20
Match length
                  145
% identity
                  37
NCBI Description HYPOTHETICAL 35.7 KD PROTEIN C26A3.11 IN CHROMOSOME I
                  >gi 1177358 emb CAA93234 (Z69240) putative amidohydrolase
                  [Schizosaccharomyces pombe]
Seq. No.
                  418270
Seq. ID
                  uC-osroM202030b07b1
Method
                  BLASTX
NCBI GI
                  q1321661
BLAST score
                  502
E value
                  7.0e-51
Match length
                  97
% identity
                  98
NCBI Description (D45423) ascorbate peroxidase [Oryza sativa]
Seq. No.
                  418271
Seq. ID
                  uC-osroM202030b08b1
Method
                  BLASTX
```

```
BLAST score
                  173
                  2.0e-12
E value
                  47
Match length
                  68
% identity
NCBI Description FLAVONOID 3',5'-HYDROXYLASE (F3'5'H) (CYTOCHROME P450 75A2)
                  (CYPLXXVA2) (P-450EG1) >gi 629713 pir S43342 flavonoid
                  hydroxylase cytochrome P450 - eggplant
                  >gi 395261 emb CAA50155 (X70824) flavonoid hydroxylase
                  (P450) [Solanum melongena]
                  418272
Seq. No.
                  uC-osroM202030b09b1
Seq. ID
                  BLASTX
Method
NCBI GI
                  g1592812
BLAST score
                  154
E value
                  4.0e-10
Match length
                  133
% identity
                  35
NCBI Description (X95957) 22 kDa polypeptide [Nicotiana tabacum]
Seq. No.
                  418273
                  uC-osroM202030b10b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1550738
BLAST score
                  211
E value
                  1.0e-16
                  122
Match length
% identity
                  44
NCBI Description
                 (Y08061) endomembrane-associated protein [Arabidopsis
                  thaliana] >gi_2982443_emb_CAA18251.1_ (AL022224)
                  endomembrane-associated protein [Arabidopsis thaliana]
                  418274
Seq. No.
Seq. ID
                  uC-osroM202030b11a1
Method
                  BLASTX
NCBI GI
                  q4538967
BLAST score
                  247
E value
                  6.0e-21
Match length
                  76
% identity
                  61
NCBI Description (AL049488) major intrinsic protein (MIP)-like [Arabidopsis
                  thaliana]
Seq. No.
                  418275
Seq. ID
                  uC-osroM202030c03a1
Method
                  BLASTN
NCBI GI
                  q2773153
BLAST score
                  393
E value
                  0.0e+00
Match length
                  401
```

% identity 100

NCBI Description Oryza sativa abscisic acid- and stress-inducible protein

(Asr1) mRNA, complete cds

418276 Seq. No.

Seq. ID uC-osroM202030c04a1

Method BLASTX

```
g1184112
NCBI GI
BLAST score
                  478
                  4.0e-48
E value
Match length
                  115
% identity
                  81
NCBI Description (U46138) Zn-induced protein [Oryza sativa]
                  418277
Seq. No.
                  uC-osroM202030c04b1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g6016845
BLAST score
                  169
E value
                  4.0e-90
Match length
                  277
% identity
                  97
NCBI Description Oryza sativa genomic DNA, chromosome 1, clone:P0711E10
Seq. No.
                  418278
                  uC-osroM202030c07a1
Seq. ID
Method
                  BLASTX
                  g4138912
NCBI GI
BLAST score
                  298
                  6.0e-27
E value
                  82
Match length
% identity
                  65
NCBI Description (AF059487) expansin precursor [Lycopersicon esculentum]
Seq. No.
                  418279
                  uC-osroM202030c10a1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2104536
BLAST score
                  485
E value
                  9.0e-49
Match length
                  171
% identity
                  53
NCBI Description (AF001308) predicted glycosyl transferase [Arabidopsis
                  thaliana]
                  418280
Seq. No.
Seq. ID
                  uC-osroM202030c12a1
Method
                  BLASTN
NCBI GI
                  g2331130
BLAST score
                  216
E value
                  1.0e-118
Match length
                  301
% identity
                  97
NCBI Description Oryza sativa glycine-rich protein (OSGRP1) mRNA, complete
Seq. No.
                  418281
Seq. ID
                  uC-osroM202030d03a1
Method
                  BLASTX
NCBI GI
                  a6094242
BLAST score
                  350
E value
                  6.0e-33
Match length
                  85
% identity
                  75
```



NCBI Description PUTATIVE SELENIUM-BINDING PROTEIN

>gi 2244759 emb CAB10182.1 (Z97335) selenium-binding

protein like [Arabidopsis thaliana]

Seq. No. 418282

Seq. ID uC-osroM202030d03b1

Method BLASTX
NCBI GI g6094242
BLAST score 312
E value 1.0e-28
Match length 72
% identity 76

NCBI Description PUTATIVE SELENIUM-BINDING PROTEIN

>gi_2244759_emb_CAB10182.1_ (Z97335) selenium-binding

protein like [Arabidopsis thaliana]

Seq. No. 418283

Seq. ID uC-osroM202030d05b1

Method BLASTX
NCBI GI g4835757
BLAST score 171
E value 5.0e-12
Match length 80
% identity 51

NCBI Description (AC007202) EST gb AA404917 comes from this gene.

[Arabidopsis thaliana]

Seq. No. 418284

Seq. ID uC-osroM202030d06a1

Method BLASTN
NCBI GI g1747295
BLAST score 45
E value 6.0e-16
Match length 69

% identity 91

NCBI Description Oryza sativa mRNA for vacuolar H+-pyrophosphatase, complete

cds

Seq. No. 418285

Seq. ID uC-osroM202030d06b1

Method BLASTX
NCBI GI g4966352
BLAST score 143
E value 9.0e-09
Match length 96
% identity 40

NCBI Description (AC006341) >F309.11 [Arabidopsis thaliana]

Seq. No.

Seq. ID uC-osroM202030d07b1

418286

Method BLASTX
NCBI GI g3941480
BLAST score 150
E value 1.0e-09
Match length 38
% identity 74

NCBI Description (AF062894) putative transcription factor [Arabidopsis

thaliana]

Seq. No. 418287

Seq. ID uC-osroM202030d10a1

Method BLASTX NCBI GI g2653446 BLAST score 331 E value 1.0e-30 Match length 65 % identity 97

NCBI Description (AB009077) proton pyrophosphatase [Vigna radiata]

Seq. No. 418288

Seq. ID uC-osroM202030d10b1

Method BLASTX NCBI GI q1747296 BLAST score 670 E value 1.0e-70 Match length 142 % identity 91

NCBI Description (D45384) vacuolar H+-pyrophosphatase [Oryza sativa] >gi_3298476_dbj_BAA31524_ (AB012766) ovp2 [Oryza sativa]

Seq. No. 418289

Seq. ID uC-osroM202030d11a1

Method BLASTX NCBI GI g1706328 BLAST score 657 E value 7.0e-69 Match length 124 % identity 100

NCBI Description PYRUVATE DECARBOXYLASE ISOZYME 2 (PDC) >gi_1009710 (U27350)

pyruvate decarboxylase 2 [Oryza sativa] >gi 1777455

(U38199) pyruvate decarboxylase 2 [Oryza sativa]

Seq. No. 418290

Seq. ID uC-osroM202030d11b1

Method BLASTX NCBI GI g1706331 BLAST score 284 E value 3.0e-25 Match length 73 % identity 78

NCBI Description PYRUVATE DECARBOXYLASE ISOZYME 3 (PDC) >gi_476284 (U07338)

pyruvate decarboxylase [Oryza sativa]

Seq. No. 418291

Seq. ID uC-osroM202030e03a1

Method BLASTX NCBI GI g2760837 BLAST score 317 E value 4.0e-29 Match length 101 % identity 52

NCBI Description (AC003105) putative cytochrome P450 [Arabidopsis thaliana]

Seq. No. 418292



Seq. ID uC-osroM202030e03b1 Method BLASTX NCBI GI g5734759 BLAST score 185 E value 1.0e-13 Match length 93 % identity 41 NCBI Description (AC007651) Similar to Cytochrome P450 [Arabidopsis thaliana] Seq. No. 418293 uC-osroM202030e04a1 Seq. ID Method BLASTX NCBI GI g5918016 BLAST score 148 E value 3.0e-09 Match length 57 % identity 53 NCBI Description (AL035525) myosin-like protein [Arabidopsis thaliana] Seq. No. 418294 Seq. ID uC-osroM202030e06a1 Method BLASTX g6063557 NCBI GI BLAST score 416 E value 1.0e-40 Match length 110 74 % identity NCBI Description (AP000615) similar to dJ522J7.2 (Z98885) [Oryza sativa] Seq. No. 418295 Seq. ID uC-osroM202030e08a1 Method BLASTX NCBI GI g3046693 BLAST score 432 E value 2.0e-42 Match length 121 % identity 63 NCBI Description (AL022140) receptor like protein (fragment) [Arabidopsis thaliana] Seq. No. 418296 Seq. ID uC-osroM202030e08b1 Method BLASTX NCBI GI q3046693 BLAST score 359 E value 4.0e-34 Match length 87 % identity 75

NCBI Description (AL022140) receptor like protein (fragment) [Arabidopsis

thaliana]

Seq. No. 418297

Seq. ID uC-osroM202030e09a1

Method BLASTX
NCBI GI g4586107
BLAST score 459

```
E value
                   9.0e-46
Match length
                  160
% identity
                  11
NCBI Description (AL049638) putative disease resistance protein [Arabidopsis
                  thaliana]
Seq. No.
                  418298
Seq. ID
                  uC-osroM202030e11a1
Method
                  BLASTX
NCBI GI
                  q4191780
BLAST score
                  173
E value
                  3.0e-12
Match length
                  41
% identity
                  71
NCBI Description (AC005917) putative cytokinin oxidase [Arabidopsis
                  thaliana]
Seq. No.
                  418299
Seq. ID
                  uC-osroM202030e11b1
Method
                  BLASTX
NCBI GI
                  g3341978
BLAST score
                  232
E value
                  3.0e-19
Match length
                  67
% identity
                  67
NCBI Description (AF044603) cytokinin oxidase [Zea mays]
Seq. No.
                  418300
Seq. ID
                  uC-osroM202030e12a1
Method
                  BLASTX
NCBI GI
                  q3550985
BLAST score
                  275
                  4.0e-24
E value
Match length
                  79
% identity
                  73
NCBI Description (AB010740) OsS5a [Oryza sativa]
Seq. No.
                  418301
Seq. ID
                  uC-osroM202030e12b1
Method
                  BLASTX
NCBI GI
                  q3550985
BLAST score
                  496
E value
                  4.0e-50
Match length
                  117
% identity
                  83
NCBI Description (AB010740) OsS5a [Oryza sativa]
Seq. No.
                  418302
                  uC-osroM202030f04a1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g585662
BLAST score
                  334
E value
                  4.0e-31
Match length
                  83
% identity
                  77
NCBI Description PEROXIDASE PRECURSOR >gi_303851 dbj BAA03911 (D16442)
                  peroxidase [Oryza sativa]
```

```
Seq. No.
                   418303
Seq. ID
                   uC-osroM202030f04b1
Method
                   BLASTX
NCBI GI
                   g585662
BLAST score
                   150
E value
                   1.0e-09
Match length
                   51
                   57
% identity
NCBI Description PEROXIDASE PRECURSOR >gi_303851_dbj_BAA03911_ (D16442)
                   peroxidase [Oryza sativa]
Seq. No.
                   418304
Seq. ID
                   uC-osroM202030f05b1
Method
                   BLASTX
NCBI GI
                   g5729707
BLAST score
                   146
E value
                   4.0e-09
Match length
                   73
% identity
                   44
NCBI Description (AC007927) unknown protein [Arabidopsis thaliana]
Seq. No.
                   418305
Seq. ID
                  uC-osroM202030f06a1
Method
                  BLASTX
NCBI GI
                   g4415931
BLAST score
                   319
E value
                   2.0e-29
Match length
                  138
% identity
                   48
                  (AC006418) unknown protein [Arabidopsis thaliana]
NCBI Description
                   >gi_4559393_gb_AAD23053.1_AC006526_18 (AC006526) unknown
                  protein [Arabidopsis thaliana]
Seq. No.
                  418306
Seq. ID
                  uC-osroM202030f06b1
Method
                  BLASTX
NCBI GI
                  g4415931
BLAST score
                  294
E value
                  2.0e-26
Match length
                  92
% identity
                  60
                  (AC006418) unknown protein [Arabidopsis thaliana]
NCBI Description
                  >gi_4559393_gb_AAD23053.1_AC006526_18 (AC006526) unknown
                  protein [Arabidopsis thaliana]
Seq. No.
                  418307
Seq. ID
                  uC-osroM202030f09a1
Method
                  BLASTX
NCBI GI
                  g3980397
BLAST score
                  357
E value
                  9.0e-34
Match length
                  161
% identity
                  47
NCBI Description
                  (AC004561) putative protein phosphatase 2C [Arabidopsis
```

thaliana]

Seq. No. 418308 Seq. ID uC-osroM202030f10a1 Method BLASTX NCBI GI q5802606 BLAST score 319 E value 2.0e-29 Match length 76 % identity 72 NCBI Description (AF174486) methylenetetrahydrofolate reductase [Zea mays] Seq. No. 418309 Seq. ID uC-osroM202030f10b1 Method BLASTX NCBI GI q5802606 BLAST score 553 7.0e-57 E value Match length 114 % identity 91 NCBI Description (AF174486) methylenetetrahydrofolate reductase [Zea mays] Seq. No. 418310 Seq. ID uC-osroM202030f12a1 Method BLASTX NCBI GI q70644 BLAST score 375 E value 7.0e-36 Match length 75 % identity 20 NCBI Description ubiquitin precursor - common sunflower (fragment) Seq. No. 418311 Seq. ID uC-osroM202030f12b1 Method BLASTX NCBI GI q418854 BLAST score 701 E value 3.0e-74Match length 142 % identity 18 NCBI Description ubiquitin precursor - parsley >gi_288112_emb_CAA45621 (X64344) polyubiquitin [Petroselinum crispum] >gi_288114_emb_CAA45622_ (X64345) polyubiquitin [Petroselinum crispum] Seq. No. 418312 Seq. ID uC-osroM202030g01a1

Method BLASTX
NCBI GI g3928543
BLAST score 145
E value 2.0e-11
Match length 154
% identity 29

NCBI Description (AB016819) UDP-glucose glucosyltransferase [Arabidopsis

thaliana]

Seq. No. 418313

Seq. ID uC-osroM202030q04a1

Method BLASTX

Method

NCBI GI

E value

BLAST score

BLASTX

235

g3123349

2.0e-19

NCBI GI q283008 BLAST score 242 E value 2.0e-20 Match length 49 % identity 96 NCBI Description sucrose synthase (EC 2.4.1.13) - rice >gi_20366_emb_CAA46017_ (X64770) sucrose synthase [Oryza sativa] Seq. No. 418314 Seq. ID uC-osroM202030q04b1 Method BLASTX NCBI GI g283008 BLAST score 612 E value 9.0e-64 Match length 136 % identity 89 NCBI Description sucrose synthase (EC 2.4.1.13) - rice >gi_20366_emb_CAA46017_ (X64770) sucrose synthase [Oryza sativa] Seq. No. 418315 Seq. ID uC-osroM202030g07a1 Method BLASTX NCBI GI g4586109 BLAST score 262 E value 1.0e-22 Match length 64 % identity NCBI Description (AL049638) putative protein [Arabidopsis thaliana] Seq. No. 418316 Seq. ID uC-osroM202030g08a1 Method BLASTX NCBI GI g4574139 BLAST score 620 E value 1.0e-64 Match length 126 % identity 100 NCBI Description (AF073697) cysteine synthase [Oryza sativa] Seq. No. 418317 Seq. ID uC-osroM202030g08b1 Method BLASTX NCBI GI q4574139 BLAST score 243 E value 1.0e-20 Match length 50 % identity 100 NCBI Description (AF073697) cysteine synthase [Oryza sativa] Seq. No. 418318 Seq. ID uC-osroM202030g09a1

```
Match length
                   63
% identity
                   71
NCBI Description (AJ005788) hypothetical protein [Cicer arietinum]
Seq. No.
                   418319
Seq. ID
                  uC-osroM202030g09b1
Method
                  BLASTX
NCBI GI
                  q2160166
BLAST score
                  366
E value
                   6.0e-35
Match length
                  137
% identity
                  57
NCBI Description (AC000132) No definition line found [Arabidopsis thaliana]
Seq. No.
                  418320
Seq. ID
                  uC-osroM202030g10b1
Method
                  BLASTX
NCBI GI
                  g5919185
BLAST score
                  290
E value
                  5.0e-26
Match length
                  92
% identity
                  61
NCBI Description (AF183809) arabinogalactan protein Pop14A9 [Populus alba x
                  Populus tremula]
Seq. No.
                  418321
Seq. ID
                  uC-osroM202030g11a1
Method
                  BLASTX
NCBI GI
                  q1350986
BLAST score
                  294
                  2.0e-26
E value
Match length
                  58
% identity
                  100
NCBI Description 40S RIBOSOMAL PROTEIN S3A (CYC07 PROTEIN)
                  >gi_483431_dbj_BAA05059_ (D26060) cyc07 [Oryza sativa]
Seq. No.
                  418322
Seq. ID
                  uC-osroM202030g11b1
Method
                  BLASTX
NCBI GI
                  g1350986
BLAST score
                  554
E value
                  6.0e-57
Match length
                  107
% identity
                  100
NCBI Description 40S RIBOSOMAL PROTEIN S3A (CYC07 PROTEIN)
                  >gi 483431 dbj BAA05059 (D26060) cyc07 [Oryza sativa]
Seq. No.
                  418323
Seq. ID
                  uC-osroM202030g12a1
Method
                  BLASTX
NCBI GI
                  g1350986
BLAST score
                  462
E value
```

% identity NCBI Description 40S RIBOSOMAL PROTEIN S3A (CYC07 PROTEIN)

5.0e-46

94

99

Match length

>gi_483431_dbj_BAA05059_ (D26060) cyc07 [Oryza sativa]

```
418324
Seq. No.
Seq. ID
                  uC-osroM202030g12b1
Method
                  BLASTX
NCBI GI
                  q1350986
BLAST score
                  548
E value
                  3.0e-56
Match length
                  106
% identity
                  100
NCBI Description 40S RIBOSOMAL PROTEIN S3A (CYC07 PROTEIN)
                  >gi_483431_dbj BAA05059 (D26060) cyc07 [Oryza sativa]
Seq. No.
                  418325
Seq. ID
                  uC-osroM202030h01b1
Method
                  BLASTX
NCBI GI
                  q3915029
BLAST score
                  615
E value
                  4.0e-64
Match length
                  120
% identity
                  97
NCBI Description ACYL-[ACYL-CARRIER PROTEIN] DESATURASE PRECURSOR
                  (STEAROYL-ACP DESATURASE) >gi_976257_dbj BAA07631 (D38753)
                  stearyl-ACP desaturase [Oryza sativa]
Seq. No.
                  418326
Seq. ID
                  uC-osroM202030h03b1
Method
                  BLASTX
NCBI GI
                  g5732035
BLAST score
                  561
                  9.0e-58
E value
Match length
                  145
% identity
                  73
NCBI Description (AF160760) contains similarity to Pfam family PF0040 - WD
                  domain, G-beta repeat; score=10.8, E=3.2, N-2 [Arabidopsis
                  thaliana]
Seq. No.
                  418327
Seq. ID
                  uC-osroM202030h08a1
Method
                  BLASTX
NCBI GI
                  g4467359
BLAST score
                  311
E value
                  2.0e-28
Match length
                  157
% identity
                  48
NCBI Description (AJ002685) Phosphatidylinositol 4-kinase [Arabidopsis
                  thaliana]
Seq. No.
                  418328
Seq. ID
                  uC-osroM202030h08b1
Method
                  BLASTX
NCBI GI
                  q1730568
BLAST score
                  268
E value
                  2.0e-23
Match length
                  122
% identity
                  46
NCBI Description PHOSPHATIDYLINOSITOL 4-KINASE (PI4-KINASE)
                  (PTDINS-4-KINASE) (PI4K-ALPHA) >gi 733528 (U23479)
```

Seq. ID

Method

NCBI GI

```
Seq. No.
                   418329
 Seq. ID
                   uC-osroM202030h10a1
 Method
                   BLASTX
 NCBI GI
                   q2832632
 BLAST score
                   261
 E value
                   2.0e-22
Match length
                   65
 % identity
                   86
NCBI Description (AL021711) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   418330
Seq. ID
                   uC-osroM202030h10b1
Method
                   BLASTX
NCBI GI
                   g4432844
BLAST score
                   267
E value
                   2.0e-23
Match length
                   88
% identity
                   57
NCBI Description (AC006283) unknown protein [Arabidopsis thaliana]
Seq. No.
                   418331
Seq. ID
                   uC-osroM202030h11b1
Method
                   BLASTX
NCBI GI
                   g5262218
BLAST score
                   155
E value
                   3.0e-10
Match length
                   101
% identity
                   36
NCBI Description (AL080254) calcium-binding protein-like [Arabidopsis
                   thalianal
Seq. No.
                   418332
Seq. ID
                  uC-osroM202031a01b1
Method
                  BLASTX
NCBI GI
                  g2632254
BLAST score
                  534
E value
                  2.0e-54
Match length
                  112
% identity
                  93
NCBI Description (Y12465) serine/threonine kinase [Sorghum bicolor]
Seq. No.
                  418333
Seq. ID
                  uC-osroM202031a04b1
Method
                  BLASTX
NCBI GI
                  g4760700
BLAST score
                  274
E value
                  4.0e-26
Match length
                  106
% identity
                  62
NCBI Description (AB024437) peroxidase 1 [Scutellaria baicalensis]
Seq. No.
                  418334
```

phosphatidylinositol 4-kinase [Dictyostelium discoideum]

54801

uC-osroM202031a05b1

BLASTX

g1685003

```
BLAST score
                    208
 E value
                   3.0e-16
 Match length
                   127
 % identity
                   39
 NCBI Description (U32643) immediate-early salicylate-induced
                   glucosyltransferase [Nicotiana tabacum]
 Seq. No.
                   418335
 Seq. ID
                   uC-osroM202031a06b1
Method
                   BLASTX
NCBI GI
                   g4415923
BLAST score
                   153
E value
                   5.0e-10
Match length
                   88
 % identity
                   40
NCBI Description
                  (AC006282) putative glucosyl transferase [Arabidopsis
                   thaliana]
Seq. No.
                   418336
Seq. ID
                   uC-osroM202031a07b1
Method
                   BLASTX
NCBI GI
                   g3132310
BLAST score
                   421
E value
                   3.0e-41
Match length
                   133
% identity
                   64
NCBI Description (AB012228) phosphoenolpyruvate carboxylase [Zea mays]
Seq. No.
                   418337
Seq. ID
                   uC-osroM202031a08b1
Method
                   BLASTX
NCBI GI
                   g854361
BLAST score
                   507
E value
                   2.0e-51
Match length
                   135
% identity
                   79
NCBI Description (X58877) beta-glucanase [Oryza sativa]
Seq. No.
                   418338
Seq. ID
                   uC-osroM202031a09b1
Method
                   BLASTX
NCBI GI
                   g4455190
BLAST score
                   433
E value
                  1.0e-42
Match length
                  119
% identity
                  73
NCBI Description
                  (AL035440) putative protein [Arabidopsis thaliana]
Seq. No.
                  418339
Seq. ID
                  uC-osroM202031a11b1
Method
                  BLASTX
NCBI GI
                  g5853313
BLAST score
                  251
E value
                  1.0e-34
Match length
                  113
% identity
                  68
NCBI Description (AF181687) metal ion transporter [Arabidopsis thaliana]
```

Seq. No. 418340 Seq. ID uC-osroM202031b01b1 Method BLASTX NCBI GI g5734756 BLAST score 256 E value 6.0e-22 Match length 128 % identity NCBI Description (AC007651) Similar to SOUL Protein [Arabidopsis thaliana] Seq. No. 418341 Seq. ID uC-osroM202031b02b1 Method BLASTX NCBI GI q2130089 BLAST score 260 E value 2.0e-22 Match length 51 % identity 90 NCBI Description 2-oxoglutarate/malate translocator (clone OMT103), mitochondrial membrane - proso millet
>gi_1100743_dbj_BAA08105_ (D45075) 2-oxoglutarate/malate translocator [Panicum miliaceum] Seq. No. 418342 Seq. ID uC-osroM202031b03b1 Method BLASTX NCBI GI g710626 BLAST score 188 E value 6.0e-14 Match length 45 % identity 69 NCBI Description (D30719) ERD15 protein [Arabidopsis thaliana] >gi_3241941 (AC004625) dehydration-induced protein ERD15 [Arabidopsis thaliana] >gi_3894181 (AC005662) ERD15 protein [Arabidopsis thaliana] Seq. No. 418343 Seq. ID uC-osroM202031b04b1 Method BLASTX NCBI GI g2979562 BLAST score 210 E value 1.0e-16 Match length 57 % identity 70 NCBI Description (AC003680) unknown protein [Arabidopsis thaliana] >gi_3386623 (AC004665) unknown protein [Arabidopsis

thaliana]

Seq. No. 418344

Seq. ID uC-osroM202031b05b1

Method BLASTX NCBI GI g82496 BLAST score 564 E value 4.0e-58 Match length 137 % identity 80

Seq. No.

```
NCBI Description phenylalanine ammonia-lyase (EC 4.3.1.5) - rice
Seq. No.
                  418345
                  uC-osroM202031b07b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q5901892
BLAST score
                  165
E value
                  3.0e-11
Match length
                  101
                  35
% identity
NCBI Description AND-1 protein >gi 3287173 emb CAA06932 (AJ006266) AND-1
                  protein [Homo sapiens]
                  418346
Seq. No.
Seq. ID
                  uC-osroM202031b08b1
                  BLASTX
Method
NCBI GI
                  g2293480
BLAST score
                  449
E value
                  1.0e-44
                  89
Match length
                  98
% identity
NCBI Description (AF011331) glycine-rich protein [Oryza sativa]
Seq. No.
                  418347
Seq. ID
                  uC-osroM202031b10b1
                  BLASTX
Method
NCBI GI
                  g4559346
BLAST score
                  172
E value
                  4.0e-12
Match length
                  100
% identity
                  38
NCBI Description (AC006585) early nodulin 16 [Arabidopsis thaliana]
Seq. No.
                  418348
                  uC-osroM202031b11b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4006829
BLAST score
                  457
E value
                  2.0e-45
Match length
                  126
% identity
NCBI Description (AC005970) putative protein kinase [Arabidopsis thaliana]
Seq. No.
                  418349
Seq. ID
                  uC-osroM202031c02b1
Method
                  BLASTX
NCBI GI
                  q1709619
BLAST score
                  556
E value
                  4.0e-57
Match length
                  118
% identity
                  47
                 PROTEIN DISULFIDE ISOMERASE PRECURSOR (PDI)
NCBI Description
                  >gi 2146814 pir S69181 protein disulfide isomerase (EC
                  5.3.4.1) precursor - maize >gi 625148 (L39014) protein
```

54804

disulfide isomerase [Zea mays]

E value

0.0e+00

```
Seq. ID
                   uC-osroM202031c06b1
Method
                   BLASTX
NCBI GI
                   q3885888
BLAST score
                   282
E value
                   6.0e-25
Match length
                   100
% identity
                   63
NCBI Description (AF093632) high mobility group protein [Oryza sativa]
Seq. No.
                   418351
Seq. ID
                  uC-osroM202031c07b1
Method
                  BLASTX
NCBI GI
                   q4099921
BLAST score
                   225
E value
                   3.0e-18
Match length
                   60
% identity
                   68
NCBI Description (U91982) EREBP-3 homolog [Stylosanthes hamata]
Seq. No.
                  418352
Seq. ID
                  uC-osroM202031c08b1
Method
                  BLASTX
NCBI GI
                  q1084461
BLAST score
                  475
E value
                  1.0e-47
Match length
                  133
% identity
                  71
NCBI Description RCc3 protein - rice >gi_786132 (L27208) RCc3 [Oryza sativa]
Seq. No.
                  418353
Seq. ID
                  uC-osroM202031c09b1
Method
                  BLASTX
NCBI GI
                  q6014937
BLAST score
                  233
E value
                  4.0e-20
Match length
                  71
% identity
                  70
                  UROPORPHYRINOGEN DECARBOXYLASE PRECURSOR (UPD) >gi 2651307
NCBI Description
                  (AC002336) putative uroporphyinogen decarboxylase
                  [Arabidopsis thaliana]
Seq. No.
                  418354
Seq. ID
                  uC-osroM202031c10b1
Method
                  BLASTX
NCBI GI
                  g4115377
BLAST score
                  483
E value
                  1.0e-48
Match length
                  148
% identity
                  61
NCBI Description (AC005967) unknown protein [Arabidopsis thaliana]
Seq. No.
                  418355
Seq. ID
                  uC-osroM202031c11b1
Method
                  BLASTN
NCBI GI
                  g3282393
BLAST score
                  360
```

NCBI Description

418361

Seq. No.

```
Match length
                   410
                   98
% identity
NCBI Description Oryza sativa aie2 mRNA, partial cds
                   418356
Seq. No.
Seq. ID
                  uC-osroM202031c12b1
Method
                  BLASTX
NCBI GI
                  g82496
BLAST score
                  817
E value
                  1.0e-87
Match length
                  164
                  99
% identity
NCBI Description phenylalanine ammonia-lyase (EC 4.3.1.5) - rice
                  418357
Seq. No.
Seq. ID
                  uC-osroM202031d01b1
Method
                  BLASTX
NCBI GI
                  g1203832
BLAST score
                  372
E value
                  1.0e-35
Match length
                  88
% identity
                  81
NCBI Description
                  (U46003) beta-D-glucan exohydrolase, isoenzyme ExoII
                   [Hordeum vulgare] >gi_1588407_prf_ 2208395A beta-D-glucan
                  exohydrolase [Hordeum vulgare]
Seq. No.
                  418358
Seq. ID
                  uC-osroM202031d02b1
Method
                  BLASTN
NCBI GI
                  g1255684
BLAST score
                  129
                  2.0e-66
E value
Match length
                  181
% identity
                  93
NCBI Description Rice mRNA for aspartic protease, complete cds
Seq. No.
                  418359
Seq. ID
                  uC-osroM202031d04b1
Method
                  BLASTX
NCBI GI
                  g4539656
BLAST score
                  284
                  3.0e-25
E value
Match length
                  68
% identity
                  85
NCBI Description
                  (AF061282) patatin-like protein [Sorghum bicolor]
Seq. No.
                  418360
Seq. ID
                  uC-osroM202031d06b1
Method
                  BLASTX
NCBI GI
                  g5051789
BLAST score
                  186
E value
                  9.0e-14
Match length
                  122
% identity
```

54806

(AL078637) putative protein [Arabidopsis thaliana]

```
uC-osroM202031d08b1
Seq. ID
Method
                  BLASTN
                  g1255684
NCBI GI
BLAST score
                  191
                  1.0e-103
E value
                  195
Match length
% identity
                  99
NCBI Description Rice mRNA for aspartic protease, complete cds
Seq. No.
                  418362
                  uC-osroM202031d09b1
Seq. ID
                  BLASTX
Method
NCBI GI
                  q4432860
BLAST score
                  318
                  3.0e-29
E value
Match length
                  141
                  41
% identity
NCBI Description (AC006300) putative glucose-induced repressor protein
                  [Arabidopsis thaliana]
Seq. No.
                  418363
Seq. ID
                  uC-osroM202031d10b1
Method
                  BLASTX
NCBI GI
                  g2827143
BLAST score
                  604
                  1.0e-62
E value
                  136
Match length
                  82
% identity
NCBI Description (AF027174) cellulose synthase catalytic subunit
                  [Arabidopsis thaliana]
                  418364
Seq. No.
Seq. ID
                  uC-osroM202031e01b1
                  BLASTX
Method
                  q3005576
NCBI GI
BLAST score
                  534
                  1.0e-54
E value
Match length
                  155
% identity
                  63
NCBI Description (AF047718) putative high affinity nitrate transporter;
                  GmNRT2 [Glycine max]
Seq. No.
                  418365
Seq. ID
                  uC-osroM202031e02b1
Method
                  BLASTX
NCBI GI
                  q4895232
BLAST score
                  224
E value
                  2.0e-18
Match length
                  114
% identity
                  42
NCBI Description (AC007660) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  418366
                  uC-osroM202031e03b1
Seq. ID
```

BLASTX

302

g2911072

Method

NCBI GI BLAST score





E value 2.0e-27 Match length 103 % identity 56

NCBI Description (AL021960) putative protein [Arabidopsis thaliana]

Seq. No. 418367

Seq. ID uC-osroM202031e04b1

Method BLASTX
NCBI GI 94406759
BLAST score 195
E value 8.0e-15
Match length 66
% identity 58

NCBI Description (AC006836) hypothetical protein [Arabidopsis thaliana]

Seq. No. 418368

Seq. ID uC-osroM202031e06b1

Method BLASTX
NCBI GI g1354849
BLAST score 254
E value 9.0e-22
Match length 103
% identity 47

NCBI Description (U57350) epoxide hydrolase [Nicotiana tabacum]

Seq. No. 418369

Seq. ID uC-osroM202031e07b1

Method BLASTX
NCBI GI g3241943
BLAST score 712
E value 2.0e-75
Match length 165
% identity 78

NCBI Description (AC004625) hypothetical protein [Arabidopsis thaliana]

Seq. No. 418370

Seq. ID uC-osroM202031e08b1

Method BLASTX
NCBI GI g4204278
BLAST score 299
E value 2.0e-28
Match length 154
% identity 49

NCBI Description (AC004146) putative Cytochrome P450 protein [Arabidopsis

thaliana]

Seq. No. 418371

Seq. ID uC-osroM202031e09b1

Method BLASTX
NCBI GI g3410961
BLAST score 616
E value 3.0e-64
Match length 152
% identity 81

NCBI Description (AB016765) 3-phosphoshikimate 1-carboxyvinyltransferase

[Oryza sativa]

E value

5.0e-20

```
418372
Seq. No.
Seq. ID
                  uC-osroM202031e10b1
Method
                  BLASTX
NCBI GI
                  g2160177
BLAST score
                  383
                  8.0e-37
E value
Match length
                  144
% identity
                  53
                 (AC000132) EST gb R64758 comes from this gene. [Arabidopsis
NCBI Description
                  thaliana]
                  418373
Seq. No.
                  uC-osroM202031f01b1
Seq. ID
Method
                  BLASTX
                  q3258637
NCBI GI
                  273
BLAST score
                  5.0e-24
E value
Match length
                  118
% identity
                  42
NCBI Description (AF041050) 4-coumarate:CoA ligase [Populus tremuloides]
Seq. No.
                  418374
                  uC-osroM202031f03b1
Seq. ID
                  BLASTX
Method
NCBI GI
                  q2832633
BLAST score
                  446
                  2.0e-44
E value
                  94
Match length
                  83
% identity
NCBI Description (AL021711) putative protein [Arabidopsis thaliana]
                   418375
Seq. No.
                  uC-osroM202031f04b1
Seq. ID
                  BLASTX
Method
NCBI GI
                  q3123745
BLAST score
                  275
                   3.0e-24
E value
                  95
Match length
% identity
                   57
NCBI Description (AB013447) aluminum-induced [Brassica napus]
                   418376
Seq. No.
Seq. ID
                   uC-osroM202031f05b1
Method
                  BLASTX
NCBI GI
                  g5702039
                   632
BLAST score
                   5.0e-66
E value
Match length
                  164
% identity
                   71
NCBI Description (Y18529) Fuct c3 protein [Vigna radiata]
                   418377
Seq. No.
Seq. ID
                   uC-osroM202031f06b1
Method
                   BLASTX
NCBI GI
                   q3860274
BLAST score
                   240
```

Match length 131 % identity 38

NCBI Description (AC005824) unknown protein [Arabidopsis thaliana]

>gi 4314397 gb AAD15607 (AC006232) putative zinc finger

protein [Arabidopsis thaliana]

Seq. No. 418378

Seq. ID uC-osroM202031f07b1

Method BLASTX
NCBI GI g1170871
BLAST score 320
E value 2.0e-29
Match length 62
% identity 98

NCBI Description MALATE OXIDOREDUCTASE, CHLOROPLAST PRECURSOR (MALIC ENZYME)

(ME) (NADP-DEPENDENT MALIC ENZYME) (NADP-ME)

>gi_1076749_pir__S46499 NADP-dependent malic enzyme - rice
>gi_415315 dbj_BAA03949_ (D16499) NADP-dependent malic

enzyme [Oryza sativa]

Seq. No. 418379

Seq. ID uC-osroM202031f10b1

Method BLASTX
NCBI GI g2129628
BLAST score 162
E value 6.0e-11
Match length 71
% identity 49

NCBI Description ketoconazole resistent protein - Arabidopsis thaliana

>gi_928938_emb_CAA61433_ (X89036) ketoconazole resistent

protein [Arabidopsis thaliana]

Seq. No. 418380

Seq. ID uC-osroM202031f12b1

Method BLASTX
NCBI GI g4098319
BLAST score 825
E value 1.0e-88
Match length 171
% identity 92

NCBI Description (U76744) beta-tubulin 1 [Triticum aestivum]

Seq. No. 418381

Seq. ID uC-osroM202031g01b1

Method BLASTX
NCBI GI g2662343
BLAST score 696
E value 2.0e-73
Match length 136
% identity 98

NCBI Description (D63581) EF-1 alpha [Oryza sativa]

Seq. No. 418382

Seq. ID uC-osroM202031g03b1

Method BLASTX NCBI GI g3790102 BLAST score 645

```
2.0e-67
E value
                  177
Match length
                  70
% identity
                  (AF095521) pyrophosphate-dependent phosphofructokinase
NCBI Description
                  alpha subunit [Citrus X paradisi]
                  418383
Seq. No.
Seq. ID
                  uC-osroM202031g04b1
Method
                  BLASTX
NCBI GI
                  q4467135
                  324
BLAST score
                  6.0e-30
E value
Match length
                  116
                  53
% identity
NCBI Description (AL035540) putative protein [Arabidopsis thaliana]
                  418384
Seq. No.
                  uC-osroM202031g05b1
Seq. ID
Method
                  BLASTX
                  g2842480
NCBI GI
                  154
BLAST score
E value
                  3.0e-10
                  95
Match length
% identity
                   42
NCBI Description (AL021749) ADP, ATP carrier-like protein [Arabidopsis
                   thaliana]
                   418385
Seq. No.
                  uC-osroM202031g06b1
Seq. ID
Method
                  BLASTX
                   g3152613
NCBI GI
                   205
BLAST score
                   6.0e-16
E value
                  167
Match length
% identity
                   31
NCBI Description (AC004482) hypothetical protein [Arabidopsis thaliana]
                   418386
Seq. No.
                   uC-osroM202031q10b1
Seq. ID
                   BLASTX
Method
NCBI GI
                   g2224915
BLAST score
                   406
E value
                   2.0e-39
Match length
                   105
% identity
NCBI Description (U95968) beta-expansin [Oryza sativa]
                   418387
Seq. No.
Seq. ID
                   uC-osroM202031g11b1
                   BLASTX
Method
                   q2842480
NCBI GI
BLAST score
                   670
                   2.0e-70
E value
Match length
                   158
% identity
                   (AL021749) ADP, ATP carrier-like protein [Arabidopsis
NCBI Description
```

thaliana]

NCBI GI

q464988

```
418388
Seq. No.
Seq. ID
                  uC-osroM202031g12b1
Method
                  BLASTX
NCBI GI
                  g5777628
BLAST score
                  550
E value
                  2.0e-56
Match length
                  141
                  77
% identity
NCBI Description (AJ245900) CAA303716.1 protein [Oryza sativa]
                  418389
Seq. No.
Seq. ID
                  uC-osroM202031h04b1
                  BLASTX
Method
NCBI GI
                  g4406780
BLAST score
                  564
E value
                  4.0e-58
Match length
                  145
                  75
% identity
NCBI Description (AC006532) putative multispanning membrane protein
                  [Arabidopsis thaliana]
                  418390
Seq. No.
Seq. ID
                  uC-osroM202031h06b1
Method
                  BLASTX
NCBI GI
                  q3342802
BLAST score
                  332
                  7.0e-31
E value
Match length
                  66
                  95
% identity
NCBI Description (AF061838) putative cytosolic 6-phosphogluconate
                  dehydrogenase [Zea mays]
Seq. No.
                  418391
Seq. ID
                  uC-osroM202032a01b1
Method
                  BLASTX
NCBI GI
                  q3445201
BLAST score
                  280
E value
                  3.0e-25
Match length
                  59
% identity
                  86
NCBI Description (AC004786) unknown protein [Arabidopsis thaliana]
Seq. No.
                  418392
                  uC-osroM202032a06b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2293480
BLAST score
                  432
E value
                  1.0e-42
Match length
                  84
% identity
NCBI Description (AF011331) glycine-rich protein [Oryza sativa]
Seq. No.
                  418393
Seq. ID
                  uC-osroM202032a07b1
Method
                  BLASTX
```

```
BLAST score
                    142
E value
                    8.0e-09
Match length
                    27
                    96
% identity
NCBI Description UBIQUITIN-CONJUGATING ENZYME E2-17 KD 11 (UBIQUITIN-PROTEIN
                    LIGASE 11) (UBIQUITIN CARRIER PROTEIN 11)
                   >gi_421856_pir__S32673 ubiquitin--protein ligase (EC
6.3.2.19) UBC11 - Arabidopsis thaliana (fragment)
                   >gi_297880_emb_CAA78716 (Z14992) ubiquitin conjugating
enzyme [Arabidopsis thaliana] >gi_349215 (L00641) ubiquitin
                    conjugating enzyme [Arabidopsis thaliana]
Seq. No.
                    418394
                   uC-osroM202032a08a1
Seq. ID
Method
                   BLASTX
NCBI GI
                    g3080389
BLAST score
                    202
                    1.0e-15
E value
Match length
                    52
% identity
                    77
NCBI Description (AL022603) putative membrane associated protein
                    [Arabidopsis thaliana]
Seq. No.
                    418395
Seq. ID
                   uC-osroM202032a10a1
Method
                   BLASTN
NCBI GI
                    g167107
BLAST score
                    37
E value
                    3.0e-11
                   132
Match length
% identity
                    89
NCBI Description Hordeum vulgare vacuolar ATPase B subunit isoform mRNA,
                    complete cds
                    418396
Seq. No.
                    uC-osroM202032a10b1
Seq. ID
Method
                   BLASTX
NCBI GI
                    g2493132
BLAST score
                    202
E value
                    1.0e-15
Match length
                    39
% identity
                    97
NCBI Description
                   VACUOLAR ATP SYNTHASE SUBUNIT B ISOFORM 2 (V-ATPASE B
                    SUBUNIT) > gi 167110 (L11873) vacuolar ATPase B subunit
                    [Hordeum vulgare]
Seq. No.
                    418397
Seq. ID
                    uC-osroM202032a11a1
Method
                    BLASTX
NCBI GI
                    g4454039
BLAST score
                    348
E value
                    7.0e-33
Match length
                    132
% identity
                    55
NCBI Description
```

thaliana]

(AL035394) putative Na+/H+-exchanging protein [Arabidopsis



```
418398
Seq. No.
Seq. ID
                  uC-osroM202032a12b1
Method
                  BLASTX
NCBI GI
                  g5729706
                  235
BLAST score
E value
                  2.0e-19
                  98
Match length
% identity
                  43
NCBI Description (AC007927) unknown protein [Arabidopsis thaliana]
Seq. No.
                  418399
Seq. ID
                  uC-osroM202032b01a1
Method
                  BLASTX
NCBI GI
                  g4467153
BLAST score
                  497
E value
                  3.0e-50
Match length
                  158
% identity
                  61
NCBI Description (AL035540) putative thaumatin-like protein [Arabidopsis
                  thaliana]
Seq. No.
                  418400
                  uC-osroM202032b04a1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g5902707
BLAST score
                  306
E value
                  7.0e-28
Match length
                  92
% identity
                  64
NCBI Description ZEAXANTHIN EPOXIDASE PRECURSOR >gi_2129941_pir__S69548
                   zeaxanthin epoxidase precursor - curled-leaved tobacco
                   >gi 1370274 emb CAA65048 (X95732) zeaxanthin epoxidase
                   [Nicotiana plumbaginifolia]
                  418401
Seq. No.
Seq. ID
                  uC-osroM202032b04b1
Method
                  BLASTN
NCBI GI
                  g1070353
BLAST score
                  51
E value
                  2.0e-19
Match length
                  71
                  93
% identity
NCBI Description H.vulgare mRNA for Hv14-3-3b
Seq. No.
                   418402
Seq. ID
                  uC-osroM202032b07b1
Method
                  BLASTX
NCBI GI
                  q6090831
BLAST score
                  184
                  1.0e-13
E value
```

Match length 81 % identity

NCBI Description (AF134485) cytidine deaminase 1 [Arabidopsis thaliana]

Seq. No. 418403

uC-osroM202032b09a1 Seq. ID

Method BLASTN

g167107 NCBI GI BLAST score 37 3.0e-11 E value 132 Match length 89 % identity NCBI Description Hordeum vulgare vacuolar ATPase B subunit isoform mRNA, complete cds 418404 Seq. No. Seq. ID uC-osroM202032b09b1 BLASTX Method NCBI GI q2493132 BLAST score 202 E value 1.0e-15 Match length 39 97 % identity NCBI Description VACUOLAR ATP SYNTHASE SUBUNIT B ISOFORM 2 (V-ATPASE B SUBUNIT) >gi 167110 (L11873) vacuolar ATPase B subunit [Hordeum vulgare] 418405 Seq. No. Seq. ID uC-osroM202032b10a1 BLASTX Method NCBI GI g1136120 BLAST score 668 E value 3.0e-70125 Match length 99 % identity NCBI Description (X91806) alpha-tubulin [Oryza sativa] Seq. No. 418406 uC-osroM202032b11b1 Seq. ID Method BLASTX NCBI GI q5729706 BLAST score 264 E value 6.0e-23 Match length 95 % identity NCBI Description (AC007927) unknown protein [Arabidopsis thaliana] 418407 Seq. No. Seq. ID uC-osroM202032b12b1 Method BLASTX NCBI GI q5729706 BLAST score 258 3.0e-22 E value Match length 83 51 % identity

Seq. No. 418408

Seq. ID uC-osroM202032c01a1

Method BLASTX
NCBI GI g129232
BLAST score 317
E value 4.0e-29
Match length 59

NCBI Description (AC007927) unknown protein [Arabidopsis thaliana]

% identity NCBI Description ORYZAIN BETA CHAIN PRECURSOR >gi 67645 pir KHRZOB oryzain (EC 3.4.22.-) beta precursor - rice >gi_218183_dbj_BAA14403_ (D90407) oryzain beta precursor [Oryza sativa] Seq. No. 418409 Seq. ID uC-osroM202032c01b1 BLASTX Method NCBI GI g129232 614 BLAST score 7.0e-64 E value Match length 119 98 % identity NCBI Description ORYZAIN BETA CHAIN PRECURSOR >gi_67645_pir__KHRZOB oryzain (EC 3.4.22.-) beta precursor - rice >gi 218183 dbj BAA14403_ (D90407) oryzain beta precursor [Oryza sativa] 418410 Seq. No. uC-osroM202032c05b1 Seq. ID Method BLASTX q4972064 NCBI GI BLAST score 432 2.0e-42 E value 158 Match length 54 % identity NCBI Description (AL078470) putative serine/threonine-specific receptor protein kinase [Arabidopsis thaliana] 418411 Seq. No. uC-osroM202032c06b1 Seq. ID BLASTX Method NCBI GI q4263822 353 BLAST score E value 2.0e-33 131 Match length % identity NCBI Description (AC006067) putative receptor protein kinase [Arabidopsis thaliana]

418412 Seq. No.

Seq. ID uC-osroM202032c07b1

Method BLASTX q1084461 NCBI GI 314 BLAST score 7.0e-29 E value 103 Match length % identity

NCBI Description RCc3 protein - rice >gi 786132 (L27208) RCc3 [Oryza sativa]

418413 Seq. No.

uC-osroM202032c09a1 Seq. ID

Method BLASTX NCBI GI g5230728 BLAST score 276 2.0e-24 E value

Match length 64 % identity

NCBI Description (AF089851) peroxisomal copper-containing amine oxidase

[Glycine max]

Seq. No. 418414

Seq. ID uC-osroM202032c09b1

BLASTX Method NCBI GI q4559342 BLAST score 844 7.0e-91 E value Match length 159 % identity 93

NCBI Description (AC007087) putative copper methylamine oxidase [Arabidopsis

thaliana]

Seq. No. 418415

Seq. ID uC-osroM202032c12b1

Method BLASTX NCBI GI q2492487 BLAST score 710 E value 4.0e-75 Match length 153 92 % identity

NCBI Description 14-3-3-LIKE PROTEIN B (14-3-3B) >gi 1070354 emb CAA63658

(X93170) Hv14-3-3b [Hordeum vulgare]

Seq. No. 418416

uC-osroM202032d07a1 Seq. ID

Method BLASTX q3204108 NCBI GI BLAST score 335 E value 3.0e-31 Match length 87 % identity

NCBI Description (AJ006764) putative deoxycytidylate deaminase [Cicer

arietinum]

Seq. No. 418417

Seq. ID uC-osroM202032d07b1

Method BLASTX NCBI GI g3204108 BLAST score 607 E value 5.0e-63Match length 125 % identity 89

NCBI Description (AJ006764) putative deoxycytidylate deaminase [Cicer

arietinum]

418418 Seq. No.

uC-osroM202032d08a1 Seq. ID

Method BLASTX NCBI GI g1155255 BLAST score 149 6.0e-10 E value Match length 34

% identity 74

```
NCBI Description (U39228) beta-glucosidase [Prunus avium]
                  418419
Seq. No.
                  uC-osroM202032d08b1
Seq. ID
Method
                  BLASTX
                  g1155255
NCBI GI
BLAST score
                  143
E value
                  3.0e-09
                  33
Match length
                  73
% identity
NCBI Description (U39228) beta-glucosidase [Prunus avium]
Seq. No.
                  418420
                  uC-osroM202032d09b1
Seq. ID
Method
                  BLASTX
                  g132110
NCBI GI
BLAST score
                  738
                  2.0e-78
E value
Match length
                  137
                  99
% identity
NCBI Description
                  RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 3B PRECURSOR
                   (RUBISCO SMALL SUBUNIT 3B) >gi_68060_pir__RKMUB3
                  ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                  B3 precursor - Arabidopsis thaliana >gi_16195_emb_CAA32702_
                   (X14564) ribulose bisphosphate carboxylase [Arabidopsis
                  thaliana]
                  418421
Seq. No.
                  uC-osroM202032d12b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3264767
BLAST score
                  175
                   2.0e-12
E value
Match length
                  118
% identity
NCBI Description (AF071893) AP2 domain containing protein [Prunus armeniaca]
                   418422
Seq. No.
                  uC-osroM202032e05a1
Seq. ID
Method
                  BLASTN
NCBI GI
                   g5852170
BLAST score
                   58
                   1.0e-23
E value
Match length
                   98
                   90
% identity
NCBI Description
                  Oryza sativa indica(GLA4) genomic DNA, chromosome 4, BAC
                   clone:t17804
                   418423
Seq. No.
Seq. ID
                  uC-osroM202032e06b1
                  BLASTX
Method
NCBI GI
                   g4886522
                   579
BLAST score
E value
                   8.0e-60
Match length
                  171
% identity
                  (AL050291) hypothetical protein [Homo sapiens]
NCBI Description
```

```
uC-osroM202032e07b1
Seq. ID
                  BLASTN
Method
NCBI GI
                  q5042437
                  42
BLAST score
                  4.0e-14
E value
                  42
Match length
                  100
% identity
NCBI Description Oryza sativa BAC T49B20 genomic sequence, complete sequence
                  418425
Seq. No.
                  uC-osroM202032e08a1
Seq. ID
                  BLASTX
Method
                  q4580721
NCBI GI
                  262
BLAST score
                   1.0e-22
E value
                   56
Match length
                   89
% identity
                  (AF136163) phosphoenolpyruvate carboxykinase 4 [Urochloa
NCBI Description
                  panicoides]
                   418426
Seq. No.
                   uC-osroM202032e08b1
Seq. ID
                  BLASTX
Method
                   g4490732
NCBI GI
BLAST score
                   815
                   2.0e-87
E value
                   172
Match length
                   87
% identity
                  (AL035709) phosphoenolpyruvate carboxykinase (ATP)-like
NCBI Description
                   protein [Arabidopsis thaliana]
                   418427
Seq. No.
                   uC-osroM202032e09b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   q3688185
BLAST score
                   151
                   1.0e-09
E value
Match length
                   47
% identity
NCBI Description (AL031804) putative protein [Arabidopsis thaliana]
                   418428
Seq. No.
                   uC-osroM202032e10a1
Seq. ID
Method
                   BLASTX
NCBI GI
                   q5007084
                   195
BLAST score
                   7.0e-15
E value
                   40
Match length
                   100
% identity
                   (AF155333) NADP-specific isocitrate dehydrogenase [Oryza
NCBI Description
                   sativa]
                   418429
Seq. No.
                   uC-osroM202032e10b1
Seq. ID
Method
                   BLASTX
```

418424

Seq. No.

```
g5007084
NCBI GI
BLAST score
                  763
                  2.0e-81
E value
Match length
                  143
                  100
% identity
                  (AF155333) NADP-specific isocitrate dehydrogenase [Oryza
NCBI Description
                  sativa]
                  418430
Seq. No.
                  uC-osroM202032e11a1
Seq. ID
                  BLASTX
Method
                  g6094021
NCBI GI
                  255
BLAST score
                  7.0e-22
E value
                  52
Match length
                  90
% identity
                 60S RIBOSOMAL PROTEIN L18 >gi 3021348 emb CAA06246_
NCBI Description
                   (AJ004961) ribosomal protein L18 [Cicer arietinum]
                  418431
Seq. No.
                  uC-osroM202032e11b1
Seq. ID
                  BLASTX
Method
NCBI GI
                  g1172977
                  692
BLAST score
                   5.0e-73
E value
                  166
Match length
                  81
% identity
                  60S RIBOSOMAL PROTEIN L18 >gi 606970 (U15741) cytoplasmic
NCBI Description
                  ribosomal protein L18 [Arabidopsis thaliana]
                   418432
Seq. No.
Seq. ID
                   uC-osroM202032f01a1
                   BLASTX
Method
NCBI GI
                   g2190551
                  184
BLAST score
                   1.0e-13
E value
Match length
                   76
% identity
                   47
                  (AC001229) Similar to C. elegans hypothetical protein
NCBI Description
                   K07C5.6 (gb_Z71181). ESTs gb_H36844,gb_AA394956 come from
                   this gene. [Arabidopsis thaliana]
                   418433
Seq. No.
                   uC-osroM202032f01b1
Seq. ID
                   BLASTX
Method
                   q4006865
NCBI GI
BLAST score
                   319
E value
                   2.0e-29
Match length
                   120
% identity
NCBI Description (299707) putative protein [Arabidopsis thaliana]
```

Seq. No. 418434

Seq. ID uC-osroM202032f03a1

Method BLASTX NCBI GI g283008 BLAST score 370



E value 2.0e-35 Match length 73 % identity 97

NCBI Description sucrose synthase (EC 2.4.1.13) - rice

>qi 20366 emb CAA46017 (X64770) sucrose synthase [Oryza

satīva]

Seq. No. 418435

Seq. ID uC-osroM202032f03b1

Method BLASTX
NCBI GI g283008
BLAST score 657
E value 5.0e-69
Match length 144
% identity 90

NCBI Description sucrose synthase (EC 2.4.1.13) - rice

>gi 20366 emb CAA46017_ (X64770) sucrose synthase [Oryza

satīva]

Seq. No. 418436

Seq. ID uC-osroM202032f04b1

Method BLASTX
NCBI GI 94567250
BLAST score 157
E value 3.0e-10
Match length 77
% identity 47

NCBI Description (AC007070) hypothetical protein [Arabidopsis thaliana]

Seq. No. 418437

Seq. ID uC-osroM202032f05a1

Method BLASTN
NCBI GI g540534
BLAST score 182
E value 1.0e-97
Match length 402
% identity 86

NCBI Description Rice mRNA for q group of receptor for activated C-kinase,

complete cds

Seq. No. 418438

Seq. ID uC-osroM202032f05b1

Method BLASTX
NCBI GI g1346109
BLAST score 559
E value 1.0e-57
Match length 109
% identity 99

NCBI Description GUANINE NUCLEOTIDE-BINDING PROTEIN BETA SUBUNIT-LIKE

PROTEIN (GPB-LR) (RWD) >gi_540535_dbj BAA07404_ (D38231)

RWD [Oryza sativa]

Seq. No. 418439

Seq. ID uC-osroM202032f06a1

Method BLASTX NCBI GI g3386621 BLAST score 177

```
E value
                   1.0e-12
Match length
                   44
                   77
% identity
                 (AC004665) unknown protein [Arabidopsis thaliana]
NCBI Description
                   418440
Seq. No.
                  uC-osroM202032f06b1
Seq. ID
                  BLASTX
Method
NCBI GI
                  g3386621
BLAST score
                   459
E value
                   6.0e-46
Match length
                  105
                   84
% identity
NCBI Description (AC004665) unknown protein [Arabidopsis thaliana]
                   418441
Seq. No.
                   uC-osroM202032f07b1
Seq. ID
                  BLASTX
Method
                  g3334320
NCBI GI
BLAST score
                   705
                   2.0e-74
E value
Match length
                   139
% identity
                   96
NCBI Description 40S RIBOSOMAL PROTEIN SA (P40) >gi 2444420 (AF020553)
                   ribosome-associated protein p40 [Glycine max]
Seq. No.
                   418442
                   uC-osroM202032g01a1
Seq. ID
                  BLASTX
Method
                   g3128218
NCBI GI
BLAST score
                   208
E value
                   2.0e-16
                   57
Match length
                   61
% identity
NCBI Description (AC004077) putative end13 protein [Arabidopsis thaliana]
Seq. No.
                   418443
Seq. ID
                   uC-osroM202032g03a1
Method
                   BLASTX
NCBI GI
                   q2384671
BLAST score
                   334
E value
                   2.0e-31
Match length
                   83
                   78
% identity
NCBI Description
                  (AF012657) putative potassium transporter AtKT2p
                   [Arabidopsis thaliana]
Seq. No.
                   418444
                   uC-osroM202032q04b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2224901
BLAST score
                   190
E value
                   3.0e-14
                   52
Match length
                   67
% identity
```

NCBI Description (U67134) PcMYB1 protein [Petroselinum crispum]

Seq. No. 418445

Seq. ID uC-osroM202032g05a1

Method BLASTX
NCBI GI g283008
BLAST score 378
E value 3.0e-36
Match length 73
% identity 100

NCBI Description sucrose synthase (EC 2.4.1.13) - rice

>gi_20366_emb_CAA46017_ (X64770) sucrose synthase [Oryza

sativa]

Seq. No. 418446

Seq. ID uC-osroM202032g05b1

Method BLASTX
NCBI GI g283008
BLAST score 662
E value 2.0e-69
Match length 146
% identity 89

NCBI Description sucrose synthase (EC 2.4.1.13) - rice

>gi_20366_emb_CAA46017_ (X64770) sucrose synthase [Oryza

sativa]

Seq. No. 418447

Seq. ID uC-osroM202032g06b1

Method BLASTX
NCBI GI g1402918
BLAST score 413
E value 3.0e-40
Match length 106
% identity 75

NCBI Description (X98320) peroxidase [Arabidopsis thaliana]

>gi_1429215_emb_CAA67310_ (X98774) peroxidase ATP6a

[Arabidopsis thaliana]

Seq. No. 418448

Seg. ID uC-osroM202032g07a1

Method BLASTN
NCBI GI g444046
BLAST score 70
E value 7.0e-31
Match length 105
% identity 91

NCBI Description Z.mays OBF1 mRNA for ocs-element binding factor

Seq. No. 418449

Seq. ID uC-osroM202032g08b1

Method BLASTX
NCBI GI g3758859
BLAST score 164
E value 4.0e-11
Match length 103
% identity 32

NCBI Description (Z98551) predicted using hexExon; MAL3P6.7 (PFC0730w),

Hypothetical protein, len: 222 aa [Plasmodium falciparum]

NCBI GI

BLAST score

Seq. No. 418450 uC-osroM202032g10b1 Seq. ID Method BLASTX NCBI GI q4406759 BLAST score 202 1.0e-15 E value Match length 110 % identity 41 NCBI Description (AC006836) hypothetical protein [Arabidopsis thaliana] Seq. No. 418451 Seq. ID uC-osroM202032g11a1 Method BLASTX NCBI GI g1350986 BLAST score 329 2.0e-30 E value Match length 66 % identity 100 NCBI Description 40S RIBOSOMAL PROTEIN S3A (CYC07 PROTEIN) >gi 483431 dbj BAA05059 (D26060) cyc07 [Oryza sativa] Seq. No. 418452 Seq. ID uC-osroM202032g11b1 Method BLASTX NCBI GI q1350986 BLAST score 750 8.0e-80 E value Match length 144 % identity 100 NCBI Description 40S RIBOSOMAL PROTEIN S3A (CYC07 PROTEIN) >gi 483431 dbj BAA05059 (D26060) cyc07 [Oryza sativa] Seq. No. 418453 uC-osroM202032g12b1 Seq. ID Method BLASTX g3264596 NCBI GI BLAST score 624 E value 5.0e-65 155 Match length 79 % identity NCBI Description (AF057183) putative tonoplast aquaporin [Zea mays] 418454 Seq. No. uC-osroM202032h01a1 Seq. ID BLASTX Method NCBI GI g2655291 BLAST score 360 3.0e - 34E value 81 Match length % identity NCBI Description (AF032974) germin-like protein 4 [Oryza sativa] 418455 Seq. No. Seq. ID uC-osroM202032h01b1 BLASTX Method

54824

q2655291



```
1.0e-43
E value
Match length
                  83
                  99
% identity
                 (AF032974) germin-like protein 4 [Oryza sativa]
NCBI Description
                  418456
Seq. No.
Seq. ID
                  uC-osroM202032h02b1
                  BLASTX
Method
NCBI GI
                  a3874228
                  149
BLAST score
                  1.0e-09
E value
                  129
Match length
                  33
% identity
                  (Z49909) cDNA EST CEMSF21F comes from this gene; cDNA EST
NCBI Description
                  EMBL: D73546 comes from this gene; cDNA EST EMBL: D73669
                  comes from this gene; cDNA EST EMBL: D70979 comes from this
                   gene; cDNA EST EMBL: D71075 comes from this gene; cDNA
Seq. No.
                   418457
Seq. ID
                  uC-osroM202032h05b1
Method
                  BLASTX
                  g5732069
NCBI GI
                   249
BLAST score
                   2.0e-21
E value
                   60
Match length
% identity
                  (AF147263) contains similarity to Pfam family PF00036 - EF
NCBI Description
                  hand; score=11.7, E=0.66, N=1 [Arabidopsis thaliana]
Seq. No.
                   418458
                   uC-osroM202032h06b1
Seq. ID
                   BLASTX
Method
                   g121332
NCBI GI
BLAST score
                   586
E value
                   8.0e-61
Match length
                   109
                   100
% identity
                  GLUTAMINE SYNTHETASE ROOT ISOZYME (GLUTAMATE--AMMONIA
NCBI Description
                   LIGASE) (CLONE LAMBDA-GS8) >gi_68590_pir__AJRZQB
                   glutamate--ammonia ligase (EC 6.3.1.2) beta, cytosolic -
                   rice >gi_20358_emb_CAA32460_ (X14244) cytosolic glutamine
                   syntethase (AA 1-357) [Oryza sativa]
                   418459
Seq. No.
                   uC-osroM202032h09b1
Seq. ID
                   BLASTX
Method
                   g2149640
NCBI GI
```

NCBI GI g2149640
BLAST score 428
E value 3.0e-42
Match length 122
% identity 67

NCBI Description (U91995) Argonaute protein [Arabidopsis thaliana]

>gi_5733867_gb_AAD49755.1_AC007932_3 (AC007932) Identical to gb_U91995 Argonaute protein from Arabidopsis thaliana. ESTs gb_H76075, gb_AA720232, gb_N65911 and gb_AA651494 come from this gene

```
418460
Seq. No.
Seq. ID
                  uC-osroM202032h10a1
Method
                  BLASTX
NCBI GI
                  g4803951
BLAST score
                  370
                  2.0e-35
E value
                  84
Match length
                  71
% identity
NCBI Description (AC006202) unknown protein [Arabidopsis thaliana]
                  418461
Seq. No.
Seq. ID
                  uC-osroM202032h11a1
                  BLASTX
Method
NCBI GI
                  g2655291
                  375
BLAST score
                  6.0e-36
E value
                  84
Match length
                  89
% identity
NCBI Description (AF032974) germin-like protein 4 [Oryza sativa]
                  418462
Seq. No.
                  uC-osroM202032h11b1
Seq. ID
                  BLASTX
Method
                  q2655291
NCBI GI
BLAST score
                  664
                  9.0e-70
E value
                  127
Match length
                  99
% identity
NCBI Description (AF032974) germin-like protein 4 [Oryza sativa]
                  418463
Seq. No.
                  uC-osroM202032h12b1
Seq. ID
Method
                  BLASTX
                  a1518388
NCBI GI
BLAST score
                  200
                  4.0e-20
E value
                  110
Match length
% identity
NCBI Description (X91172) korean-radish isoperoxidase [Raphanus sativus]
Seq. No.
                  418464
                  uC-osroM202033a02a1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3319354
BLAST score
                  248
                  5.0e-21
E value
Match length
                  72
                  65
% identity
NCBI Description (AF077407) contains similarity to sugar transporters (Pfam:
                  sugar tr.hmm, score: 395.39) [Arabidopsis thaliana]
                  418465
Seq. No.
                  uC-osroM202033a05a1
Seq. ID
```

Method BLASTN
NCBI GI g2331130
BLAST score 204
E value 1.0e-111



304 Match length 96 % identity

Oryza sativa glycine-rich protein (OSGRP1) mRNA, complete NCBI Description

cds

418466 Seq. No.

Seq. ID uC-osroM202033a05b1

BLASTN Method g2331130 NCBI GI BLAST score 40 3.0e-13E value 48 Match length

96 % identity

Oryza sativa glycine-rich protein (OSGRP1) mRNA, complete NCBI Description

cds

418467 Seq. No.

Seq. ID uC-osroM202033a06a1

BLASTX Method g5688947 NCBI GI 252 BLAST score 1.0e-21 E value 46 Match length 100 % identity

(AB017428) succinate dehydrogenase iron-protein subunit NCBI Description

(SDHB) [Oryza sativa] >gi 5688949 dbj BAA82750.1

(AB017429) succinate dehydrogenase iron-protein subunit

(SDHB) [Oryza sativa]

418468 Seq. No.

Seq. ID uC-osroM202033a06b1

BLASTX Method NCBI GI q5688945 235 BLAST score E value 6.0e-20 55 Match length 75 % identity

(AB017427) mitochondrial ribosomal protein S14 [Oryza NCBI Description

sativa] >gi 5688950 dbj BAA82751.1 (AB017429) mitochondrial ribosomal portein S14 [Oryza sativa]

Seq. No. 418469

Seq. ID uC-osroM202033a09b1

BLASTX Method NCBI GI q1345644 BLAST score 318 3.0e-29 E value Match length 93 62 % identity

NCBI Description CYTOCHROME P450 86A1 (CYPLXXXVI) >gi 940446 emb CAA62082_

(X90458) cytochrome p450 [Arabidopsis thaliana]

Seq. No. 418470

uC-osroM202033a10b1 Seq. ID

BLASTX Method NCBI GI g3176690 BLAST score 208



E value 2.0e-16 Match length 122 % identity 47

NCBI Description (AC003671) Similar to ubiquitin ligase gb_D63905 from S.

cerevisiae. EST gb R65295 comes from this gene.

[Arabidopsis thaliana]

Seq. No. 418471

Seq. ID uC-osroM202033a12a1

Method BLASTX
NCBI GI g3548808
BLAST score 410
E value 4.0e-40
Match length 148
% identity 57

NCBI Description (AC005313) unknown protein [Arabidopsis thaliana]

Seq. No. 418472

Seq. ID uC-osroM202033a12b1

Method BLASTX
NCBI GI g5688947
BLAST score 155
E value 1.0e-10
Match length 33
% identity 85

NCBI Description (AB017428) succinate dehydrogenase iron-protein subunit

(SDHB) [Oryza sativa] >gi 5688949 dbj BAA82750.1_

(AB017429) succinate dehydrogenase iron-protein subunit

(SDHB) [Oryza sativa]

Seq. No. 418473

Seq. ID uC-osroM202033b01a1

Method BLASTX
NCBI GI g5281051
BLAST score 288
E value 1.0e-25
Match length 70
% identity 79

NCBI Description (AL080318) stress-induced protein stil-like protein

[Arabidopsis thaliana]

Seq. No. 418474

Seq. ID uC-osroM202033b01b1

Method BLASTX
NCBI GI g3445201
BLAST score 192
E value 3.0e-16
Match length 70
% identity 60

NCBI Description (AC004786) unknown protein [Arabidopsis thaliana]

Seq. No. 418475

Seq. ID uC-osroM202033b02b1

Method BLASTX
NCBI GI g3757515
BLAST score 178
E value 8.0e-13

% identity

NCBI Description

76

```
Match length
                  50
                  70
% identity
                  (AC005167) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                  >gi 4581130 gb AAD24620.1 AC005825 27 (AC005825)
                  hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  418476
Seq. ID
                  uC-osroM202033b05a1
                  BLASTX
Method
NCBI GI
                  q1076746
BLAST score
                  325
                  4.0e-30
E value
                  97
Match length
                  70
% identity
                  heat shock protein 70 - rice (fragment)
NCBI Description
                  >gi 763160 emb CAA47948 (X67711) heat shock protein 70
                  [Oryza sativa]
Seq. No.
                  418477
Seq. ID
                  uC-osroM202033b05b1
                  BLASTX
Method
NCBI GI
                  g166765
BLAST score
                  208
                  8.0e-17
E value
                  57
Match length
                  72
% identity
NCBI Description (M23106) heat shock protein HSP70-1 [Arabidopsis thaliana]
                  418478
Seq. No.
                  uC-osroM202033b06a1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4191782
BLAST score
                  293
                  3.0e-26
E value
                  78
Match length
                  67
% identity
NCBI Description (AC005917) WD-40 repeat protein [Arabidopsis thaliana]
Seq. No.
                  418479
Seq. ID
                  uC-osroM202033b06b1
Method
                  BLASTX
NCBI GI
                  q4191782
BLAST score
                  433
E value
                  1.0e-42
Match length
                  102
% identity
                  77
NCBI Description (AC005917) WD-40 repeat protein [Arabidopsis thaliana]
Seq. No.
                  418480
                  uC-osroM202033b07b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3757515
BLAST score
                  252
E value
                  6.0e-23
Match length
                  79
```

54829

(AC005167) hypothetical protein [Arabidopsis thaliana]

>gi_4581130_gb_AAD24620.1_AC005825_27 (AC005825)
hypothetical protein [Arabidopsis thaliana]

Seq. No. 418481

Seq. ID uC-osroM202033b08a1

Method BLASTX
NCBI GI g3757515
BLAST score 453
E value 5.0e-45
Match length 162
% identity 58

NCBI Description (AC005167) hypothetical protein [Arabidopsis thaliana]

>gi 4581130 gb AAD24620.1_AC005825_27 (AC005825)

hypothetical protein [Arabidopsis thaliana]

Seq. No. 418482

Seq. ID uC-osroM202033b09a1

Method BLASTX
NCBI GI g3319340
BLAST score 157
E value 2.0e-10
Match length 66
% identity 53

NCBI Description (AF077407) contains similarity to E. coli cation transport

protein ChaC (GB:D90756) [Arabidopsis thaliana]

Seq. No. 418483

Seq. ID uC-osroM202033b11a1

Method BLASTX
NCBI GI g1076620
BLAST score 176
E value 1.0e-12
Match length 58
% identity 59

NCBI Description cyclin - common tobacco >gi_599933_emb_CAA86032_ (Z37978)

Cyclin [Nicotiana tabacum]

Seq. No. 418484

Seq. ID uC-osroM202033b11b1

Method BLASTX
NCBI GI g2130119
BLAST score 471
E value 1.0e-48
Match length 132
% identity 73

NCBI Description cyclin Ia - maize

Seq. No. 418485

Seq. ID uC-osroM202033c01a1

Method BLASTX
NCBI GI 94314378
BLAST score 250
E value 2.0e-21
Match length 112
% identity 41

NCBI Description (AC006232) putative lipase [Arabidopsis thaliana]

>gi_5306262_gb_AAD41994.1_AC006233_5 (AC006233) putative



lipase [Arabidopsis thaliana]

```
418486
Seq. No.
                  uC-osroM202033c01b1
Seq. ID
                  BLASTN
Method
                  q3298473
NCBI GI
                  335
BLAST score
                  0.0e+00
E value
Match length
                  379
                  97
% identity
NCBI Description Oryza sativa gene for ovpl, complete cds
                  418487
Seq. No.
                  uC-osroM202033c02a1
Seq. ID
                  BLASTX
Method
                  q1747294
NCBI GI
                  710
BLAST score
                  3.0e-75
E value
                  165
Match length
% identity
NCBI Description (D45383) vacuolar H+-pyrophosphatase [Oryza sativa]
                  418488
Seq. No.
                  uC-osroM202033c03b1
Seq. ID
                  BLASTX
Method
NCBI GI
                  q5281051
                  288
BLAST score
                  8.0e-26
E value
Match length
                  97
                   29
% identity
NCBI Description (AL080318) stress-induced protein stil-like protein
                   [Arabidopsis thaliana]
                   418489
Seq. No.
                  uC-osroM202033c04b1
Seq. ID
Method
                  BLASTX
                   g2952328
NCBI GI
                   701
BLAST score
                   4.0e-74
E value
                   137
Match length
% identity
NCBI Description (AF049889) 1-aminocyclopropane-1-carboxylate oxidase [Oryza
                   sativa]
Seq. No.
                   418490
                   uC-osroM202033c05a1
Seq. ID
                   BLASTN
Method
                   q287400
NCBI GI
                   419
BLAST score
E value
                   0.0e + 00
                   446
Match length
                   98
% identity
NCBI Description Rice mRNA for peroxidase, complete cds
```

Seq. No. 418491

Seq. ID uC-osroM202033c06a1

Method BLASTX

g2589164 NCBI GI BLAST score 364 E value 1.0e-34 Match length 111 66 % identity NCBI Description (D88452) aldehyde oxidase-2 [Zea mays] 418492 Seq. No. Seq. ID uC-osroM202033c06b1 Method BLASTN NCBI GI q1532047 BLAST score 61 1.0e-25 E value Match length 163 % identity 86 NCBI Description O.sativa mRNA for S-adenosylmethionine decarboxylase 418493 Seq. No. Seq. ID uC-osroM202033c08a1 Method BLASTX NCBI GI g4314378 BLAST score 222 E value 3.0e-18 Match length 88 44 % identity NCBI Description (AC006232) putative lipase [Arabidopsis thaliana] >gi 5306262 gb AAD41994.1 AC006233 5 (AC006233) putative lipase [Arabidopsis thaliana] Seq. No. 418494 Seq. ID uC-osroM202033c08b1 Method BLASTX NCBI GI g1519251 BLAST score 666 E value 4.0e-70 Match length 133 99 % identity NCBI Description (U65957) GF14-c protein [Oryza sativa] Seq. No. 418495 Seq. ID uC-osroM202033c09a1 BLASTN Method NCBI GI g1519250 BLAST score 411 E value 0.0e + 00Match length 415 100 % identity NCBI Description Oryza sativa GF14-c protein mRNA, complete cds 418496 Seq. No. Seq. ID uC-osroM202033c10a1 BLASTX Method

Method BLASTX
NCBI GI g3184098
BLAST score 250
E value 3.0e-21
Match length 163
% identity 39



```
(AL023777) coenzyme a synthetase [Schizosaccharomyces
NCBI Description
                  pombe]
                  418497
Seq. No.
                  uC-osroM202033c11a1
Seq. ID
                  BLASTX
Method
                  g3929545
NCBI GI
BLAST score
                  172
                  4.0e-12
E value
Match length
                  61
                  67
% identity
                  (AF067194) S-adenosylmethionine decarboxylase [Oryza
NCBI Description
                  sativa]
                  418498
Seq. No.
                  uC-osroM202033c11b1
Seq. ID
                  BLASTX
Method
                  g585661
NCBI GI
                  242
BLAST score
                  1.0e-20
E value
Match length
                  61
                  77
% identity
NCBI Description PEROXIDASE PRECURSOR >gi_287401_dbj_BAA03644_ (D14997)
                  peroxidase [Oryza sativa]
                  418499
Seq. No.
Seq. ID
                  uC-osroM202033d01a1
Method
                  BLASTX
                  g3108053
NCBI GI
BLAST score
                  196
E value
                   4.0e-15
Match length
                   46
% identity
                   80
                  (AF056326) myo-inositol 1-phosphate synthase; INO1 [Zea
NCBI Description
                  mays]
Seq. No.
                   418500
                   uC-osroM202033d01b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   q129232
BLAST score
                   412
E value
                   2.0e-40
Match length
                   80
                   96
% identity
NCBI Description ORYZAIN BETA CHAIN PRECURSOR >gi 67645_pir KHRZOB oryzain
                   (EC 3.4.22.-) beta precursor - rice
                   >gi_218183_dbj_BAA14403_ (D90407) oryzain beta precursor
                   [Oryza sativa]
                   418501
Seq. No.
                   uC-osroM202033d02b1
Seq. ID
```

Method BLASTX NCBI GI g6056371

BLAST score 458 1.0e-45 E value Match length 126 % identity 69

Method

BLASTX



```
NCBI Description (AC009894) nucleolar protein [Arabidopsis thaliana]
                   418502
Seq. No.
                  uC-osroM202033d03a1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3860319
BLAST score
                  394
                   3.0e-38
E value
Match length
                  92
                  82
% identity
NCBI Description (AJ012686) nucleolar protein [Cicer arietinum]
                   418503
Seq. No.
                  uC-osroM202033d04a1
Seq. ID
Method
                  BLASTX
NCBI GI
                   g3860319
BLAST score
                   417
                   7.0e-41
E value
                  101
Match length
% identity
                   80
NCBI Description (AJ012686) nucleolar protein [Cicer arietinum]
Seq. No.
                   418504
                  uC-osroM202033d04b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3560531
BLAST score
                   529
                   1.0e-53
E value
Match length
                   130
% identity
                  (AF042332) cycloartenol-C24-methyltransferase [Oryza sativa
NCBI Description
                   subsp. japonica]
Seq. No.
                   418505
Seq. ID
                   uC-osroM202033d05b1
Method
                   BLASTX
NCBI GI
                   q5281051
BLAST score
                   226
E value
                   1.0e-18
                   73
Match length
% identity
                   59
                  (AL080318) stress-induced protein stil-like protein
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                   418506
                   uC-osroM202033d06b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2459575
                   183
BLAST score
E value
                   2.0e-13
                   77
Match length
                   53
% identity
NCBI Description (U75346) envelope protein [Chlamydomonas reinhardtii]
Seq. No.
                   418507
Seq. ID
                   uC-osroM202033d07a1
```

BLAST score

246

```
NCBI GI
                  g129232
BLAST score
                  372
                  1.0e-35
E value
Match length
                  65
                  100
% identity
                  ORYZAIN BETA CHAIN PRECURSOR >gi_67645_pir__KHRZOB oryzain
NCBI Description
                  (EC 3.4.22.-) beta precursor - rice
                  >gi_218183_dbj_BAA14403_ (D90407) oryzain beta precursor
                  [Oryza sativa]
                  418508
Seq. No.
                  uC-osroM202033d08a1
Seq. ID
                  BLASTX
Method
                  q3860319
NCBI GI
BLAST score
                  219
                  1.0e-17
E value
                  95
Match length
                  54
% identity
NCBI Description (AJ012686) nucleolar protein [Cicer arietinum]
                  418509
Seq. No.
                  uC-osroM202033d10b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q6056371
                  334
BLAST score
E value
                  2.0e-31
                  89
Match length
                  70
% identity
NCBI Description (AC009894) nucleolar protein [Arabidopsis thaliana]
Seq. No.
                   418510
                   uC-osroM202033d12a1
Seq. ID
                  BLASTX
Method
NCBI GI
                  g2952328
BLAST score
                  236
E value
                   1.0e-19
Match length
                   46
% identity
                   100
NCBI Description (AF049889) 1-aminocyclopropane-1-carboxylate oxidase [Oryza
                   sativa]
                   418511
Seq. No.
                   uC-osroM202033e01a1
Seq. ID
                   BLASTX
Method
                   q4455210
NCBI GI
BLAST score
                   231
E value
                   4.0e-19
                   51
Match length
% identity
                  (AL035440) putative aspartate-tRNA ligase [Arabidopsis
NCBI Description
                   thaliana]
                   418512
Seq. No.
Seq. ID
                   uC-osroM202033e03a1
                   BLASTX
Method
NCBI GI
                   g1076746
```

7.0e-21 E value Match length 64 77 % identity heat shock protein 70 - rice (fragment) NCBI Description >gi_763160_emb_CAA47948_ (X67711) heat shock protein 70 [Oryza satīva] 418513 Seq. No. uC-osroM202033e03b1 Seq. ID Method BLASTN g3298473 NCBI GI 307 BLAST score E value 1.0e-172 339 Match length 97 % identity NCBI Description Oryza sativa gene for ovpl, complete cds 418514 Seq. No. uC-osroM202033e07b1 Seq. ID BLASTX Method g5731763 NCBI GI 345 BLAST score 2.0e-32 E value 110 Match length 59 % identity (X92419) SNAP25A protein [Arabidopsis thaliana] NCBI Description >gi 5731764 emb CAB52583.1_ (X92420) SNAP25AB protein [Arabidopsis thaliana] 418515 Seq. No. uC-osroM202033e08b1 Seq. ID Method BLASTX q1076746 NCBI GI 605 BLAST score 2.0e-67 E value Match length 134 % identity 99 heat shock protein 70 - rice (fragment) NCBI Description >gi_763160_emb_CAA47948_ (X67711) heat shock protein 70 [Oryza sativa] Seq. No. 418516 uC-osroM202033e09a1 Seq. ID BLASTX Method NCBI GI g1747294 BLAST score 732 E value 9.0e-78

Match length 167 % identity 90

NCBI Description (D45383) vacuolar H+-pyrophosphatase [Oryza sativa]

Seq. No. 418517

uC-osroM202033e11a1 Seq. ID

BLASTX Method NCBI GI g3063445 BLAST score 169 8.0e-12 E value

```
73
Match length
% identity
                  (AC003981) F22013.7 [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  418518
                  uC-osroM202033e12a1
Seq. ID
                  BLASTN
Method
                  q3560530
NCBI GI
BLAST score
                  299
                  1.0e-167
E value
Match length
                  299
                  100
% identity
NCBI Description Oryza sativa subsp. japonica
                  cycloartenol-C24-methyltransferase mRNA, complete cds
                  418519
Seq. No.
                  uC-osroM202033f01a1
Seq. ID
                  BLASTX
Method
                  g3108053
NCBI GI
BLAST score
                  229
E value
                  6.0e-19
                  45
Match length
                  100
% identity
NCBI Description (AF056326) myo-inositol 1-phosphate synthase; INO1 [Zea
                  mays]
                   418520
Seq. No.
                  uC-osroM202033f01b1
Seq. ID
                  BLASTX
Method
NCBI GI
                  q3062907
BLAST score
                  404
                   1.0e-39
E value
Match length
                  77
% identity
NCBI Description (AB012107) myo-inositol phosphate synthase [Oryza sativa]
Seq. No.
                   418521
                   uC-osroM202033f02b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   q4262147
BLAST score
                  199
E value
                   1.0e-15
Match length
                  72
% identity
                  (AC005275) putative homolog of transport inhibitor response
NCBI Description
                   1 [Arabidopsis thaliana]
                   418522
Seq. No.
                   uC-osroM202033f03a1
Seq. ID
                   BLASTN
Method
NCBI GI
                   g20280
BLAST score
                   391
E value
                   0.0e+00
Match length
                   391
                   100
% identity
```

NCBI Description Rice gene for phenylalanine ammonia-lyase (EC 4.3.1.5)

418523 Seq. No. uC-osroM202033f05b1 Seq. ID Method BLASTX NCBI GI q129591 BLAST score 196 5.0e-15 E value Match length 110 44 % identity PHENYLALANINE AMMONIA-LYASE >qi 295824 emb CAA34226 NCBI Description (X16099) phenylalanine ammonia-lyase [Oryza sativa] 418524 Seq. No. uC-osroM202033f07a1 Seq. ID Method BLASTX NCBI GI q5453379 BLAST score 426 5.0e-42 E value Match length 103 79 % identity (AF155124) bacterial-induced peroxidase precursor NCBI Description [Gossypium hirsutum] 418525 Seq. No. uC-osroM202033f08b1 Seq. ID Method BLASTX NCBI GI g129591 BLAST score 383 5.0e-37E value Match length 94 80 % identity NCBI Description PHENYLALANINE AMMONIA-LYASE >gi 295824 emb_CAA34226 (X16099) phenylalanine ammonia-lyase [Oryza sativa] 418526 Seq. No. uC-osroM202033f10b1 Seq. ID Method BLASTX NCBI GI q4582436 BLAST score 152 E value 2.0e-14 Match length 132 % identity 43 NCBI Description (AC007196) unknown protein [Arabidopsis thaliana] Seq. No. 418527 uC-osroM202033f11b1 Seq. ID Method BLASTX NCBI GI g2827141 BLAST score 513

E value 2.0e-52 Match length 108 % identity 82

NCBI Description (AF027173) cellulose synthase catalytic subunit [Arabidopsis thaliana] >gi_4914447_emb_CAB43650.1

(AL050351) cellulose synthase catalytic subunit (Ath-A)

[Arabidopsis thaliana]

Seq. No. 418528



uC-osroM202033f12b1 Seq. ID BLASTX Method q4886522 NCBI GI 415 BLAST score 9.0e-41 E value 121 Match length 68 % identity (AL050291) hypothetical protein [Homo sapiens] NCBI Description 418529 Seq. No. uC-osroM202033g01b1 Seq. ID BLASTX Method q4584525 NCBI GI BLAST score 181 4.0e-13 E value 57 Match length 68 % identity (AL049607) protein phosphatase 2C-like protein [Arabidopsis NCBI Description thaliana] 418530 Seq. No. uC-osroM202033g02a1 Seq. ID BLASTX Method g4510425 NCBI GI 306 BLAST score 8.0e-28 E value Match length 70 % identity 81 NCBI Description (AC006929) unknown protein [Arabidopsis thaliana] 418531 Seq. No. uC-osroM202033g02b1 Seq. ID Method BLASTX q4510426 NCBI GI 350 BLAST score E value 4.0e-33 Match length 121 % identity 55 NCBI Description (AC006929) hypothetical protein [Arabidopsis thaliana] 418532 Seq. No. Seq. ID uC-osroM202033g04a1 BLASTX Method q861170 NCBI GI 284 BLAST score E value 3.0e-25 Match length 59 % identity 92 NCBI Description (X03697) heat shock protein 70 [Zea mays] 418533 Seq. No. Seq. ID uC-osroM202033q04b1

Method BLASTX
NCBI GI g123650
BLAST score 608
E value 3.0e-67
Match length 165

```
% identity
                  HEAT SHOCK COGNATE 70 KD PROTEIN >gi_82245 pir S03250 heat
NCBI Description
                  shock protein 70 (clone pMON9743) - garden petunia
                  >qi 20557 emb CAA30018 (X06932) heat shock protein 70
                  [Petunia x hybrida]
                  418534
Seq. No.
                  uC-osroM202033g05a1
Seq. ID
                  BLASTX
Method
                  q129591
NCBI GI
BLAST score
                  269
                  2.0e-23
E value
                  49
Match length
                  100
% identity
NCBI Description PHENYLALANINE AMMONIA-LYASE >gi 295824 emb CAA34226
                  (X16099) phenylalanine ammonia-lyase [Oryza sativa]
                  418535
Seq. No.
                  uC-osroM202033g05b1
Seq. ID
                  BLASTX
Method
                  g82496
NCBI GI
                  534
BLAST score
                  1.0e-54
E value
Match length
                  144
                  79
% identity
NCBI Description phenylalanine ammonia-lyase (EC 4.3.1.5) - rice
                  418536
Seq. No.
                  uC-osroM202033g07a1
Seq. ID
                  BLASTX
Method
NCBI GI
                  g1497987
                  152
BLAST score
                   7.0e-10
E value
Match length
                  40
                   72
% identity
NCBI Description (U62798) SCARECROW [Arabidopsis thaliana]
                   418537
Seq. No.
                   uC-osroM202033g08b1
Seq. ID
                   BLASTX
Method
NCBI GI
                   g3135263
BLAST score
                   145
E value
                   4.0e-09
                  54
Match length
% identity
NCBI Description (AC003058) hypothetical protein [Arabidopsis thaliana]
                   418538
Seq. No.
                   uC-osroM202033g09b1
Seq. ID
                   BLASTN
Method
                   q3077789
NCBI GI
                   43
BLAST score
                   9.0e-15
E value
                   71
Match length
                   90
% identity
NCBI Description Oryza sativa RINO1 mRNA for myo-inositol phosphate
```

54840

synthase, complete cds

Method

BLASTX

Seq. No. 418539 uC-osroM202033g10a1 Seq. ID Method BLASTX NCBI GI q2244965 144 BLAST score 8.0e-09 E value Match length 77 39 % identity NCBI Description (Z97340) hypothetical protein [Arabidopsis thaliana] 418540 Seq. No. Seq. ID uC-osroM202033g11a1Method BLASTX NCBI GI g2133430 329 BLAST score E value 1.0e-30 Match length 136 % identity 44 NCBI Description cathepsin L (EC 3.4.22.15) precursor - Paramecium tetraurelia (SGC5) >gi 1403087 emb CAA62869 (X91754) cathepsin L [Paramecium tetraurelia] Seq. No. 418541 uC-osroM202033g12a1 Seq. ID Method BLASTX NCBI GI q5932555 BLAST score 4445.0e-44E value Match length 111 76 % identity NCBI Description (AC009465) putative ribose 5-phosphate isomerase [Arabidopsis thaliana] Seq. No. 418542 Seq. ID uC-osroM202033h01b1 Method BLASTX NCBI GI g4926827 BLAST score 173 E value 2.0e-12 Match length 55 % identity NCBI Description (AC004135) T17H7.12 [Arabidopsis thaliana] Seq. No. 418543 uC-osroM202033h02a1 Seq. ID Method BLASTN NCBI GI g5410347 BLAST score 35 E value 5.0e-10 43 Match length % identity 95 NCBI Description Sorghum bicolor BAC clone 110K5, partial sequence 418544 Seq. No. uC-osroM202033h02b1 Seq. ID

```
q4926827
NCBI GI
BLAST score
                  191
                  7.0e-18
E value
                  83
Match length
                  58
% identity
NCBI Description (AC004135) T17H7.12 [Arabidopsis thaliana]
                  418545
Seq. No.
Seq. ID
                  uC-osroM202033h03a1
                  BLASTX
Method
NCBI GI
                  q6006872
BLAST score
                  160
E value
                  9.0e-11
                  71
Match length
                  46
% identity
NCBI Description (AC009540) s-syntaxin-like protein [Arabidopsis thaliana]
                   418546
Seq. No.
Seq. ID
                  uC-osroM202033h07a1
Method
                  BLASTX
                  q3128218
NCBI GI
                  149
BLAST score
                   2.0e-09
E value
                  38
Match length
                   68
% identity
NCBI Description (AC004077) putative end13 protein [Arabidopsis thaliana]
                   418547
Seq. No.
Seq. ID
                   uC-osroM202033h07b1
Method
                   BLASTX
                   q4926827
NCBI GI
                   432
BLAST score
                   2.0e-42
E value
                   125
Match length
% identity
                   72
NCBI Description (AC004135) T17H7.12 [Arabidopsis thaliana]
                   418548
Seq. No.
                   uC-osroM202033h08b1
Seq. ID
Method
                   BLASTN
                   q5410347
NCBI GI
BLAST score
                   81
                   1.0e-37
E value
                   145
Match length
                   89
% identity
NCBI Description Sorghum bicolor BAC clone 110K5, partial sequence
                   418549
Seq. No.
                   uC-osroM202033h12b1
Seq. ID
                   BLASTX
Method
NCBI GI
                   g20559
BLAST score
                   139
E value
                   6.0e-09
                   49
Match length
                   59
% identity
NCBI Description (X13301) hsp70 (AA 6 - 651) [Petunia x hybrida]
```

Seq. No. 418550 Seq. ID uC-osroM202034a01b1 Method BLASTX NCBI GI q2459430 BLAST score 175 2.0e-12 E value Match length 69 % identity 52 (AC002332) putative CUC2 protein [Arabidopsis thaliana] NCBI Description 418551 Seq. No. uC-osroM202034a02b1 Seq. ID Method BLASTX NCBI GI q6056189 BLAST score 367 6.0e - 35E value Match length 150 % identity 51 NCBI Description (AC009400) hypothetical protein [Arabidopsis thaliana] 418552 Seq. No. uC-osroM202034a03b1 Seq. ID BLASTX Method NCBI GI q113385 BLAST score 651 3.0e-68 E value Match length 128 95 % identity NCBI Description ALCOHOL DEHYDROGENASE 3 >gi 82349 pir S04040 alcohol dehydrogenase (EC 1.1.1.1) 3 - barley >gi_18886_emb_CAA31231_ (X12734) alcohol dehydrogenase [Hordeum vulgare] Seq. No. 418553 uC-osroM202034a04a1 Seq. ID Method BLASTN NCBI GI g2773153 227 BLAST score E value 1.0e-124 Match length 343 92 % identity NCBI Description Oryza sativa abscisic acid- and stress-inducible protein (Asr1) mRNA, complete cds 418554 Seq. No. Seq. ID uC-osroM202034a04b1 BLASTX Method

Method BLASTX
NCBI GI g2773154
BLAST score 257
E value 5.0e-22
Match length 128
% identity 46

NCBI Description (AF039573) abscisic acid- and stress-inducible protein

[Oryza sativa]

Seq. No. 418555

Seq. ID uC-osroM202034a05a1



```
BLASTN
Method
                  g4158220
NCBI GI
BLAST score
                  163
                  2.0e-86
E value
                  246
Match length
                  93
% identity
NCBI Description Oryza sativa mRNA for reversibly glycosylated polypeptide
                  418556
Seq. No.
                  uC-osroM202034a05b1
Seq. ID
                  BLASTX
Method
                  g3646373
NCBI GI
                  658
BLAST score
                  4.0e-69
E value
                  141
Match length
                  90
% identity
NCBI Description (AJ011078) RGP1 protein [Oryza sativa]
                  418557
Seq. No.
Seq. ID
                  uC-osroM202034a11b1
Method
                  BLASTX
                  g5734634
NCBI GI
                  293
BLAST score
                  2.0e-26
E value
                   81
Match length
                  70
% identity
                  (AP000391) Similar to putative lipase (AC006232) [Oryza
NCBI Description
                   sativa]
                   418558
Seq. No.
Seq. ID
                  uC-osroM202034b01b1
Method
                  BLASTX
                   g2385410
NCBI GI
BLAST score
                   212
E value
                   7.0e-17
Match length
                   149
                   34
% identity
                  (AB001372) TFIID subunit taf72p [Schizosaccharomyces pombe]
NCBI Description
                   >gi 3859081 emb CAA21958 (AL033406) tfiid subunit taf72p.
                   [Schizosaccharomyces pombe]
                   418559
Seq. No.
Seq. ID
                   uC-osroM202034b02b1
                   BLASTX
Method
                   q4835757
NCBI GI
BLAST score
                   258
                   4.0e-22
E value
                   119
Match length
                   54
% identity
NCBI Description (AC007202) EST gb AA404917 comes from this gene.
                   [Arabidopsis thaliana]
```

Seq. No. 418560

Seq. ID uC-osroM202034b03b1

Method BLASTN
NCBI GI g2773153
BLAST score 464

0.0e + 00E value 476 Match length 99 % identity NCBI Description Oryza sativa abscisic acid- and stress-inducible protein (Asr1) mRNA, complete cds 418561 Seq. No. uC-osroM202034b05b1 Seq. ID BLASTN Method g2331130 NCBI GI 98 BLAST score 1.0e-47 E value 321 Match length 90 % identity NCBI Description Oryza sativa glycine-rich protein (OSGRP1) mRNA, complete cds 418562 Seq. No. uC-osroM202034b06b1 Seq. ID BLASTN Method NCBI GI g6016845 107 BLAST score 6.0e-53 E value 351 Match length 83 % identity NCBI Description Oryza sativa genomic DNA, chromosome 1, clone:P0711E10 418563 Seq. No. Seq. ID uC-osroM202034b07b1 BLASTX Method NCBI GI g3757527 BLAST score 192 2.0e-14 E value 48 Match length 79 % identity NCBI Description (AC005167) putative ribosomal protein L27 [Arabidopsis thaliana] 418564 Seq. No. Seq. ID uC-osroM202034b08b1 BLASTX Method NCBI GI q4895189 154 BLAST score E value 6.0e-10 78 Match length % identity NCBI Description (AC007661) unknown protein [Arabidopsis thaliana] 418565 Seq. No. uC-osroM202034b11b1 Seq. ID Method BLASTX NCBI GI g3790102 BLAST score 448 E value 2.0e-44Match length 142

(AF095521) pyrophosphate-dependent phosphofructokinase

60

% identity

NCBI Description

NCBI GI

E value

BLAST score

Match length

q4454464

301 3.0e-27

77

alpha subunit [Citrus X paradisi]

418566 Seq. No. Seq. ID uC-osroM202034c01b1 Method BLASTX q2696221 NCBI GI BLAST score 567 E value 2.0e-58 147 Match length 73 % identity NCBI Description (D55708) chitinase [Oryza sativa] Seq. No. 418567 uC-osroM202034c02b1 Seq. ID Method BLASTX NCBI GI g1729971 BLAST score 500 E value 1.0e-50 Match length 145 % identity 71 TONOPLAST INTRINSIC PROTEIN, GAMMA (GAMMA TIP) NCBI Description (AQUAPORIN-TIP) >gi 1076745 pir S52004 gamma-Tip protein rice >gi 473997 dbj_BAA05017_ (D25534) gamma-Tip [Oryza sativa] 418568 Seq. No. uC-osroM202034c07b1 Seq. ID Method BLASTX NCBI GI g2499489 BLAST score 647 8.0e-68 E value Match length 149 81 % identity NCBI Description PYROPHOSPHATE--FRUCTOSE 6-PHOSPHATE 1-PHOSPHOTRANSFERASE BETA SUBUNIT (PFP) (6-PHOSPHOFRUCTOKINASE (PYROPHOSPHATE)) (PYROPHOSPHATE-DEPENDENT 6-PHOSPHOFRUCTOSE-1-KINASE) (PPI-PFK) >gi 483536 emb CAA83683 (Z32850) pyrophosphate-dependent phosphofructokinase beta subunit [Ricinus communis] Seq. No. 418569 uC-osroM202034c11a1 Seq. ID BLASTX Method q4454464 NCBI GI BLAST score 400 9.0e-39 E value 94 Match length 74 % identity NCBI Description (AC006234) unknown protein [Arabidopsis thaliana] 418570 Seq. No. uC-osroM202034c12a1 Seq. ID Method BLASTX

Match length

135

% identity (AC006234) unknown protein [Arabidopsis thaliana] NCBI Description Seq. No. 418571 Seq. ID uC-osroM202034d01b1 BLASTX Method q1729971 NCBI GI BLAST score 579 8.0e-60 E value 162 Match length % identity 73 TONOPLAST INTRINSIC PROTEIN, GAMMA (GAMMA TIP) NCBI Description (AQUAPORIN-TIP) >gi 1076745 pir S52004 gamma-Tip protein rice >gi_473997_dbj_BAA05017_ (D25534) gamma-Tip [Oryza sativa] 418572 Seq. No. uC-osroM202034d02a1 Seq. ID Method BLASTX q4314378 NCBI GI BLAST score 152 3.0e-10 E value 51 Match length % identity 47 (AC006232) putative lipase [Arabidopsis thaliana] NCBI Description >gi 5306262 gb AAD41994.1 AC006233 5 (AC006233) putative lipase [Arabidopsis thaliana] Seq. No. 418573 Seq. ID uC-osroM202034d02b1 BLASTX Method NCBI GI q4314378 BLAST score 209 E value 2.0e-16 Match length 89 % identity 51 (AC006232) putative lipase [Arabidopsis thaliana] NCBI Description >gi 5306262 gb AAD41994.1 AC006233 5 (AC006233) putative lipase [Arabidopsis thaliana] Seq. No. 418574 uC-osroM202034d03b1 Seq. ID BLASTX Method g1136122 NCBI GI BLAST score 711 3.0e-75 E value Match length 141 % identity 94 NCBI Description (X91807) alfa-tubulin [Oryza sativa] 418575 Seq. No. uC-osroM202034d04b1 Seq. ID Method BLASTX NCBI GI g6006848 BLAST score 368 3.0e-35 E value

% identity

61

```
55
% identity
                  (AC009540) unknown protein, 5' partial [Arabidopsis
NCBI Description
                  thaliana]
                  418576
Seq. No.
                  uC-osroM202034d05a1
Seq. ID
                  BLASTN
Method
                  g287400
NCBI GI
                  339
BLAST score
                  0.0e + 00
E value
                  386
Match length
                  97
% identity
NCBI Description Rice mRNA for peroxidase, complete cds
                  418577
Seq. No.
                  uC-osroM202034d05b1
Seq. ID
                  BLASTX
Method
                  g585661
NCBI GI
                  514
BLAST score
                  3.0e-52
E value
Match length
                  114
                  88
% identity
NCBI Description PEROXIDASE PRECURSOR >gi_287401_dbj_BAA03644_ (D14997)
                  peroxidase [Oryza sativa]
                   418578
Seq. No.
                  uC-osroM202034d06b1
Seq. ID
                  BLASTX
Method
                   g585661
NCBI GI
                   \bar{4}44
BLAST score
E value
                   4.0e-44
                   97
Match length
                   90
% identity
NCBI Description PEROXIDASE PRECURSOR >gi 287401 dbj BAA03644 (D14997)
                  peroxidase [Oryza sativa]
                   418579
Seq. No. Seq. ID
                   uC-osroM202034d08b1
                   BLASTX
Method
NCBI GI
                   g399015
                   736
BLAST score
                   3.0e-78
E value
Match length
                   150
                   93
% identity
NCBI Description ADP, ATP CARRIER PROTEIN PRECURSOR (ADP/ATP TRANSLOCASE)
                   (ADENINE NUCLEOTIDE TRANSLOCATOR) (ANT)
                   >gi_218145_dbj_BAA02161_ (D12637) ATP/ADP translocator
                   [Oryza sativa]
                   418580
Seq. No.
Seq. ID
                   uC-osroM202034d09b1
                   BLASTX
Method
                   q4455246
NCBI GI
BLAST score
                   177
E value
                   1.0e-12
Match length
                   64
```

Seq. ID Method

BLASTX

```
NCBI Description (AL035523) putative protein [Arabidopsis thaliana]
                  418581
Seq. No.
                  uC-osroM202034d11a1
Seq. ID
Method
                  BLASTX
                  g3341693
NCBI GI
                  206
BLAST score
                  3.0e-16
E value
Match length
                  69
% identity
                  58
                  (AC003672) unknown protein [Arabidopsis thaliana]
NCBI Description
                   418582
Seq. No.
                  uC\hbox{-}osroM202034e01a1
Seq. ID
                  BLASTX
Method
NCBI GI
                  g129591
                   317
BLAST score
                   4.0e-29
E value
                   70
Match length
                   86
% identity
                 PHENYLALANINE AMMONIA-LYASE >gi 295824_emb_CAA34226
NCBI Description
                   (X16099) phenylalanine ammonia-Tyase [Oryza sativa]
                   418583
Seq. No.
                   uC-osroM202034e01b1
Seq. ID
                   BLASTX
Method
NCBI GI
                   g82496
                   667
BLAST score
                   4.0e-70
E value
                   150
Match length
                   87
% identity
NCBI Description phenylalanine ammonia-lyase (EC 4.3.1.5) - rice
                   418584
Seq. No.
                   uC-osroM202034e02b1
Seq. ID
                   BLASTX
Method
                   q4126809
NCBI GI
                   660
BLAST score
                   1.0e-69
E value
                   135
Match length
                   55
% identity
NCBI Description (AB017042) glyoxalase I [Oryza sativa]
                   418585
Seq. No.
                   uC-osroM202034e04b1
Seq. ID
                   BLASTX
Method
                   q129591
NCBI GI
                   150
BLAST score
                   4.0e-25
E value
                   95
Match length
                   76
% identity
NCBI Description PHENYLALANINE AMMONIA-LYASE >gi_295824_emb_CAA34226_
                   (X16099) phenylalanine ammonia-lyase [Oryza sativa]
Seq. No.
                   418586
                   uC-osroM202034e05a1
```

Method

BLASTN

```
q3023713
NCBI GI
                  271
BLAST score
                  9.0e-24
E value
                  62
Match length
% identity
                  84
                  ENOLASE (2-PHOSPHOGLYCERATE DEHYDRATASE)
NCBI Description
                  (2-PHOSPHO-D-GLYCERATE HYDRO-LYASE) (OSE1) >gi_780372
                  (U09450) enolase [Oryza sativa]
                  418587
Seq. No.
                  uC-osroM202034e05b1
Seq. ID
                  BLASTX
Method
                  q3023713
NCBI GI
                  664
BLAST score
                  7.0e-70
E value
                  130
Match length
                  100
% identity
                  ENOLASE (2-PHOSPHOGLYCERATE DEHYDRATASE)
NCBI Description
                   (2-PHOSPHO-D-GLYCERATE HYDRO-LYASE) (OSE1) >gi_780372
                   (U09450) enolase [Oryza sativa]
Seq. No.
                   418588
                  uC-osroM202034e06b1
Seq. ID
                  BLASTX
Method
                  q300264
NCBI GI
                   478
BLAST score
                   6.0e-48
E value
                   138
Match length
                  70
% identity
                  (S59747) HSP68=68 kda heat-stress DnaK homolog [Solanum
NCBI Description
                   tuberosum=potatoes, Peptide Mitochondrial, 682 aa] [Solanum
                   tuberosum]
                   418589
Seq. No.
                   uC-osroM202034e07b1
Seq. ID
                   BLASTX
Method
                   g129591
NCBI GI
                   700
BLAST score
                   4.0e-74
E value
                   144
Match length
                   97
% identity
NCBI Description PHENYLALANINE AMMONIA-LYASE >gi_295824_emb_CAA34226
                   (X16099) phenylalanine ammonia-lyase [Oryza sativa]
Seq. No.
                   418590
Seq. ID
                   uC-osroM202034e08b1
                   BLASTX
Method
                   q4567312
NCBI GI
                   152
BLAST score
                   1.0e-09
E value
Match length
                   66
% identity
NCBI Description (AC005956) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   418591
                   uC-osroM202034e10a1
Seq. ID
```

```
g20280
NCBI GI
                  382
BLAST score
                  0.0e + 00
E value
                  430
Match length
                  97
% identity
NCBI Description Rice gene for phenylalanine ammonia-lyase (EC 4.3.1.5)
                  418592
Seq. No.
                  uC-osroM202034e10b1
Seq. ID
                  BLASTX
Method
                  g129591
NCBI GI
                  424
BLAST score
                  7.0e-42
E value
                  102
Match length
                  81
% identity
NCBI Description PHENYLALANINE AMMONIA-LYASE >gi 295824 emb CAA34226
                  (X16099) phenylalanine ammonia-lyase [Oryza sativa]
                  418593
Seq. No.
Seq. ID
                  uC-osroM202034e11a1
Method
                  BLASTX
                  q4097342
NCBI GI
                  187
BLAST score
                  5.0e-14
E value
                  42
Match length
                  76
% identity
NCBI Description (U57640) Bowman-Birk type trypsin inhibitor [Oryza sativa]
                   418594
Seq. No.
                  uC-osroM202034e11b1
Seq. ID
                  BLASTX
Method
                  g1800227
NCBI GI
                   456
BLAST score
                   2.0e-45
E value
                  121
Match length
                   40
% identity
NCBI Description (U76004) Bowman-Birk proteinase inhibitor [Oryza sativa]
                   418595
Seq. No.
Seq. ID
                   uC-osroM202034f01b1
                   BLASTX
Method
                   q4126809
NCBI GI
                   548
BLAST score
                   5.0e-70
E value
                  135
Match length
% identity
NCBI Description (AB017042) glyoxalase I [Oryza sativa]
                   418596
Seq. No.
                   uC-osroM202034f02b1
Seq. ID
Method
                   BLASTX
                   q4126809
NCBI GI
                   680
BLAST score
E value
                   1.0e-71
Match length
                   127
% identity
NCBI Description (AB017042) glyoxalase I [Oryza sativa]
```

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418597
Seq. No.
Seq. ID
                  uC-osroM202034f05b1
                  BLASTX
Method
NCBI GI
                  q4455335
                  158
BLAST score
                  2.0e-10
E value
Match length
                  75
                  47
% identity
NCBI Description (AL035525) putative protein [Arabidopsis thaliana]
                  418598
Seq. No.
Seq. ID
                  uC-osroM202034f07a1
Method
                  BLASTX
NCBI GI
                  g3341693
BLAST score
                  223
                  3.0e-18
E value
Match length
                  69
                  59
% identity
NCBI Description (AC003672) unknown protein [Arabidopsis thaliana]
                  418599
Seq. No.
Seq. ID
                  uC-osroM202034f09a1
Method
                  BLASTX
NCBI GI
                  q1729971
                  288
BLAST score
                  8.0e-26
E value
                  60
Match length
% identity
                  88
NCBI Description
                  TONOPLAST INTRINSIC PROTEIN, GAMMA (GAMMA TIP)
                  (AQUAPORIN-TIP) >gi_1076745_pir__S52004 gamma-Tip protein -
                  rice >gi 473997 dbj BAA05017 (D25534) gamma-Tip [Oryza
                  418600
Seq. No.
                  uC-osroM202034f09b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1729971
BLAST score
                  429
E value
                  2.0e-42
Match length
                  115
                  76
% identity
NCBI Description TONOPLAST INTRINSIC PROTEIN, GAMMA (GAMMA TIP)
                   (AQUAPORIN-TIP) >gi_1076745_pir__S52004 gamma-Tip protein -
                  rice >gi 473997 dbj BAA05017 (D25534) gamma-Tip [Oryza
                  sativa]
                  418601
Seq. No.
Seq. ID
                  uC-osroM202034f10b1
Method
                  BLASTX
                  g3122914
NCBI GI
BLAST score
                  598
                  5.0e-62
E value
                  169
Match length
% identity
                  62
NCBI Description VALYL-TRNA SYNTHETASE (VALINE--TRNA LIGASE) (VALRS)
                  >gi 1890130 gb AAB49704.1 (U89986) valyl tRNA synthetase
```

[Arabidopsis thaliana]

418602 Seq. No. uC-osroM202034f11b1 Seq. ID BLASTX Method g2196466 NCBI GI BLAST score 480 3.0e-48E value 145 Match length 63 % identity (Y13673) TATA binding protein-associated factor NCBI Description [Arabidopsis thaliana] 418603 Seq. No. uC-osroM202034f12b1 Seq. ID BLASTX Method g3461835 NCBI GI BLAST score 160 E value 9.0e-11 Match length 50 60 % identity (AC005315) putative protein kinase [Arabidopsis thaliana] NCBI Description >qi 3927840 (AC005727) putative protein kinase [Arabidopsis thaliana] 418604 Seq. No. Seq. ID uC-osroM202034g01b1 BLASTX Method g1184774 NCBI GI BLAST score 524 2.0e-53 E value Match length 107 91 % identity NCBI Description (U45856) cytosolic glyceroldehyde-3-phosphate dehydrogenase GAPC3 [Zea mays] 418605 Seq. No. uC-osroM202034g02a1 Seq. ID BLASTX Method NCBI GI g2497538 BLAST score 147 3.0e-09 E value Match length 34 85 % identity NCBI Description PYRUVATE KINASE, CYTOSOLIC ISOZYME >gi_466350 (L08632) pyruvate kinase [Glycine max] 418606 Seq. No. Seq. ID uC-osroM202034g02b1 BLASTX Method g2497538 NCBI GI BLAST score 559 E value 2.0e-57 Match length 134 79 % identity NCBI Description PYRUVATE KINASE, CYTOSOLIC ISOZYME >gi_466350 (L08632)

54853

pyruvate kinase [Glycine max]

418607 Seq. No. uC-osroM202034g03b1 Seq. ID BLASTX Method NCBI GI q1184774 609 BLAST score 2.0e-63 E value 144 Match length 82 % identity (U45856) cytosolic glyceroldehyde-3-phosphate dehydrogenase NCBI Description GAPC3 [Zea mays] 418608 Seq. No. Seq. ID uC-osroM202034g04b1 Method BLASTX NCBI GI g1332579 BLAST score 395 E value 2.0e-38 Match length 123 % identity NCBI Description (X98063) polyubiquitin [Pinus sylvestris] 418609 Seq. No. Seq. ID uC-osroM202034g05b1 Method BLASTX NCBI GI g5672692 BLAST score 573 4.0e-59 E value Match length 122 % identity 82 NCBI Description (AB028448) nuclease I [Hordeum vulgare] 418610 Seq. No. Seq. ID uC-osroM202034q06b1 Method BLASTX NCBI GI g2244865 BLAST score 156 E value 3.0e-10 Match length 128 % identity 38 NCBI Description (Z97337) hypothetical protein [Arabidopsis thaliana] Seq. No. 418611 uC-osroM202034g07b1 Seq. ID Method BLASTX NCBI GI g4895219 BLAST score 222 6.0e-18 E value Match length 106 % identity NCBI Description (AC007660) hypothetical protein [Arabidopsis thaliana] Seq. No. 418612 uC-osroM202034g10b1 Seq. ID BLASTX Method q3834322 NCBI GI

54854

252

BLAST score

```
2.0e-21
E value
                  86
Match length
                  57
% identity
                  (AC005679) EST gb_R30300 comes from this gene. [Arabidopsis
NCBI Description
                  thaliana]
                  418613
Seq. No.
                  uC-osroM202034g11b1
Seq. ID
                  BLASTX
Method
                  g1353516
NCBI GI
                  409
BLAST score
                  7.0e-40
E value
                  113
Match length
                  70
% identity
NCBI Description (U38651) sugar transporter [Medicago truncatula]
                  418614
Seq. No.
                  uC-osroM202034g12a1
Seq. ID
                  BLASTX
Method
                  q99758
NCBI GI
BLAST score
                  160
                  9.0e-11
E value
                  46
Match length
                  67
% identity
NCBI Description monosaccharid transport protein STP4 - Arabidopsis thaliana
                  >gi 16524_emb_CAA47325_ (X66857) sugar transport protein
                   [Arabidopsis thaliana]
                   418615
Seq. No.
                   uC-osroM202034g12b1
Seq. ID
                  BLASTX
Method
                   q1353516
NCBI GI
                   320
BLAST score
                   1.0e-29
E value
                   82
Match length
                   73
% identity
NCBI Description (U38651) sugar transporter [Medicago truncatula]
                   418616
Seq. No.
                   uC-osroM202034h01b1
Seq. ID
                  BLASTX
Method
NCBI GI
                   g6093997
                   270
BLAST score
                   5.0e - 24
E value
                   71
Match length
                   82
% identity
NCBI Description 60S RIBOSOMAL PROTEIN L11 >gi_2570507 (AF022736) ribosomal
                   protein [Oryza sativa]
                   418617
Seq. No.
                   uC-osroM202034h03b1
Seq. ID
                   BLASTX
Method
                   q3126967
NCBI GI
 BLAST score
                   533
 E value
                   1.0e-54
                   119
Match length
 % identity
                   16
```

```
NCBI Description (AF061807) polyubiquitin [Elaeagnus umbellata]
                  418618
Seq. No.
Seq. ID
                  uC-osroM202034h04b1
                  BLASTX
Method
                  g4588012
NCBI GI
                  454
BLAST score
                  3.0e-45
E value
                  131
Match length
                  68
% identity
                  (AF085717) putative callose synthase catalytic subunit
NCBI Description
                  [Gossypium hirsutum]
                  418619
Seq. No.
                  uC-osroM202034h09b1
Seq. ID
                  BLASTX
Method
                  g2832617
NCBI GI
BLAST score
                  235
                  7.0e-20
E value
Match length
                  71
% identity
                  61
NCBI Description (AL021711) putative protein [Arabidopsis thaliana]
                  418620
Seq. No.
Seq. ID
                  uC-osroM202034h10b1
Method
                  BLASTX
                  g4588012
NCBI GI
                  559
BLAST score
                  2.0e-57
E value
                  146
Match length
                  73
% identity
NCBI Description (AF085717) putative callose synthase catalytic subunit
                   [Gossypium hirsutum]
Seq. No.
                   418621
                  uC-osroM202034h11b1
Seq. ID
Method
                  BLASTX
                  g1771160
NCBI GI
                   356
BLAST score
E value
                   9.0e - 34
                  138
Match length
                   49
% identity
                  (X98929) SBT1 [Lycopersicon esculentum]
NCBI Description
                   >gi 3687305_emb_CAA06999.1_ (AJ006378) subtilisin-like
                   protease [Lycopersicon esculentum]
                   418622
Seq. No.
                   uC-osroM202035a02a1
Seq. ID
                   BLASTX
Method
NCBI GI
                   g4680197
BLAST score
                   416
                   7.0e-41
E value
Match length
                   102
% identity
                   78
                  (AF114171) putative beta-ketoacyl-CoA synthase [Sorghum
NCBI Description
```

bicolor]

```
Seq. ID
                  uC-osroM202035a03b1
Method
                  BLASTX
NCBI GI
                  g2501189
BLAST score
                  480
                  3.0e-48
E value
                  127
Match length
                  76
% identity
                  THIAMINE BIOSYNTHETIC ENZYME 1-1 PRECURSOR
NCBI Description
                  >gi 2130146 pir S61419 thiamine biosynthetic enzyme thi1-1
                   - maize >gi_596078 (U17350) thiamine biosynthetic enzyme
                  [Zea mays]
                  418624
Seq. No.
Seq. ID
                  uC-osroM202035a05a1
                  BLASTX
Method
                  g1710590
NCBI GI
BLAST score
                  150
E value
                  1.0e-09
Match length
                  89
                  44
% identity
NCBI Description 60S ACIDIC RIBOSOMAL PROTEIN P1 (L12) >gi 1209701 (U40147)
                  ribosomal protein L12 [Zea mays]
Seq. No.
                  418625
Seq. ID
                  uC-osroM202035a05b1
                  BLASTX
Method
NCBI GI
                  q2431769
BLAST score
                  272
E value
                  8.0e-24
                  110
Match length
% identity
NCBI Description (U62752) acidic ribosomal protein Pla [Zea mays]
Seq. No.
                   418626
                  uC-osroM202035a06a1
Seq. ID
                  BLASTN
Method
NCBI GI
                  g20280
BLAST score
                  286
E value
                   1.0e-160
Match length
                  314
% identity
                   98
NCBI Description Rice gene for phenylalanine ammonia-lyase (EC 4.3.1.5)
Seq. No.
                   418627
                  uC-osroM202035a06b1
Seq. ID
Method
                  BLASTX
NCBI GI
                   g129591
BLAST score
                   432
E value
                   1.0e-42
Match length
                  112
% identity
                   76
NCBI Description PHENYLALANINE AMMONIA-LYASE >gi 295824 emb_CAA34226_
                   (X16099) phenylalanine ammonia-lyase [Oryza sativa]
                   418628
Seq. No.
                   uC-osroM202035a08a1
Seq. ID
                                      54857
```

Seq. No.

NCBI Description

```
BLASTX
Method
NCBI GI
                  q3395432
                  604
BLAST score
                  9.0e-63
E value
Match length
                  144
                  76
% identity
NCBI Description
                  (AC004683) unknown protein [Arabidopsis thaliana]
                  >gi 5731261_gb_AAD48838.1_AF166352_1 (AF166352)
                  alanine:glyoxylate aminotransferase 2 homolog [Arabidopsis
                  thaliana]
                  418629
Seq. No.
Seq. ID
                  uC-osroM202035a08b1
                  BLASTX
Method
                  q3395432
NCBI GI
                  183
BLAST score
                  2.0e-13
E value
                  42
Match length
% identity
                   69
                  (AC004683) unknown protein [Arabidopsis thaliana]
NCBI Description
                  >gi 5731261_gb_AAD48838.1_AF166352_1 (AF166352)
                  alanine:glyoxylate aminotransferase 2 homolog [Arabidopsis
                  thaliana]
                   418630
Seq. No.
                  uC-osroM202035a09b1
Seq. ID
Method
                  BLASTX
                   g283008
NCBI GI
BLAST score
                   783
E value
                   1.0e-83
                   167
Match length
                   91
% identity
                   sucrose synthase (EC 2.4.1.13) - rice
NCBI Description
                   >qi 20366 emb CAA46017 (X64770) sucrose synthase [Oryza
                   sativa]
                   418631
Seq. No.
                   uC-osroM202035a10b1
Seq. ID
Method
                   BLASTX
                   g4314378
NCBI GI
BLAST score
                   302
                   2.0e-27
E value
                   139
Match length
                   44
% identity
                   (AC006232) putative lipase [Arabidopsis thaliana]
NCBI Description
                   >gi 5306262_gb_AAD41994.1_AC006233_5 (AC006233) putative
                   lipase [Arabidopsis thaliana]
                   418632
Seq. No.
                   uC-osroM202035a11b1
Seq. ID
                   BLASTX
Method
                   g5672692
NCBI GI
                   570
BLAST score
                   8.0e-59
E value
                   120
Match length
% identity
```

54858

(AB028448) nuclease I [Hordeum vulgare]

Seq. ID

```
418633
Seq. No.
Seq. ID
                  uC-osroM202035a12b1
                  BLASTX
Method
                  q129591
NCBI GI
BLAST score
                  402
                  3.0e-39
E value
                  98
Match length
                  81
% identity
NCBI Description PHENYLALANINE AMMONIA-LYASE >gi 295824 emb CAA34226
                  (X16099) phenylalanine ammonia-lyase [Oryza sativa]
                  418634
Seq. No.
                  uC-osroM202035b01a1
Seq. ID
                  BLASTX
Method
NCBI GI
                  g3355533
                  177
BLAST score
                  1.0e-12
E value
                  101
Match length
                  36
% identity
                  (AL021331) dJ366N23.1 (putative C. elegans UNC-93 (protein
NCBI Description
                  1, C46F11.1) LIKE protein) [Homo sapiens]
                   418635
Seq. No.
                  uC-osroM202035b04b1
Seq. ID
                  BLASTX
Method
                   g5919185
NCBI GI
                   290
BLAST score
                   6.0e-26
E value
Match length
                   92
% identity
                   61
NCBI Description (AF183809) arabinogalactan protein Pop14A9 [Populus alba x
                   Populus tremula]
Seq. No.
                   418636
                   uC-osroM202035b05b1
Seq. ID
                   BLASTX
Method
                   g4102839
NCBI GI
                   407
BLAST score
E value
                   1.0e-39
                   93
Match length
% identity
                   77
NCBI Description (AF016713) LeOPT1 [Lycopersicon esculentum]
                   418637
Seq. No.
                   uC-osroM202035b06b1
Seq. ID
                   BLASTX
Method
NCBI GI
                   g4335747
BLAST score
                   274
                   4.0e-24
E value
Match length
                   74
                   68
% identity
                   (AC006284) putative A3 protein [Vigna unguiculata]
NCBI Description
                   (integral membrane protein) [Arabidopsis thaliana]
Seq. No.
                   418638
```

54859

uC-osroM202035b07a1

NCBI GI

BLAST score

285

```
BLASTX
Method
                  g4539324
NCBI GI
BLAST score
                  147
                  3.0e-09
E value
                  53
Match length
                  57
% identity
                  (AL035679) kinesin like protein [Arabidopsis thaliana]
NCBI Description
                  418639
Seq. No.
                  uC-osroM202035b07b1
Seq. ID
                  BLASTX
Method
                  g5263326
NCBI GI
                  283
BLAST score
                  5.0e-25
E value
                  74
Match length
% identity
                  68
                  (ACO07727) Similar to gb_U06698 neuronal kinesin heavy
NCBI Description
                  chain from Homo sapiens and contains a PF_00225 Kinesin
                  motor domain. EST gb_AA042507 comes from this gene.
                  [Arabidopsis thaliana]
                  418640
Seq. No.
                  uC-osroM202035b09b1
Seq. ID
                  BLASTX
Method
                  g82496
NCBI GI
BLAST score
                  666
                  5.0e-70
E value
                  149
Match length
                  87
% identity
NCBI Description phenylalanine ammonia-lyase (EC 4.3.1.5) - rice
                   418641
Seq. No.
Seq. ID
                  uC-osroM202035b10b1
                  BLASTX
Method
NCBI GI
                  q4432865
                   629
BLAST score
                   1.0e-65
E value
                  177
Match length
                   68
% identity
NCBI Description (AC006300) putative cellulose synthase catalytic subunit
                   [Arabidopsis thaliana]
                   418642
Seq. No.
                   uC-osroM202035c01b1
Seq. ID
                   BLASTX
Method
NCBI GI
                   q4335739
BLAST score
                   148
                   2.0e-09
E value
                   49
Match length
                   57
% identity
NCBI Description (AC006248) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   418643
                   uC-osroM202035c03a1
Seq. ID
                   BLASTX
Method
                   q6015059
```

```
2.0e-25
E value
Match length
                  56
                  98
% identity
                  ELONGATION FACTOR 1-ALPHA (EF-1-ALPHA) >gi 2996096
NCBI Description
                  (AF030517) translation elongation factor-1 alpha; EF-1
                  alpha [Oryza sativa]
                  418644
Seq. No.
                  uC-osroM202035c03b1
Seq. ID
                  BLASTX
Method
                  q2662343
NCBI GI
BLAST score
                  706
                  1.0e-80
E value
                  153
Match length
                  99
% identity
NCBI Description (D63581) EF-1 alpha [Oryza sativa]
                  418645
Seq. No.
Seq. ID
                  uC-osroM202035c07a1
Method
                  BLASTN
NCBI GI
                  q3560532
BLAST score
                  56
                  1.0e-22
E value
                  230
Match length
                  93
% identity
NCBI Description Oryza sativa 24-methylene lophenol C24(1)methyltransferase
                  mRNA, complete cds
Seq. No.
                  418646
Seq. ID
                  uC-osroM202035c07b1
                  BLASTX
Method
                  q3560533
NCBI GI
BLAST score
                  653
                  1.0e-68
E value
Match length
                  123
                  98
% identity
NCBI Description (AF042333) 24-methylene lophenol C24(1)methyltransferase
                   [Oryza sativa]
Seq. No.
                  418647
Seq. ID
                  uC-osroM202035c08b1
Method
                  BLASTX
                  q3915019
NCBI GI
                  548
BLAST score
                  4.0e-56
E value
                  121
Match length
                  88
% identity
NCBI Description SUCROSE-PHOSPHATE SYNTHASE (UDP-GLUCOSE-FRUCTOSE-PHOSPHATE
                  GLUCOSYLTRANSFERASE) >gi_421958_pir__S34172
                   sucrose-phosphate synthase (EC 2.4.1.14) - potato
                   >gi_313265_emb_CAA51872_ (X73477) sucrose-phosphate
                   synthase [Solanum tuberosum]
                   418648
Seq. No.
                  uC-osroM202035c09b1
Seq. ID
```

BLASTX

g322525

Method NCBI GI

BLAST score

E value

313 1.0e-28

```
496
BLAST score
                   4.0e-50
E value
Match length
                  138
                   67
% identity
                  omnipotent suppressor protein SUP1 homolog (clone A18) -
NCBI Description
                  Arabidopsis thaliana (fragment) >gi 16512 emb CAA49171
                   (X69374) similar to yeast omnipotent suppressor protein
                   SUP1 (SUP45); ORF [Arabidopsis thaliana]
                   418649
Seq. No.
Seq. ID
                  uC-osroM202035c10a1
                  BLASTX
Method
                  g2388566
NCBI GI
BLAST score
                  178
                   6.0e-13
E value
                  73
Match length
                   51
% identity
                  (AC000098) Similar to Arabidopsis Fe(II) transport protein
NCBI Description
                   (gb U27590). [Arabidopsis thaliana]
                   418650
Seq. No.
Seq. ID
                   uC-osroM202035c10b1
                  BLASTX
Method
NCBI GI
                  g4836773
BLAST score
                   277
                   2.0e-24
E value
                   105
Match length
                   51
% identity
                  (AF136580) iron-regulated transporter 2 [Lycopersicon
NCBI Description
                   esculentum]
                   418651
Seq. No.
Seq. ID
                   uC-osroM202035c11a1
Method
                   BLASTX
NCBI GI
                   g2244898
BLAST score
                   359
                   4.0e-34
E value
                   182
Match length
                   44
% identity
NCBI Description (Z97338) phosphatase like protein [Arabidopsis thaliana]
Seq. No.
                   418652
                   uC-osroM202035c12b1
Seq. ID
                   BLASTX
Method
NCBI GI
                   q1684851
BLAST score
                   186
                   8.0e-14
E value
Match length
                   62
                   60
% identity
NCBI Description (U77935) DnaJ-like protein [Phaseolus vulgaris]
Seq. No.
                   418653
Seq. ID
                   uC-osroM202035d01a1
Method
                   BLASTX
                   g729135
NCBI GI
```

Method

NCBI GI

E value

BLAST score

```
Match length
                  70
% identity
                  81
                  CAFFEIC ACID 3-O-METHYLTRANSFERASE
NCBI Description
                  (S-ADENOSYSL-L-METHIONINE: CAFFEIC ACID
                  3-O-METHYLTRANSFERASE) (COMT) >gi 283034 pir S28612
                  catechol O-methyltransferase (EC 2.1.1.6) - maize
                  >qi 168532 (M73235) O-methyltransferase [Zea mays]
                  418654
Seq. No.
Seq. ID
                  uC-osroM202035d01b1
                  BLASTX
Method
NCBI GI
                  q4104220
BLAST score
                  478
                  6.0e-48
E value
                  150
Match length
% identity
                  (AF033538) caffeic acid O-methyltransferase; LPOMT1 [Lolium
NCBI Description
                  perenne]
                  418655
Seq. No.
                  uC-osroM202035d03b1
Seq. ID
                  BLASTX
Method
                  q4220527
NCBI GI
BLAST score
                  316
                  4.0e-29
E value
                  139
Match length
                  45
% identity
NCBI Description (AL035356) putative protein [Arabidopsis thaliana]
Seq. No.
                  418656
                  uC-osroM202035d04b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3063471
BLAST score
                  318
                  3.0e-29
E value
                  93
Match length
                  62
% identity
NCBI Description (AC003981) F22013.33 [Arabidopsis thaliana]
Seq. No.
                  418657
                  uC-osroM202035d06a1
Seq. ID
Method
                  BLASTX
                  q2499613
NCBI GI
                  265
BLAST score
                  5.0e-23
E value
                  68
Match length
                  68
% identity
NCBI Description MITOGEN-ACTIVATED PROTEIN KINASE HOMOLOG MMK2
                  >gi_1204129_emb_CAA57719_ (X82268) protein kinase [Medicago
                  sativa]
                   418658
Seq. No.
                  uC-osroM202035d06b1
Seq. ID
                  BLASTX
```

54863

g2499608

2.0e-56



```
Match length
                  129
% identity
                  MITOGEN-ACTIVATED PROTEIN KINASE HOMOLOG 4 (MAP KINASE 4)
NCBI Description
                  (ATMPK4) >gi_2129645_pir__S40470 mitogen-activated protein
                  kinase 4 (EC 2.7.1.-) - Arabidopsis thaliana
                  >gi_457400_dbj_BAA04867_ (D21840) MAP kinase [Arabidopsis
                  thaliana]
                  418659
Seq. No.
Seq. ID
                  uC-osroM202035d07a1
                  BLASTX
Method
                  q2388560
NCBI GI
BLAST score
                  162
                  5.0e-11
E value
                  71
Match length
% identity
NCBI Description (AC000098) YUP8H12.1 [Arabidopsis thaliana]
Seq. No.
                  418660
                  uC-osroM202035d07b1
Seq. ID
                  BLASTX
Method
NCBI GI
                  g3935137
                  419
BLAST score
E value
                  5.0e-41
                  125
Match length
% identity
NCBI Description (AC005106) T25N20.1 [Arabidopsis thaliana]
Seq. No.
                  418661
                  uC-osroM202035d10b1
Seq. ID
                  BLASTX
Method
NCBI GI
                  g3201618
BLAST score
                  724
E value
                  8.0e-77
Match length
                  157
                  82
% identity
NCBI Description (AC004669) Sop2p-like protein [Arabidopsis thaliana]
Seq. No.
                  418662
                  uC-osroM202035d11b1
Seq. ID
Method
                  BLASTX
                  q1161566
NCBI GI
                  162
BLAST score
                  7.0e-11
E value
Match length
                  66
% identity
                  45
NCBI Description (X94943) peroxidase [Lycopersicon esculentum]
                  418663
Seq. No.
                  uC-osroM202035d12a1
Seq. ID
                  BLASTX
Method
                  g417154
NCBI GI
```

Method BLASTX
NCBI GI g417154
BLAST score 421
E value 3.0e-41
Match length 90
% identity 91

NCBI Description HEAT SHOCK PROTEIN 82 >gi_100685_pir__S25541 heat shock

protein 82 - rice (strain Taichung Native One)
>gi_20256_emb_CAA77978_ (Z11920) heat shock protein 82
(HSP82) [Oryza sativa]

Seq. No. 418664

Seq. ID uC-osroM202035d12b1

Method BLASTX
NCBI GI g417154
BLAST score 495
E value 5.0e-50
Match length 148
% identity 68

NCBI Description HEAT SHOCK PROTEIN 82 >gi 100685 pir S25541 heat shock

protein 82 - rice (strain Taichung Native One)

>gi_20256_emb_CAA77978_ (Z11920) heat shock protein 82

(HSP82) [Oryza sativa]

Seq. No. 418665

Seq. ID uC-osroM202035e01a1

Method BLASTX
NCBI GI g2827143
BLAST score 341
E value 7.0e-32
Match length 136
% identity 49

NCBI Description (AF027174) cellulose synthase catalytic subunit

[Arabidopsis thaliana]

Seq. No. 418666

Seq. ID uC-osroM202035e01b1

Method BLASTX
NCBI GI g5081779
BLAST score 339
E value 1.0e-31
Match length 68
% identity 90

NCBI Description (AF150630) cellulose synthase [Gossypium hirsutum]

Seq. No. 418667

Seq. ID uC-osroM202035e02a1

Method BLASTX
NCBI GI g2781433
BLAST score 232
E value 3.0e-19
Match length 109
% identity 46

NCBI Description (AF030052) RSW1-like cellulose synthase catalytic subunit

[Oryza sativa subsp. japonica]

Seq. No. 418668

Seq. ID uC-osroM202035e02b1

Method BLASTX
NCBI GI g5081779
BLAST score 189
E value 5.0e-19
Match length 74
% identity 67

```
NCBI Description (AF150630) cellulose synthase [Gossypium hirsutum]
Seq. No.
                   418669
                  uC-osroM202035e03b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q6056385
BLAST score
                   672
                  1.0e-70
E value
Match length
                  170
% identity
                  69
NCBI Description (AC009894) Unknown protein [Arabidopsis thaliana]
                   418670
Seq. No.
                  uC-osroM202035e04b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3540181
BLAST score
                  248
E value
                  6.0e-21
Match length
                  155
% identity
                  39
NCBI Description (AC004122) Unknown protein [Arabidopsis thaliana]
Seq. No.
                   418671
                  uC-osroM202035e09a1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g425794
BLAST score
                  83
E value
                  6.0e-39
Match length
                  123
% identity
                  92
NCBI Description
                  Rice mRNA for heat shock protein 82 (gene name AD167),
                  partial cds
Seq. No.
                  418672
                  uC-osroM202035e10a1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g829283
BLAST score
                  175
                  4.0e-14
E value
                  48
Match length
                  92
% identity
NCBI Description (Z15018) heat shock protein hsp82 [Oryza sativa]
                  418673
Seq. No.
                  uC-osroM202035e10b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g417154
BLAST score
                  628
E value
                  1.0e-65
Match length
                  130
% identity
                  98
NCBI Description HEAT SHOCK PROTEIN 82 >gi_100685_pir__S25541 heat shock
                  protein 82 - rice (strain Taichung Native One)
                  >gi_20256_emb_CAA77978_ (Z11920) heat shock protein 82
                   (HSP82) [Oryza sativa]
Seq. No.
                  418674
```

% identity

36

uC-osroM202035e12a1 Seq. ID Method BLASTX NCBI GI q3033381 BLAST score 185 1.0e-13 E value 43 Match length 74 % identity NCBI Description (AC004238) putative UDP-galactose-4-epimerase [Arabidopsis thaliana] 418675 Seq. No. Seq. ID uC-osroM202035e12b1 Method BLASTX q4587518 NCBI GI BLAST score 239 6.0e-20 E value Match length 90 % identity 59 NCBI Description (AC007060) Strong similarity to F19I3.8 gi 3033381 putative UDP-galactose-4-epimerase from Arabidopsis thaliana BAC gb AC004238 and is a member of PF 01370 the NAD dependent epimerase/dehydratase family. EST gb AA59 Seq. No. 418676 uC-osroM202035f01a1 Seq. ID BLASTX Method NCBI GI q584825 BLAST score 305 E value 1.0e-27 Match length 81 72 % identity NCBI Description B2 PROTEIN >gi 322726 pir S32124 B2 protein - carrot >gi 297889 emb CAA51078 (X72385) B2 protein [Daucus carota] 418677 Seq. No. uC-osroM202035f02a1 Seq. ID Method BLASTX NCBI GI g584825 BLAST score 325 E value 5.0e-30 Match length 84 73 % identity B2 PROTEIN >gi 322726 pir S32124 B2 protein - carrot NCBI Description >gi 297889 emb CAA51078 (X72385) B2 protein [Daucus carota] 418678 Seq. No. uC-osroM202035f03a1 Seq. ID Method BLASTX NCBI GI g4894862 BLAST score 146 E value 5.0e-09 Match length 116

NCBI Description (AF135438) de novo DNA methyltransferase 3 [Danio rerio]

Seq. ID

Method

NCBI GI

Seq. No. 418679 Seq. ID uC-osroM202035f04a1 Method BLASTN NCBI GI q474002 BLAST score 52 E value 2.0e-20 Match length 71 % identity 94 NCBI Description Rice mRNA, partial homologous to ribosomal protein L39 gene Seq. No. 418680 Seq. ID uC-osroM202035f04b1 Method BLASTX NCBI GI q1710551 BLAST score 281 E value 5.0e-25 Match length 51 % identity 100 NCBI Description 60S RIBOSOMAL PROTEIN L39 >gi 1177369 emb CAA64728.1 (X95458) ribosomal protein L3 $\overline{9}$ [Zea mays] Seq. No. 418681 Seq. ID uC-osroM202035f06b1 Method BLASTX NCBI GI g3201625 BLAST score 364 E value 1.0e-34 Match length 149 % identity 56 NCBI Description (AC004669) hypothetical protein [Arabidopsis thaliana] Seq. No. 418682 Seq. ID uC-osroM202035f09a1 Method BLASTX NCBI GI g3927836 BLAST score 257 E value 4.0e-22 Match length 55 % identity 82 NCBI Description (AC005727) unknown protein [Arabidopsis thaliana] Seq. No. 418683 uC-osroM202035f10b1 Seq. ID Method BLASTX NCBI GI q3287695 BLAST score 413 E value 2.0e-40 Match length 172 % identity 47 NCBI Description (AC003979) Similar to hypothetical protein C34B7.2 gb_1729503 from C. elegans cosmid gb Z83220. [Arabidopsis thaliana] Seq. No. 418684

54868

uC-osroM202035f11b1

BLASTX

g3046815

```
BLAST score
                   548
E value
                   4.0e-56
Match length
                  164
% identity
NCBI Description (AL021687) cytochrome P450 [Arabidopsis thaliana]
Seq. No.
                  418685
                  uC-osroM202035f12a1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q6041853
BLAST score
                  313
                  1.0e-28
E value
Match length
                  77
% identity
NCBI Description (AC009853) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  418686
Seq. ID
                  uC-osroM202035f12b1
Method
                  BLASTX
NCBI GI
                  q6041853
BLAST score
                  429
                  3.0e-42
E value
Match length
                  128
% identity
                  62
NCBI Description (AC009853) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  418687
Seq. ID
                  uC-osroM202035g02a1
Method
                  BLASTX
NCBI GI
                  q5679838
BLAST score
                  244
E value
                  1.0e-20
Match length
                  110
% identity
                  43
NCBI Description (AJ243961) has similarity to Arabidopsis thaliana
                  gi 3068705 [Oryza sativa]
                  418688
Seq. No.
Seq. ID
                  uC-osroM202035g03b1
Method
                  BLASTX
                  g4220527
NCBI GI
BLAST score
                  175
E value
                  1.0e-12
Match length
                  53
% identity
                  62
NCBI Description (AL035356) putative protein [Arabidopsis thaliana]
                  418689
Seq. No.
Seq. ID
                  uC-osroM202035g06b1
Method
                  BLASTX
NCBI GI
                  g3927826
BLAST score
                  233
                  3.0e-19
E value
Match length
                  100
% identity
                  46
NCBI Description (AC005727) hypothetical protein [Arabidopsis thaliana]
```

```
418690
Seq. No.
Seq. ID
                   uC-osroM202035g07b1
                   BLASTX
Method
NCBI GI
                   g3132310
BLAST score
                   872
                   4.0e-94
E value
                   175
Match length
% identity
NCBI Description (AB012228) phosphoenolpyruvate carboxylase [Zea mays]
                   418691
Seq. No.
                  uC-osroM202035g08a1
Seq. ID
Method
                   BLASTX
NCBI GI
                  g3757515
BLAST score
                  156
E value
                   1.0e-10
Match length
                   93
% identity
                   44
NCBI Description
                  (AC005167) hypothetical protein [Arabidopsis thaliana]
                   >gi_4581130_gb_AAD24620.1 AC005825 27 (AC005825)
                   hypothetical protein [Arabidopsis thaliana]
                   418692
Seq. No.
Seq. ID
                   uC-osroM202035g08b1
Method
                   BLASTX
NCBI GI
                  g3757515
BLAST score
                   329
                  1.0e-30
E value
Match length
                   88
% identity
                  (AC005167) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                  >gi 4581130 gb AAD24620.1 AC005825 27 (AC005825)
                  hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   418693
Seq. ID
                  uC-osroM202035g10a1
Method
                  BLASTN
NCBI GI
                   g1777454
BLAST score
                   132
E value
                   5.0e-68
Match length
                   215
% identity
NCBI Description
                  Oryza sativa pyruvate decarboxylase 2 (pdc2) gene, complete
                  cds
                   418694
Seq. No.
                  uC-osroM202035g10b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1706331
BLAST score
                  301
E value
                  3.0e-27
Match length
                  78
                  78
% identity
```

Seq. No. 418695

NCBI Description PYRUVATE DECARBOXYLASE ISOZYME 3 (PDC) >gi_476284 (U07338) pyruvate decarboxylase [Oryza sativa]

Seq. No.

```
uC-osroM202035q11b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1657621
BLAST score
                  628
E value
                  2.0e-65
                  154
Match length
                  77
% identity
NCBI Description (U72505) G6p [Arabidopsis thaliana] >gi 3068711 (AF049236)
                  putative acyl-coA dehydrogenase [Arabidopsis thaliana]
                  >gi 5478795 dbj BAA82478.1_ (AB017643) Short-chain acyl CoA
                  oxidase [Arabidopsis thaliana]
Seq. No.
                  418696
                  uC-osroM202035g12b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4103635
BLAST score
                  201
                  2.0e-15
E value
Match length
                  78
% identity
                  47
NCBI Description (AF026538) ABA-responsive protein [Hordeum vulgare]
Seq. No.
                  418697
Seq. ID
                  uC-osroM202035h01b1
Method
                  BLASTX
NCBI GI
                  g4835771
BLAST score
                  163
E value
                  5.0e-11
Match length
                  70
% identity
                  51
                 (AC007202) Similar to gi 3844599 F31D5.2 gene product from
NCBI Description
                  Caenorhabditis elegans cosmid gb U28941 and contains
                  PF 00097 Zinc (Ring) finger C3HC4 domain. ESTs gb_F19963
                  and gb_T42582 come from this gene. [Arabidops
Seq. No.
                  418698
                  uC-osroM202035h03b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2492834
BLAST score
                  156
E value
                  3.0e-10
Match length
                  98
% identity
                  43
NCBI Description PUTATIVE AMIDASE >gi 1224069 (U49269) amidase [Moraxella
                  catarrhalis]
Seq. No.
                  418699
                  uC-osroM202035h04a1
Seq. ID
Method'
                  BLASTN
NCBI GI
                  g340520
BLAST score
                  34
E value
                  2.0e-09
                  62
Match length
% identity
                  89
NCBI Description Coptis japonica triosphosphate isomerase mRNA, complete cds
```

Seq. ID uC-osroM202035h04b1 Method BLASTX g136057 NCBI GI BLAST score 424 E value 1.0e-41 Match length 120 68 % identity TRIOSEPHOSPHATE ISOMERASE, CYTOSOLIC (TIM) NCBI Description >gi_99499_pir__A32187 (S)-tetrahydroberberine oxidase -Coptis japonica >gi_556171 (J04121) triosephosphate isomerase [Coptis japonica] 418701 Seq. No. Seq. ID uC-osroM202035h05b1 Method BLASTX NCBI GI g5802955 BLAST score 227 E value 1.0e-18 101 Match length 48 % identity NCBI Description (AF178990) stress related protein [Vitis riparia] 418702 Seq. No. uC-osroM202035h06b1 Seq. ID Method BLASTX NCBI GI g4678372 BLAST score 159 E value 1.0e-10 Match length 91 % identity 44 NCBI Description (AL049656) putative protein [Arabidopsis thaliana] 418703 Seq. No. uC-osroM202035h07a1 Seq. ID Method BLASTX NCBI GI g4490736 BLAST score 152 6.0e-10 E value Match length 59 % identity NCBI Description (AL035708) putative protein [Arabidopsis thaliana] 418704 Seq. No. Seq. ID uC-osroM202035h07b1 Method BLASTX NCBI GI q4490736 BLAST score 524 E value 2.0e-53 Match length 154 % identity

NCBI Description (AL035708) putative protein [Arabidopsis thaliana]

Seq. No. 418705

Seq. ID uC-osroM202035h08b1

Method BLASTX NCBI GI g6056375 BLAST score 317



E value 3.0e-29 Match length 137 % identity 47

NCBI Description (AC009894) Similar to serine/threonine kinases [Arabidopsis

thaliana]

Seq. No. 418706

Seq. ID uC-osroM202035h11b1

Method BLASTX
NCBI GI g1155261
BLAST score 716
E value 7.0e-76
Match length 153
% identity 90

NCBI Description (U40217) eukaryotic release factor 1 homolog [Arabidopsis

thaliana]

Seq. No. 418707

Seq. ID uC-osroM202035h12b1

Method BLASTX
NCBI GI g3128176
BLAST score 325
E value 4.0e-30
Match length 111
% identity 54

NCBI Description (AC004521) unknown protein [Arabidopsis thaliana]

Seq. No. 418708

Seq. ID uC-osroM202036a05a1

Method BLASTN
NCBI GI g809513
BLAST score 152
E value 3.0e-80
Match length 184
% identity 96

NCBI Description Rice mRNA for ferredoxin-nitrite reductase, complete cds

Seq. No. 418709

Seq. ID uC-osroM202036a05b1

Method BLASTX
NCBI GI g2130072
BLAST score 509
E value 8.0e-52
Match length 109
% identity 92

NCBI Description ferredoxin--nitrite reductase (EC 1.7.7.1) - rice

>gi 809514 dbj BAA09122 (D50556) ferredoxin-nitrite

reductase [Oryza sativa]

Seq. No. 418710

Seq. ID uC-osroM202036a08b1

Method BLASTX
NCBI GI g5360230
BLAST score 825
E value 1.0e-88
Match length 150
% identity 99

```
NCBI Description (AB015287) Ran [Oryza sativa]
                  418711
Seq. No.
Seq. ID
                  uC-osroM202036a10b1
Method
                  BLASTX
NCBI GI
                  q548770
BLAST score
                  595
E value
                  8.0e-62
                  124
Match length
% identity
NCBI Description 60S RIBOSOMAL PROTEIN L3 >gi 481228 pir S38359 ribosomal
                  protein L3 - rice >gi 303853 dbj BAA02155 (D12630)
                  ribosomal protein L3 [Oryza sativa]
                  418712
Seq. No.
                  uC-osroM202036a11a1
Seq. ID
Method
                  BLASTN
NCBI GI
                  q809513
BLAST score
                  56
E value
                  9.0e-23
                  116
Match length
% identity
NCBI Description Rice mRNA for ferredoxin-nitrite reductase, complete cds
                  418713
Seq. No.
                  uC-osroM202036a11b1
Seq. ID
                  BLASTX
Method
NCBI GI
                  q1350969
BLAST score
                  346
E value
                  2.0e-32
Match length
                  66
                  95
% identity
NCBI Description 40S RIBOSOMAL PROTEIN S26 (S31) >gi 971284 dbj BAA07208
                  (D38011) ribosomal protein S31 [Oryza sativa]
Seq. No.
                  418714
                  uC-osroM202036a12a1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2245136
BLAST score
                  178
E value
                  3.0e-13
                  65
Match length
% identity
                  48
NCBI Description (Z97344) trehalose-6-phosphate synthase like protein
                  [Arabidopsis thaliana]
                  418715
Seq. No.
                  uC-osroM202036b01b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3860277
BLAST score
                  414
E value
                  2.0e-40
Match length
                  132
% identity
                  64
                  (AC005824) putative ribosomal protein L10 [Arabidopsis
NCBI Description
                  thaliana] >gi_4314394_gb_AAD15604_ (AC006232) putative
                  ribosomal protein L10A [Arabidopsis thaliana]
```

Method

BLASTX

Seq. No. 418716 uC-osroM202036b02b1 Seq. ID Method BLASTX NCBI GI q3860277 BLAST score 589 E value 6.0e-61 Match length 157 % identity 73 (AC005824) putative ribosomal protein L10 [Arabidopsis NCBI Description thaliana] >gi 4314394 gb AAD15604 (AC006232) putative ribosomal protein L10A [Arabidopsis thaliana] Seq. No. 418717 uC-osroM202036b04b1 Seq. ID Method BLASTX NCBI GI q4467099 BLAST score 597 E value 6.0e-62 Match length 146 % identity 85 NCBI Description (AL035538) glycine hydroxymethyltransferase like protein [Arabidopsis thaliana] Seq. No. 418718 Seq. ID uC-osroM202036b05b1 Method BLASTX NCBI GI q2832643 BLAST score 179 E value 5.0e-13 Match length 66 % identity 55 NCBI Description (AL021710) hypothetical protein [Arabidopsis thaliana] 418719 Seq. No. uC-osroM202036b07a1 Seq. ID Method BLASTX NCBI GI q4510402 BLAST score 180 E value 1.0e-13 Match length 40 % identity 85 NCBI Description (AC006587) putative AP2 domain [Arabidopsis thaliana] 418720 Seq. No. uC-osroM202036b08a1 Seq. ID Method BLASTN NCBI GI g5042437 BLAST score 211 1.0e-115 E value Match length 306 93 % identity NCBI Description Oryza sativa BAC T49B20 genomic sequence, complete sequence Seq. No. 418721 uC-osroM202036b08b1 Seq. ID

```
NCBI GI
                  g5042456
BLAST score
                  583
E value
                  2.0e-60
Match length
                  109
% identity
                  100
                 (AC007789) putative pathogenesis related protein [Oryza
NCBI Description
                  sativa]
                  418722
Seq. No.
                  uC-osroM202036b09b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1839188
BLAST score
                  555
                  1.0e-57
E value
Match length
                  134
% identity
                  85
NCBI Description (U86081) root hair defective 3 [Arabidopsis thaliana]
                  418723
Seq. No.
                  uC-osroM202036b10a1
Seq. ID
                  BLASTN
Method
NCBI GI
                  q20365
BLAST score
                  162
                  4.0e-86
E value
                  210
Match length
% identity
                  94
NCBI Description O.sativa RSs1 gene for sucrose synthase
Seq. No.
                  418724
                  uC-osroM202036b10b1
Seq. ID
                  BLASTX
Method
NCBI GI
                  g283008
BLAST score
                  784
                  7.0e-84
E value
                  168
Match length
                  90
% identity
NCBI Description
                  sucrose synthase (EC 2.4.1.13) - rice
                  >gi_20366_emb_CAA46017_ (X64770) sucrose synthase [Oryza
                  sativa]
                  418725
Seq. No.
Seq. ID
                  uC-osroM202036b12b1
Method
                  BLASTX
NCBI GI
                  g1203832
BLAST score
                  307
                  2.0e-28
E value
Match length
                  90
% identity
                  79
NCBI Description
                  (U46003) beta-D-glucan exohydrolase, isoenzyme ExoII
                   [Hordeum vulgare] >gi_1588407_prf__2208395A beta-D-glucan
                  exohydrolase [Hordeum vulgare]
```

g2613143 BLAST score 515

BLASTX

418726

uC-osroM202036c02b1

Seq. No.

Seq. ID Method

NCBI GI

Seq. No.

418732

```
E value
                   2.0e-52
Match length
                   114
% identity
                   85
NCBI Description (AF030548) tubulin [Oryza sativa]
Seq. No.
                  418727
Seq. ID
                  uC-osroM202036c06a1
Method
                  BLASTN
NCBI GI
                  g1261857
BLAST score
                  281
                  1.0e-157
E value
Match length
                  301
% identity
                  98
NCBI Description Rice CatA gene for catalase, complete cds
Seq. No.
                  418728
Seq. ID
                  uC-osroM202036c06b1
Method
                  BLASTX
NCBI GI
                  g2130069
BLAST score
                  836
E value
                  6.0e-90
Match length
                  157
% identity
                  99
NCBI Description catalase (EC 1.11.1.6) catA - rice
                  >gi_1261858_dbj_BAA06232_ (D29966) catalase [Oryza sativa]
Seq. No.
                  418729
Seq. ID
                  uC-osroM202036c10b1
Method
                  BLASTX
NCBI GI
                  g4539459
BLAST score
                  256
                  6.0e-22
E value
Match length
                  82
% identity
                  57
NCBI Description (AL049500) putative protein [Arabidopsis thaliana]
Seq. No.
                  418730
Seq. ID
                  uC-osroM202036d01a1
Method
                  BLASTN
NCBI GI
                  g20280
BLAST score
                  146
E value
                  1.0e-76
Match length
                  170
% identity
                  96
NCBI Description Rice gene for phenylalanine ammonia-lyase (EC 4.3.1.5)
Seq. No.
                  418731
Seq. ID
                  uC-osroM202036d01b1
Method
                  BLASTX
NCBI GI
                  g82496
BLAST score
                  603
E value
                  1.0e-62
Match length
                  150
% identity
NCBI Description phenylalanine ammonia-lyase (EC 4.3.1.5) - rice
```

E value

1.0e-12

uC-osroM202036d02b1 Seq. ID Method BLASTX q4835227 NCBI GI BLAST score 270 E value 1.0e-23 Match length 128 47 % identity NCBI Description (AL049862) glycosyltransferase-like protein [Arabidopsis thaliana] 418733 Seq. No. uC-osroM202036d03a1 Seq. ID Method BLASTN NCBI GI g20243 BLAST score 94 2.0e-45 E value Match length 122 93 % identity NCBI Description O.sativa GP28 gene (partial) 418734 Seq. No. uC-osroM202036d03b1 Seq. ID Method BLASTX g478740 NCBI GI 419 BLAST score 9.0e-42 E value Match length 101 % identity NCBI Description phenylalanine ammonia-lyase (EC 4.1.3.5) - rice Seq. No. 418735 Seq. ID uC-osroM202036d04b1 Method BLASTN NCBI GI q20367 BLAST score 75 E value 3.0e - 34Match length 167 86 % identity NCBI Description Oryza sativa shoot GS1 mRNA for cytosolic glutamine synthetase (EC 6.3.1.2) (clone lambda-GS28) 418736 Seq. No. uC-osroM202036d05a1 Seq. ID BLASTX Method NCBI GI q3033397 BLAST score 169 E value 2.0e-12 Match length 38 87 % identity NCBI Description (AC004238) unknown protein [Arabidopsis thaliana] Seq. No. 418737 uC-osroM202036d05b1 Seq. ID Method BLASTX NCBI GI g3033397 BLAST score 176

Match length 43 % identity 77

NCBI Description (AC004238) unknown protein [Arabidopsis thaliana]

Seq. No. 418738

Seq. ID uC-osroM202036d06a1

Method BLASTN
NCBI GI g1255684
BLAST score 233
E value 1.0e-128
Match length 237
% identity 100

NCBI Description Rice mRNA for aspartic protease, complete cds

Seq. No. 418739

Seq. ID uC-osroM202036d06b1

Method BLASTX
NCBI GI g2499819
BLAST score 879
E value 6.0e-95
Match length 173
% identity 99

NCBI Description ASPARTIC PROTEINASE ORYZASIN 1 PRECURSOR

>gi_2130068_pir___S66516 aspartic proteinase 1 precursor rice >gi_1030715_dbj_BAA06876_ (D32165) aspartic protease
[Oryza sativa] >gi_1711289_dbj_BAA06875_ (D32144) aspartic

protease [Oryza sativa]

Seq. No. 418740

Seq. ID uC-osroM202036d08b1

Method BLASTX
NCBI GI g2352492
BLAST score 536
E value 8.0e-55
Match length 155
% identity 63

NCBI Description (AF005047) transport inhibitor response 1 [Arabidopsis

thaliana] >gi 2352494 (AF005048) transport inhibitor

response 1 [Arabidopsis thaliana]

Seq. No. 418741

Seq. ID uC-osroM202036d12b1

Method BLASTX
NCBI GI g543711
BLAST score 534
E value 2.0e-54
Match length 109
% identity 100

NCBI Description 14-3-3-LIKE PROTEIN S94 >gi_419796_pir__S30927 14-3-3

protein homolog - rice >gi 303859 dbj BAA03711 (D16140)

brain specific protein [Oryza satīva]

Seq. No. 418742

Seq. ID uC-osroM202036e01b1

Method BLASTX NCBI GI g4503521 BLAST score 397 E value 2.0e-38 Match length 170 % identity 47 murine mammary tumor integration site 6 (oncogene homolog) NCBI Description >gi 2498490 sp Q64252 INT6 MOUSE VIRAL INTEGRATION SITE PROTEIN INT-6 > gi 2114363 (U62962) similar to mouse Int-6 [Homo sapiens] >q1 2351382 (U54562) eIF3-p48 [Homo sapiens] >qi 2688818 (U85947) Int-6 [Homo sapiens] >qi 2695701 (U94175) mammary tumor-associated protein INT6 [Homo sapiens] Seq. No. 418743 uC-osroM202036e04b1 Seq. ID Method BLASTX NCBI GI q401140 BLAST score 883 E value 2.0e-95 Match length 165 % identity 98 NCBI Description SUCROSE SYNTHASE 2 (SUCROSE-UDP GLUCOSYLTRANSFERASE 2) >gi 20095 emb CAA41774 (X59046) sucrose-UDP glucosyltransferase (isoenzyme 2) [Oryza sativa] >gi 1587662 prf 2207194A sucrose synthase:ISOTYPE=2 [Oryza satīva] Seq. No. 418744 Seq. ID uC-osroM202036e05b1 Method BLASTX NCBI GI q5882723 BLAST score 204 E value 8.0e-16 Match length 120 % identity 39 NCBI Description (AC008263) F25A4.3 [Arabidopsis thaliana] Seq. No. 418745 uC-osroM202036e06b1 Seq. ID Method BLASTX NCBI GI q5031281 BLAST score 350 E value 5.0e-33 Match length 117 60 % identity NCBI Description (AF139499) unknown [Prunus armeniaca] 418746 Seq. No. uC-osroM202036e07b1 Seq. ID ${\tt BLASTX}$ Method NCBI GI g4753882 BLAST score 197

Method BLASTX
NCBI GI g4753882
BLAST score 197
E value 4.0e-15
Match length 89
% identity 48

NCBI Description (AL049754) putative aspartate aminotransferase

[Streptomyces coelicolor]

Seq. No. 418747



Seq. ID uC-osroM202036e08b1

Method BLASTX
NCBI GI g1705678
BLAST score 810
E value 7.0e-87
Match length 163
% identity 95

NCBI Description CELL DIVISION CYCLE PROTEIN 48 HOMOLOG (VALOSIN CONTAINING

PROTEIN HOMOLOG) (VCP) >gi_862480 (U20213) valosin-containing protein [Glycine max]

Seq. No. 418748

Seq. ID uC-osroM202036e09b1

Method BLASTX
NCBI GI g2275211
BLAST score 753
E value 3.0e-80
Match length 169
% identity 86

NCBI Description (AC002337) RNA helicase isolog [Arabidopsis thaliana]

Seq. No. 418749

Seq. ID uC-osroM202036e10b1

Method BLASTX
NCBI GI g129916
BLAST score 643
E value 2.0e-69
Match length 149
% identity 89

NCBI Description PHOSPHOGLYCERATE KINASE, CYTOSOLIC >gi 66911 pir TVWTGY

phosphoglycerate kinase (EC 2.7.2.3), cytosolic - wheat
>gi 21835 emb CAA33302 (X15232) phosphoglycerate kinase

(AA 1 - 401) [Triticum aestivum]

Seq. No. 418750

Seq. ID uC-osroM202036e11b1

Method BLASTX
NCBI GI g285636
BLAST score 210
E value 1.0e-21
Match length 66
% identity 82

NCBI Description (D14161) ORF [Hordeum vulgare]

Seq. No. 418751

Seq. ID uC-osroM202036f02b1

Method BLASTX
NCBI GI g1352613
BLAST score 239
E value 5.0e-20
Match length 53
% identity 92

NCBI Description OCS-ELEMENT BINDING FACTOR 1 (OCSBF-1)

>gi_444047_emb_CAA44607_ (X62745) ocs-binding factor 1 [Zea

mays]

Seq. No. 418752

Seq. ID uC-osroM202036f03b1 Method BLASTX NCBI GI q1351856 BLAST score 854 E value 5.0e-92 Match length 169 93 % identity NCBI Description ACONITATE HYDRATASE, CYTOPLASMIC (CITRATE HYDRO-LYASE) (ACONITASE) >gi_868003_dbj_BAA06108_ (D29629) aconitase [Cucurbita sp.] Seq. No. 418753 Seq. ID uC-osroM202036f04b1 Method BLASTX NCBI GI g3548810 BLAST score 178 E value 7.0e-13Match length 51 % identity 69 NCBI Description (AC005313) putative chloroplast nucleoid DNA binding protein [Arabidopsis thaliana] Seq. No. 418754 Seq. ID uC-osroM202036f05b1 Method BLASTX NCBI GI g710626 BLAST score 188 6.0e-14 E value Match length 45 % identity 69 NCBI Description (D30719) ERD15 protein [Arabidopsis thaliana] >gi 3241941 (AC004625) dehydration-induced protein ERD15 [Arabidopsis thaliana] >gi_3894181 (AC005662) ERD15 protein [Arabidopsis thaliana] Seq. No. 418755 Seq. ID uC-osroM202036f06a1 Method BLASTN NCBI GI q218203 BLAST score 204 E value 1.0e-111 Match length 231 97 % identity NCBI Description Rice mRNA for GTP binding protein Seq. No. 418756 Seq. ID uC-osroM202036f06b1 Method BLASTX g3024552 NCBI GI BLAST score 739 E value 1.0e-78

Match length 146 % identity 99

NCBI Description RAS-RELATED PROTEIN RGP2 (GTP-BINDING REGULATORY PROTEIN RGP2) >gi_419797_pir__S30273 GTP-binding protein rgp2 -

rice >gi_218204_dbj_BAA02437 (D13152) GTP binding protein [Oryza sativa] >gi_446772_prf__1912297A rgp2 gene [Oryza

Method

NCBI GI

BLASTX

g2493318

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sativa]
```

```
Seq. No.
                   418757
                   uC-osroM202036f07a1
Seq. ID
Method
                   BLASTX
NCBI GI
                   q113301
BLAST score
                   293
E value
                   3.0e-28
                   66
Match length
                   90
% identity
NCBI Description
                  ACTIN, PLASMODIAL ISOFORM >gi 2144826 pir ATFY actin -
                   slime mold (Physarum polycephalum) >gi 3187 emb CAA30629
                   (X07792) actin [Physarum polycephalum]
                   >gi 3191 emb CAA43201 (X60788) actin [Physarum
                   polycephalum] >gi 161208 (M21500) actin PpA35 [Physarum
                  polycephalum] >qi 161210 (M21501) actin PpA5 [Physarum
                   polycephalum] >gi 161212 (M15272) actin [Physarum
                  polycephalum]
Seq. No.
                   418758
Seq. ID
                   uC-osroM202036f07b1
Method
                   BLASTX
NCBI GI
                   g113213
BLAST score
                   927
E value
                   1.0e-100
Match length
                   180
% identity
                   98
NCBI Description
                  ACTIN 1 >gi_71630_pir__ATAX actin - Acanthamoeba
                   castellanii >gi 5566 emb CAA23399 (V00002) actin
                   [Acanthamoeba castellanii]
Seq. No.
                   418759
Seq. ID
                   uC-osroM202036f09b1
Method
                  BLASTX
NCBI GI
                   g3399767
BLAST score
                   252
E value
                   2.0e-21
                  92
Match length
% identity
                   46
NCBI Description
                 (U76298) uclacyanin I [Arabidopsis thaliana] >gi 3831466
                   (AC005700) uclacyanin I [Arabidopsis thaliana]
Seq. No.
                   418760
Seq. ID
                  uC-osroM202036f10b1
Method
                  BLASTX
                  g1747296
NCBI GI
BLAST score
                  574
E value
                  3.0e-59
Match length
                  162
% identity
                  72
                  (D45384) vacuolar H+-pyrophosphatase [Oryza sativa]
NCBI Description
                  >gi_3298476_dbj_BAA31524_ (AB012766) ovp2 [Oryza sativa]
Seq. No.
                  418761
Seq. ID
                  uC-osroM202036f11b1
```

Match length

159

```
BLAST score
                   219
E value
                   1.0e-17
Match length
                   88
                   48
% identity
NCBI Description
                  BLUE COPPER PROTEIN PRECURSOR >gi 562779 emb CAA80963
                   (Z25471) blue copper protein [Pisum sativum]
                  >gi 1098264 prf 2115352A blue Cu protein [Pisum sativum]
                   418762
Seq. No.
                   uC-osroM202036g01b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3377509
BLAST score
                   453
                   4.0e-45
E value
Match length
                  125
% identity
                  70
NCBI Description (AF056027) auxin transport protein REH1 [Oryza sativa]
Seq. No.
                   418763
                  uC-osroM202036q02b1
Seq. ID
Method
                  BLASTX
NCBI GI
                   g4689108
BLAST score
                   306
                   9.0e-28
E value
Match length
                  152
% identity
                   43
                  (AF077030) hypothetical 43.2 kDa protein [Homo sapiens]
NCBI Description
                  >gi 4929577 gb AAD34049.1 AF151812 1 (AF151812) CGI-54
                  protein [Homo sapiens]
Seq. No.
                   418764
Seq. ID
                  uC-osroM202036g03b1
Method
                  BLASTX
NCBI GI
                  g82496
BLAST score
                   671
E value
                  1.0e-70
Match length
                  150
% identity
                  87
NCBI Description phenylalanine ammonia-lyase (EC 4.3.1.5) - rice
                   418765
Seq. No.
                  uC-osroM202036g04b1
Seq. ID
Method
                  BLASTX
                  g4874269
NCBI GI
BLAST score
                  254
                  1.0e-21
E value
Match length
                  169
% identity
                  37
NCBI Description (AC007354) T16B5.7 [Arabidopsis thaliana]
                  418766
Seq. No.
Seq. ID
                  uC-osroM202036g05b1
Method
                  BLASTX
NCBI GI
                  q2618699
BLAST score
                  201
E value
                  2.0e-15
```

Seq. No.

418772

```
% identity
                  (AC002510) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   418767
Seq. ID
                   uC-osroM202036g07a1
Method
                   BLASTN
NCBI GI
                   g5042437
BLAST score
                   40
E value
                   4.0e-13
Match length
                   64
% identity
                   91
NCBI Description Oryza sativa BAC T49B20 genomic sequence, complete sequence
Seq. No.
                   418768
Seq. ID
                   uC-osroM202036g09b1
Method
                   BLASTX
NCBI GI
                   q4468979
BLAST score
                   423
E value
                   1.0e-41
Match length
                   111
% identity
                   65
NCBI Description
                  (AL035605) putative protein [Arabidopsis thaliana]
Seq. No.
                   418769
Seq. ID
                   uC-osroM202036g10b1
Method
                   BLASTX
NCBI GI
                   g1449179
BLAST score
                   341
E value
                   7.0e-32
Match length
                   128
% identity
                   55
NCBI Description
                  (D86506) N-ethylmaleimide sensitive fusion protein
                   [Nicotiana tabacum]
Seq. No.
                   418770
Seq. ID
                   uC-osroM202036g11b1
Method
                   BLASTX
NCBI GI
                   g3023817
BLAST score
                   592
                   2.0e-61
E value
Match length
                   158
                   74
% identity
NCBI Description
                  GLUCOSE-6-PHOSPHATE 1-DEHYDROGENASE, CHOLOROPLAST ISOFORM
                   PRECURSOR (G6PD) >gi 1480344 emb CAA67782 (X99405)
                   glucose-6-phosphate dehydrogenase [Nicotiana tabacum]
Seq. No.
                   418771
Seq. ID
                   uC-osroM202036h01b1
Method
                  BLASTX
NCBI GI
                  g3451072
BLAST score
                   368
E value
                   3.0e - 35
Match length
                  91
% identity
NCBI Description
                  (AL031326) putative protein [Arabidopsis thaliana]
```

```
uC-osroM202036h02b1
Seq. ID
Method
                  BLASTX
                  q3451072
NCBI GI
BLAST score
                  455
E value
                  2.0e-45
                  109
Match length
                  76
% identity
NCBI Description (AL031326) putative protein [Arabidopsis thaliana]
                  418773
Seq. No.
                  uC-osroM202036h06b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g5732040
                  395
BLAST score
                  3.0e-38
E value
Match length
                  104
                  70
% identity
NCBI Description (AF147262) contains similarity to mouse and human SL15
                  proteins (GB:AF038961 and U41996) [Arabidopsis thaliana]
                  418774
Seq. No.
                  uC-osroM202036h07b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q417745
BLAST score
                  692
                  4.0e-73
E value
Match length
                  136
                  95
% identity
NCBI Description ADENOSYLHOMOCYSTEINASE (S-ADENOSYL-L-HOMOCYSTEINE
                  HYDROLASE) (ADOHCYASE) >qi 170773 (L11872)
                  S-adenosyl-L-homocysteine hydrolase [Triticum aestivum]
Seq. No.
                  418775
Seq. ID
                  uC-osroM202036h08a1
Method
                  BLASTX
NCBI GI
                  g3128180
BLAST score
                  169
E value
                  5.0e-14
Match length
                  65
% identity
NCBI Description (AC004521) citrate synthetase [Arabidopsis thaliana]
                  418776
Seq. No.
                  uC-osroM202036h08b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g461745
BLAST score
                  321
                  2.0e-29
E value
Match length
                  142
% identity
                  44
                  CITRATE SYNTHASE, MITOCHONDRIAL PRECURSOR
NCBI Description
                  >gi 1070508 pir YKBY citrate (si)-synthase (EC 4.1.3.7)
                  precursor, mitochondrial - yeast (Saccharomyces cerevisiae)
                  >gi_313750_emb_CAA80781_ (Z23259) mitochondrial citrate
```

>gi 496718 emb CAA54569 (X77395) mitochodrial citrate

synthase [Saccharomyces cerevisiae]

synthase [Saccharomyces cerevisiae]

>gi_1302469_emb_CAA96277_ (Z71616) ORF YNR001c [Saccharomyces cerevisiae]

Seq. No. 418777

Seq. ID uC-osroM202036h09b1

Method BLASTX
NCBI GI g5702186
BLAST score 417
E value 9.0e-41
Match length 121
% identity 70

NCBI Description (AF106085) 4-coumarate:CoA ligase 2 [Arabidopsis thaliana]

>gi_5702188_gb_AAD47193.1_AF106086_1 (AF106086)
4-coumarate:CoA ligase 2 [Arabidopsis thaliana]

Seq. No. 418778

Seq. ID uC-osroM202036h10a1

Method BLASTX
NCBI GI g113622
BLAST score 144
E value 3.0e-09
Match length 32
% identity 88

NCBI Description FRUCTOSE-BISPHOSPHATE ALDOLASE, CYTOPLASMIC ISOZYME

>gi_68197_pir__ADRZY fructose-bisphosphate aldolase (EC
4.1.2.13), cytosolic - rice >gi 20204 emb CAA37290

(X53130) fructose-diphosphate aldolase (AA 1-358) [Oryza

sativa]

Seq. No. 418779

Seq. ID uC-osroM202036h10b1

Method BLASTX
NCBI GI g113622
BLAST score 673
E value 8.0e-71
Match length 130
% identity 100

NCBI Description FRUCTOSE-BISPHOSPHATE ALDOLASE, CYTOPLASMIC ISOZYME

>gi_68197_pir__ADRZY fructose-bisphosphate aldolase (EC
4.1.2.13), cytosolic - rice >gi_20204_emb_CAA37290_
(X53130) fructose-diphosphate aldolase (AA 1-358) [Oryza

sativa]

Seq. No. 418780

Seq. ID uC-osroM202037a01b1

Method BLASTX
NCBI GI g2995990
BLAST score 292
E value 3.0e-26
Match length 125
% identity 49

NCBI Description (AF053746) dormancy-associated protein [Arabidopsis

thaliana] >gi 2995992 (AF053747) dormancy-associated

protein [Arabidopsis thaliana]

Seq. No. 418781

Seq. ID uC-osroM202037a02b1

```
Method
                   BLASTX
NCBI GI
                   g2736155
                   171
BLAST score
                   2.0e-13
E value
                   58
Match length
                   63
% identity
NCBI Description
                   (AF022082) sulfolipid biosynthesis protein [Arabidopsis
                   thaliana] >gi 3688184 emb_CAA21212 (AL031804) sulfolipid
                   biosynthesis protein SQD1 [Arabidopsis thaliana]
Seq. No.
                   418782
Seq. ID
                   uC-osroM202037a04a1
Method
                   BLASTX
NCBI GI
                   q129591
BLAST score
                   284
                   3.0e-25
E value
                   53
Match length
% identity
                   98
                  PHENYLALANINE AMMONIA-LYASE >qi 295824 emb CAA34226
NCBI Description
                   (X16099) phenylalanine ammonia-lyase [Oryza sativa]
                   418783
Seq. No.
                   uC-osroM202037a04b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g82496
BLAST score
                   648
E value
                   7.0e-68
Match length
                   147
% identity
                   86
NCBI Description phenylalanine ammonia-lyase (EC 4.3.1.5) - rice
                   418784
Seq. No.
                  uC-osroM202037a07b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g1360090
BLAST score
                   362
E value
                   2.0e-34
                  146
Match length
                   47
% identity
NCBI Description
                  (X95576) C1C-Nt1 [Nicotiana tabacum]
                   418785
Seq. No.
Seq. ID
                  uC-osroM202037a08b1
Method
                  BLASTX
NCBI GI
                  g2736155
BLAST score
                  165
E value
                   2.0e-11
Match length
                   47
% identity
                   66
NCBI Description
                  (AF022082) sulfolipid biosynthesis protein [Arabidopsis
                   thaliana] >gi_3688184_emb_CAA21212_ (AL031804) sulfolipid
                  biosynthesis protein SQD1 [Arabidopsis thaliana]
```

Seq. No. 418786

Seq. ID uC-osroM202037a10b1

Method BLASTX NCBI GI g3337356

BLAST score

209

```
BLAST score
                   677
                   3.0e-71
E value
                   139
Match length
                   96
% identity
NCBI Description
                   (AC004481) putative protein transport protein SEC61 alpha
                   subunit [Arabidopsis thaliana]
                   418787
Seq. No.
                   uC-osroM202037a11a1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g4836904
BLAST score
                   195
E value
                   7.0e-15
Match length
                   43
                   81
% identity
NCBI Description
                  (AC007369) 1cl prt seq No definition line found
                   [Arabidopsis thaliana]
                   418788
Seq. No.
Seq. ID
                   uC-osroM202037a11b1
Method
                   BLASTX
NCBI GI
                   g4836904
BLAST score
                   324
E value
                   5.0e-30
Match length
                   103
% identity
                   59
NCBI Description
                  (AC007369) lcl prt seq No definition line found
                   [Arabidopsis thaliana]
                   418789
Seq. No.
                   uC-osroM202037a12a1
Seq. ID
Method
                   BLASTX
                   g129231
NCBI GI
BLAST score
                   619
E value
                   1.0e-64
Match length
                   128
% identity
                   94
                  ORYZAIN ALPHA CHAIN PRECURSOR >gi 67644_pir__KHRZOA oryzain
NCBI Description
                   (EC 3.4.22.-) alpha precursor - rice
                   >gi_218181_dbj_BAA14402_ (D90406) oryzain alpha precursor
                   [Oryza sativa]
Seq. No.
                   418790
Seq. ID
                   uC-osroM202037a12b1
Method
                   BLASTN
NCBI GI
                   g218180
BLAST score
                   303
E value
                   1.0e-170
Match length
                   348
                   96
% identity
NCBI Description Rice mRNA for oryzain alpha (EC 3.4.22)
Seq. No.
                   418791
Seq. ID
                   uC-osroM202037b01b1
Method
                  BLASTX
NCBI GI
                   g3643611
```

```
E value
                   2.0e-16
Match length
                   57
% identity
                   70
NCBI Description (AC005395) putative casein kinase [Arabidopsis thaliana]
Seq. No.
                   418792
Seq. ID
                   uC-osroM202037b03a1
Method
                   BLASTX
NCBI GI
                   q2832660
BLAST score
                   246
E value
                   7.0e-21
                   96
Match length
% identity
                   52
NCBI Description (AL021710) lipase-like protein [Arabidopsis thaliana]
Seq. No.
                   418793
                   uC-osroM202037b04a1
Seq. ID
Method
                   BLASTX
NCBI GI
                   q6041834
BLAST score
                   383
E value
                   6.0e-37
Match length
                   138
% identity
                   52
NCBI Description
                  (AC009853) putative glucan endo-1-3-beta-glucosidase
                   [Arabidopsis thaliana]
Seq. No.
                   418794
Seq. ID
                   uC-osroM202037b05b1
Method
                   BLASTX
NCBI GI
                   g1305549
BLAST score
                   332
E value
                   6.0e-31
Match length
                  118
% identity
                   58
NCBI Description (U55874) asparagine synthetase [Glycine max]
Seq. No.
                   418795
                  uC-osroM202037b06a1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q5915836
BLAST score
                   406
E value
                  2.0e-39
Match length
                  151
% identity
                  50
NCBI Description CYTOCHROME P450 71D7 >gi_1762144 (U48435) putative
                  cytochrome P450 [Solanum chacoense]
Seq. No.
                  418796
Seq. ID
                  uC-osroM202037b08a1
Method
                  BLASTX
NCBI GI
                  q125606
BLAST score
                  417
E value
                  7.0e-41
Match length
                  101
% identity
                  83
```

NCBI Description PYRUVATE KINASE, CYTOSOLIC ISOZYME >gi_100463_pir__S12248 pyruvate kinase (EC 2.7.1.40) - potato

```
tuberosum]
Seq. No.
                   418797
Seq. ID
                   uC-osroM202037b10b1
Method
                   BLASTX
NCBI GI
                   g2995990
BLAST score
                   176
E value
                   1.0e-12
Match length
                   122
                   37
% identity
NCBI Description
                   (AF053746) dormancy-associated protein [Arabidopsis
                   thaliana] >gi_2995992 (AF053747) dormancy-associated
                   protein [Arabidopsis thaliana]
Seq. No.
                   418798
Seq. ID
                   uC-osroM202037b11a1
Method
                   BLASTX
NCBI GI
                   g129231
BLAST score
                   558
E value
                   1.0e-57
Match length
                   110
                   98
% identity
NCBI Description
                   ORYZAIN ALPHA CHAIN PRECURSOR >gi 67644 pir KHRZOA oryzain
                   (EC 3.4.22.-) alpha precursor - rice
                   >gi_218181_dbj_BAA14402_ (D90406) oryzain alpha precursor
                   [Oryza sativa]
Seq. No.
                   418799
Seq. ID
                   uC-osroM202037b11b1
Method
                   BLASTN
NCBI GI
                   g218180
BLAST score
                   415
E value
                   0.0e + 00
Match length
                   440
% identity
                   98
NCBI Description Rice mRNA for oryzain alpha (EC 3.4.22)
Seq. No.
                   418800
Seq. ID
                   uC-osroM202037b12a1
Method
                   BLASTX
NCBI GI
                   g82496
BLAST score
                   155
E value
                   3.0e-10
Match length
                   45
% identity
NCBI Description phenylalanine ammonia-lyase (EC 4.3.1.5) - rice
Seq. No.
                   418801
Seq. ID
                   uC-osroM202037b12b1
Method
                  BLASTX
NCBI GI
                  g3184098
BLAST score
                  150
E value
                  2.0e-09
Match length
                  76
% identity
                   47
NCBI Description
                  (AL023777) coenzyme a synthetase [Schizosaccharomyces
                                      54891
```

>gi_22576 emb_CAA37727_ (X53688) pyruvate kinase [Solanum

```
Seq. No.
                   418802
Seq. ID
                   uC-osroM202037c02a1
Method
                   BLASTX
NCBI GI
                   q3790587
BLAST score
                   157
E value
                   7.0e-14
Match length
                   88
% identity
                   53
NCBI Description (AF079182) RING-H2 finger protein RHF2a [Arabidopsis
                   thaliana]
Seq. No.
                   418803
Seq. ID
                   uC-osroM202037c04a1
Method
                   BLASTX
NCBI GI
                   g1707998
BLAST score
                   158
E value
                   1.0e-10
Match length
                   31
% identity
                   97
NCBI Description
                   SERINE HYDROXYMETHYLTRANSFERASE, MITOCHONDRIAL PRECURSOR
                   (SERINE METHYLASE) (GLYCINE HYDROXYMETHYLTRANSFERASE)
                   (SHMT) >gi 481944 pir S40218 glycine
                   hydroxymethyltransferase (EC 2.1.2.1) - potato
                   >gi 438247 emb CAA81082 (Z25863) glycine
                   hydroxymethyltransferase [Solanum tuberosum]
Seq. No.
                   418804
Seq. ID
                  uC-osroM202037c04b1
Method
                  BLASTX
NCBI GI
                   g5031275
BLAST score
                  588
E value
                  8.0e-61
Match length
                  148
% identity
                  72
NCBI Description (AF139496) unknown [Prunus armeniaca]
Seq. No.
                   418805
Seq. ID
                  uC-osroM202037c05b1
Method
                  BLASTX
NCBI GI
                  g1208496
BLAST score
                  263
E value
                  8.0e-23
Match length
                  87
% identity
                  63
NCBI Description (D38124) EREBP-3 [Nicotiana tabacum]
Seq. No.
                  418806
Seq. ID
                  uC-osroM202037c06a1
Method
                  BLASTX
NCBI GI
                  q5257275
BLAST score
                  411
E value
                  2.0e-40
Match length
                  80
% identity
NCBI Description (AP000364) ESTs AU030740(E60171), AU030739(E60171)
```

pombe]

correspond to a region of the predicted gene.; Similar to Populus tremuloides caffeoyl-CoA 3-O-methyltransferase. (U27116) [Oryza sativa]

Seq. No. 418807

Seq. ID uC-osroM202037c06b1

Method BLASTX NCBI GI q5257275 BLAST score 355 E value 6.0e-34 Match length 92 % identity 77

(AP000364) ESTs AU030740(E60171), AU030739(E60171) NCBI Description

> correspond to a region of the predicted gene.; Similar to Populus tremuloides caffeoyl-CoA 3-O-methyltransferase.

(U27116) [Oryza sativa]

Seq. No. 418808

Seq. ID uC-osroM202037c08b1

Method BLASTX NCBI GI q3790587 BLAST score 143 E value 5.0e-09 Match length 60 % identity 55

(AF079182) RING-H2 finger protein RHF2a [Arabidopsis NCBI Description

thaliana]

418809 Seq. No.

Seq. ID uC-osroM202037c09b1

Method BLASTX NCBI GI g1684851 BLAST score 246 E value 9.0e-21 Match length 103

% identity 50

NCBI Description (U77935) DnaJ-like protein [Phaseolus vulgaris]

418810 Seq. No.

Seq. ID uC-osroM202037c10b1

Method BLASTX g4467099 NCBI GI BLAST score 628 2.0e-65 E value Match length 149 % identity 86

NCBI Description (AL035538) glycine hydroxymethyltransferase like protein

[Arabidopsis thaliana]

Seq. No. 418811

Seq. ID uC-osroM202037c11a1

Method BLASTX NCBI GI q5257275 BLAST score 503 E value 6.0e-51 Match length 98 % identity 99

NCBI Description (AP000364) ESTs AU030740(E60171), AU030739(E60171) correspond to a region of the predicted gene.; Similar to Populus tremuloides caffeoyl-CoA 3-O-methyltransferase. (U27116) [Oryza sativa] 418812 Seq. No. Seq. ID uC-osroM202037c12a1 Method BLASTX NCBI GI g5257275 BLAST score 445 E value 3.0e-4490 Match length 96 % identity NCBI Description (AP000364) ESTs AU030740(E60171), AU030739(E60171) correspond to a region of the predicted gene.; Similar to Populus tremuloides caffeoyl-CoA 3-0-methyltransferase. (U27116) [Oryza sativa] Seq. No. 418813 uC-osroM202037c12b1 Seq. ID Method BLASTX NCBI GI g5257275 BLAST score 645 E value 1.0e-67 Match length 130 % identity 98 (AP000364) ESTs AU030740(E60171), AU030739(E60171) NCBI Description correspond to a region of the predicted gene.; Similar to Populus tremuloides caffeoyl-CoA 3-O-methyltransferase. (U27116) [Oryza sativa] Seq. No. 418814 Seq. ID uC-osroM202037d01a1 Method BLASTX NCBI GI g3790587 BLAST score 394 E value 4.0e-38 Match length 126 % identity 63 NCBI Description (AF079182) RING-H2 finger protein RHF2a [Arabidopsis thaliana] 418815 Seq. No. Seq. ID uC-osroM202037d01b1 Method BLASTX NCBI GI g4894963 BLAST score 479 E value 4.0e-48 Match length 131 % identity NCBI Description (AF140553) DNA-binding protein WRKY3 [Avena sativa]

Seq. No. 418816

Seq. ID uC-osroM202037d02b1

Method BLASTX NCBI GI g1491615 BLAST score 190 E value 3.0e-14 Match length 60 % identity 63 NCBI Description (X99923) male sterility 2-like protein [Arabidopsis thaliana] Seq. No. 418817 uC-osroM202037d03a1 Seq. ID Method BLASTX NCBI GI g4263781 BLAST score 198 E value 3.0e-15 Match length 77 48 % identity NCBI Description (AC006068) putative membrane transport protein [Arabidopsis thaliana] Seq. No. 418818 Seq. ID uC-osroM202037d05a1 Method BLASTX NCBI GI g2118183 BLAST score 182 E value 2.0e-13 Match length 39 % identity 92 NCBI Description inorganic pyrophosphatase (EC 3.6.1.1), H+-translocating (clone TVP17), vacuolar membrane - common tobacco (fragment) >qi 790475 emb CAA58699 (X83728) inorganic pyrophosphatase [Nicotiana tabacum] 418819 Seq. No. uC-osroM202037d06b1 Seq. ID BLASTX Method NCBI GI g5031275 BLAST score 548 3.0e-56 E value Match length 140 % identity 71 NCBI Description (AF139496) unknown [Prunus armeniaca] 418820 Seq. No. uC-osroM202037d07b1 Seq. ID Method BLASTX NCBI GI g3790587 BLAST score 497 E value 4.0e-50 128 Match length % identity 77

NCBI Description (AF079182) RING-H2 finger protein RHF2a [Arabidopsis

thaliana]

Seq. No. 418821

Seq. ID uC-osroM202037d08b1

Method BLASTX
NCBI GI g114193
BLAST score 221
E value 7.0e-18

Match length 43 % identity 98

NCBI Description PHOSPHO-2-DEHYDRO-3-DEOXYHEPTONATE ALDOLASE 1 PRECURSOR

(PHOSPHO-2-KETO-3-DEOXYHEPTONATE ALDOLASE 1) (DAHP

SYNTHETASE 1) (3-DEOXY-D-ARABINO-HEPTULOSONATE 7-PHOSPHATE

SYNTHASE 1) >gi_170225 (M64261)

3-deoxy-D-arabino-heptulosonate 7-phosphate synthase

[Nicotiana tabacum] >gi 228697 prf 1808327A

deoxyheptulosonate phosphate synthase [Nicotiana tabacum]

Seq. No. 418822

Seq. ID uC-osroM202037d09a1

Method BLASTX
NCBI GI g343151
BLAST score 228
E value 1.0e-18
Match length 84
% identity 52

NCBI Description (M80906) cytochrome oxidase subunit II [Phyllostomus

hastatusl

Seq. No. 418823

Seq. ID uC-osroM202037d09b1

Method BLASTX
NCBI GI g2245004
BLAST score 346
E value 1.0e-32
Match length 116
% identity 56

NCBI Description (Z97341) membrane transporter like protein [Arabidopsis

thaliana]

Seq. No. 418824

Seq. ID uC-osroM202037d10a1

Method BLASTX
NCBI GI g2642448
BLAST score 177
E value 1.0e-12
Match length 162
% identity 36

NCBI Description (AC002391) hypothetical protein [Arabidopsis thaliana]

>gi_3169187_gb_AAC17830.1_ (AC004401) hypothetical protein

[Arabidopsis thaliana]

Seq. No. 418825

Seq. ID uC-osroM202037d11a1

Method BLASTX
NCBI GI g5031275
BLAST score 325
E value 5.0e-30
Match length 76
% identity 76

NCBI Description (AF139496) unknown [Prunus armeniaca]

Seq. No. 418826

Seq. ID uC-osroM202037d11b1

Method BLASTX

E value

6.0e-28

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NCBI GI
                  g1747296
BLAST score
                  269
E value
                  2.0e-23
Match length
                  78
% identity
                  71
                  (D45384) vacuolar H+-pyrophosphatase [Oryza sativa]
NCBI Description
                  >gi 3298476 dbj BAA31524 (AB012766) ovp2 [Oryza sativa]
                  418827
Seq. No.
                  uC-osroM202037d12a1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g5031275
BLAST score
                  309
E value
                  3.0e-28
Match length
                  72
                  76
% identity
NCBI Description (AF139496) unknown [Prunus armeniaca]
Seq. No.
                  418828
Seq. ID
                  uC-osroM202037e01b1
Method
                  BLASTX
NCBI GI
                  g5441879
BLAST score
                  274
E value
                  4.0e-24
Match length
                  63
% identity
                  (AP000367) ESTs AU070372(S13446), AU075541(S0353) correspond
NCBI Description
                  to a region of the predicted gene.; Similar to Arabidopsis
                  thaliana BAC genomic sequence. (AC002292) [Oryza sativa]
                  418829
Seq. No.
                  uC-osroM202037e02a1
Seq. ID
                  BLASTX
Method
NCBI GI
                  g2541876
BLAST score
                  282
                  5.0e-25
E value
                  107
Match length
% identity
                  51
NCBI Description (D26015) CND41, chloroplast nucleoid DNA binding protein
                   [Nicotiana tabacum]
                  418830
Seq. No.
Seq. ID
                  uC-osroM202037e03a1
Method
                  BLASTX
NCBI GI
                  g3702323
                  401
BLAST score
E value
                  6.0e-39
Match length
                  98
                  76
% identity
NCBI Description (AC005397) unknown protein [Arabidopsis thaliana]
                  418831
Seq. No.
Seq. ID
                  uC-osroM202037e03b1
Method
                  BLASTX
NCBI GI
                  g2226329
BLAST score
                  307
```

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Match length
                   115
% identity
NCBI Description (AF001634) physical impedance induced protein [Zea mays]
Seq. No.
                   418832
                   uC-osroM202037e04a1
Seq. ID
Method
                   BLASTX
NCBI GI
                   q1877279
BLAST score
                   247
E value
                   7.0e-21
Match length
                   91
% identity
                   55
NCBI Description (Z92770) fadE2 [Mycobacterium tuberculosis]
Seq. No.
                   418833
Seq. ID
                   uC-osroM202037e05a1
Method
                   BLASTX
NCBI GI
                   q129591
BLAST score
                   246
E value
                   8.0e-21
Match length
                   49
% identity
                   94
NCBI Description PHENYLALANINE AMMONIA-LYASE >gi 295824 emb CAA34226
                   (X16099) phenylalanine ammonia-lyase [Oryza sativa]
Seq. No.
                   418834
Seq. ID
                   uC-osroM202037e06a1
Method
                   BLASTX
NCBI GI
                   g451193
BLAST score
                   393
                   5.0e-38
E value
Match length
                  108
% identity
                  71
NCBI Description (L28008) wali7 [Triticum aestivum]
                  >gi 1090845 prf 2019486B wali7 gene [Triticum aestivum]
Seq. No.
                   418835
Seq. ID
                  uC-osroM202037e06b1
Method
                  BLASTX
NCBI GI
                  g1841391
BLAST score
                  236
E value
                  1.0e-19
Match length
                  82
% identity
                  76
NCBI Description (D64039) EL3 [Oryza sativa]
Seq. No.
                  418836
Seq. ID
                  uC-osroM202037e07a1
Method
                  BLASTX
NCBI GI
                  g2541876
BLAST score
                  273
E value
                   6.0e-24
Match length
                  99
% identity
                  53
                  (D26015) CND41, chloroplast nucleoid DNA binding protein
NCBI Description
                   [Nicotiana tabacum]
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Seq. No.
                   418837
Seq. ID
                   uC-osroM202037e07b1
Method
                   BLASTX
NCBI GI
                   g82496
BLAST score
                   592
E value
                   2.0e-61
Match length
                   144
% identity
                   81
NCBI Description phenylalanine ammonia-lyase (EC 4.3.1.5) - rice
Seq. No.
                   418838
Seq. ID
                   uC-osroM202037e08a1
Method
                   BLASTX
NCBI GI
                   g3702323
BLAST score
                   146
E value
                   9.0e-13
Match length
                  91
% identity
                  52
NCBI Description (AC005397) unknown protein [Arabidopsis thaliana]
Seq. No.
                   418839
Seq. ID
                  uC-osroM202037e10a1
Method
                  BLASTX
NCBI GI
                  g3859597
BLAST score
                  143
E value
                  1.0e-08
Match length
                  81
% identity
                  51
NCBI Description (AF104919) No definition line found [Arabidopsis thaliana]
Seq. No.
                  418840
Seq. ID
                  uC-osroM202037e10b1
Method
                  BLASTX
NCBI GI
                  g1877279
BLAST score
                  535
E value
                  1.0e-54
Match length
                  159
% identity
                  65
NCBI Description (Z92770) fadE2 [Mycobacterium tuberculosis]
Seq. No.
                  418841
Seq. ID
                  uC-osroM202037e11a1
Method
                  BLASTX
NCBI GI
                  g1841391
BLAST score
                  269
E value
                  2.0e-23
Match length
                  85
% identity
                  66
NCBI Description (D64039) EL3 [Oryza sativa]
Seq. No.
                  418842
Seq. ID
                  uC-osroM202037e11b1
Method
                  BLASTX
NCBI GI
                  q82496
BLAST score
                  665
E value
                  6.0e-70
Match length
                  152
```

Seq. No.

418848

```
% identity
NCBI Description
                   phenylalanine ammonia-lyase (EC 4.3.1.5) - rice
Seq. No.
                   418843
Seq. ID
                   uC-osroM202037f02b1
Method
                   BLASTX
NCBI GI
                   g2160322
BLAST score
                   436
E value
                   3.0e-43
Match length
                   130
% identity
                   68
NCBI Description
                  (D16139) cytokinin binding protein CBP57 [Nicotiana
                   sylvestris]
Seq. No.
                   418844
Seq. ID
                   uC-osroM202037f03b1
Method
                   BLASTX
NCBI GI
                   g2160322
BLAST score
                   226
E value
                   1.0e-18
Match length
                   91
% identity
                   60
NCBI Description
                  (D16139) cytokinin binding protein CBP57 [Nicotiana
                   sylvestris]
Seq. No.
                   418845
Seq. ID
                   uC-osroM202037f04a1
Method
                   BLASTX
NCBI GI
                   g3868754
BLAST score
                   352
E value
                   3.0e - 33
Match length
                   69
% identity
                   96
NCBI Description (D64013) catalase [Oryza sativa]
Seq. No.
                   418846
Seq. ID
                   uC-osroM202037f06b1
Method
                  BLASTX
NCBI GI
                  q3320104
BLAST score
                   169
E value
                   9.0e-12
Match length
                  137
% identity
                   32
NCBI Description (AJ007366) calcium-dependent protein kinase [Zea mays]
Seq. No.
                  418847
Seq. ID
                  uC-osroM202037f08a1
Method
                  BLASTX
NCBI GI
                  q5123545
BLAST score
                  436
E value
                  4.0e-43
Match length
                  101
% identity
                  78
NCBI Description
                  (AL079344) arginine methyltransferase (pam1) [Arabidopsis
                  thaliana]
```

Seq. ID uC-osroM202037f08b1 Method BLASTX NCBI GI g2160322 BLAST score 566 E value 2.0e-58 Match length 156 % identity 74 NCBI Description (D16139) cytokinin binding protein CBP57 [Nicotiana sylvestris] Seq. No. 418849 uC-osroM202037f09b1 Seq. ID Method BLASTX NCBI GI g4589961 BLAST score 208 E value 1.0e-16 Match length 95 % identity 43 NCBI Description (AC007169) unknown protein [Arabidopsis thaliana] Seq. No. 418850 uC-osroM202037f10a1 Seq. ID Method BLASTX NCBI GI g3334346 BLAST score 150 9.0e-20 E value Match length 57 % identity 93 NCBI Description PROTEIN TRANSLATION FACTOR SUI1 HOMOLOG >gi 2852445 dbj BAA24697 (AB003378) SUI1 homolog [Salix bakko] 418851 Seq. No. Seq. ID uC-osroM202037f10b1 Method BLASTX NCBI GI g3868754 BLAST score 707 E value 3.0e-85 Match length 160 % identity 98 NCBI Description (D64013) catalase [Oryza sativa] Seq. No. 418852 Seq. ID uC-osroM202037g01b1 Method BLASTN NCBI GI g5410347 BLAST score 43 E value 9.0e-15 Match length 115 % identity NCBI Description Sorghum bicolor BAC clone 110K5, partial sequence

Seq. No. 418853

Seq. ID uC-osroM202037g02b1

Method BLASTX NCBI GI g3023713 BLAST score 700

```
E value
                   5.0e-74
Match length
                   151
% identity
                   91
NCBI Description
                   ENOLASE (2-PHOSPHOGLYCERATE DEHYDRATASE)
                   (2-PHOSPHO-D-GLYCERATE HYDRO-LYASE) (OSE1) >gi 780372
                   (U09450) enolase [Oryza sativa]
Seq. No.
                   418854
Seq. ID
                   uC-osroM202037g03a1
Method
                   BLASTX
NCBI GI
                   q4510383
BLAST score
                   269
E value
                   1.0e-23
Match length
                   73
                   75
% identity
NCBI Description (AC007017) unknown protein [Arabidopsis thaliana]
Seq. No.
                   418855
Seq. ID
                   uC-osroM202037g05a1
Method
                   BLASTX
NCBI GI
                   g2913891
BLAST score
                   289
E value
                   8.0e-26
Match length
                   59
                   93
% identity
NCBI Description (AB011367) LIP9 [Oryza sativa]
Seq. No.
                   418856
Seq. ID
                  uC-osroM202037g05b1
Method
                  BLASTN
NCBI GI
                   q5410347
BLAST score
                  39
E value
                  2.0e-12
Match length
                  115
% identity
                  83
NCBI Description Sorghum bicolor BAC clone 110K5, partial sequence
Seq. No.
                  418857
Seq. ID
                  uC-osroM202037g06a1
Method
                  BLASTX
NCBI GI
                  g2913891
BLAST score
                  293
E value
                  3.0e-26
Match length
                  58
% identity
                  95
NCBI Description (AB011367) LIP9 [Oryza sativa]
Seq. No.
                  418858
Seq. ID
                  uC-osroM202037g06b1
Method
                  BLASTX
NCBI GI
                  g3023817
BLAST score
                  624
E value
                  5.0e-65
Match length
                  170
% identity
                  72
NCBI Description GLUCOSE-6-PHOSPHATE 1-DEHYDROGENASE, CHOLOROPLAST ISOFORM
                  PRECURSOR (G6PD) >gi_1480344_emb_CAA67782_ (X99405)
```

glucose-6-phosphate dehydrogenase [Nicotiana tabacum]

Seq. No. 418859

Seq. ID uC-osroM202037g07a1

Method BLASTN
NCBI GI g780371
BLAST score 300
E value 1.0e-168
Match length 324
% identity 98

NCBI Description Oryza sativa enolase mRNA, complete cds

Seq. No. 418860

Seq. ID uC-osroM202037g07b1

Method BLASTX
NCBI GI g1172874
BLAST score 178
E value 1.0e-15
Match length 113
% identity 47

NCBI Description DEHYDRATION-RESPONSIVE PROTEIN RD22 PRECURSOR

>gi_479589_pir__S34823 dehydration-induced protein RD22 Arabidopsis thaliana >gi_391608_dbj_BAA01546_ (D10703) rd22
[Arabidopsis thaliana] >gi_447134_prf__1913421A rd22 gene

[Arabidopsis thaliana]

Seq. No. 418861

Seq. ID uC-osroM202037g10a1

Method BLASTX
NCBI GI g3123130
BLAST score 145
E value 4.0e-09
Match length 44
% identity 64

NCDI Description

NCBI Description HYPOTHETICAL 61.8 KD TRP-ASP REPEATS CONTAINING PROTEIN

T32G6.2 IN CHROMOSOME II >gi 2618685 (AC002510) putative

small nuclear ribonucleoprotein Prp4p [Arabidopsis thaliana] >gi_3241948 (AC004625) putative small nuclear

ribonucleoprotein Prp4p [Arabidopsis thaliana]

Seq. No. 418862

Seq. ID uC-osroM202037g10b1

Method BLASTX
NCBI GI g5882746
BLAST score 225
E value 3.0e-18
Match length 102
% identity 46

NCBI Description (AC008263) ESTs gb T04421 and gb AA586001 come from this

gene. [Arabidopsis thaliana]

Seq. No. 418863

Seq. ID uC-osroM202037g11a1

Method BLASTX
NCBI GI g2276346
BLAST score 369
E value 3.0e-35

```
Match length
                   89
% identity
                   78
NCBI Description
                   (AJ000183) Glucose-6-phosphate dehydrogenase [Spinacia
                   oleracea]
                   418864
Seq. No.
Seq. ID
                   uC-osroM202037q11b1
Method
                   BLASTX
NCBI GI
                   q1657843
BLAST score
                   311
                   2.0e-28
E value
Match length
                   132
% identity
                   53
NCBI Description
                  (U73210) cold acclimation protein WCOR410b [Triticum
                   aestivum]
Seq. No.
                   418865
Seq. ID
                   uC-osroM202037q12b1
Method
                   BLASTX
NCBI GI
                   q1657843
BLAST score
                   190
E value
                   3.0e-14
Match length
                   130
% identity
                   39
NCBI Description
                  (U73210) cold acclimation protein WCOR410b [Triticum
                   aestivum]
Seq. No.
                   418866
Seq. ID
                   uC-osroM202037h01a1
Method
                   BLASTX
NCBI GI
                   q282994
BLAST score
                   475
E value
                   2.0e-48
                   150
Match length
                   71
% identity
NCBI Description Sipl protein - barley >gi 167100 (M77475) seed imbibition
                   protein [Hordeum vulgare]
                   418867
Seq. No.
Seq. ID
                   uC-osroM202037h01b1
Method
                   BLASTX
NCBI GI
                   g1203832
BLAST score
                   460
                   6.0e-46
E value
Match length
                   124
% identity
                   73
NCBI Description
                  (U46003) beta-D-glucan exohydrolase, isoenzyme ExoII
                   [Hordeum vulgare] >gi_1588407_prf__2208395A beta-D-glucan
                   exohydrolase [Hordeum vulgare]
                   418868
Seq. No.
Seq. ID
                   uC-osroM202037h02b1
Method
                   BLASTN
NCBI GI
                   q167099
BLAST score
                   95
```

7.0e-46

179

E value Match length

```
% identity
                   88
                  Hordeum vulgare seed imbitition protein (Sip1) gene,
NCBI Description
                   complete cds
                   418869
Seq. No.
                  uC-osroM202037h04b1
Seq. ID
Method
                  BLASTX
                   g1084461
NCBI GI
                   392
BLAST score
                  2.0e-41
E value
Match length
                  106
% identity
                  88
NCBI Description RCc3 protein - rice >gi 786132 (L27208) RCc3 [Oryza sativa]
Seq. No.
                   418870
                  uC-osroM202037h05a1
Seq. ID
                  BLASTX
Method
NCBI GI
                   g2913891
BLAST score
                   271
                   1.0e-23
E value
Match length
                  54
% identity
                   96
NCBI Description (AB011367) LIP9 [Oryza sativa]
                   418871
Seq. No.
                   uC-osroM202037h05b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   q3941480
BLAST score
                   150
                   1.0e-09
E value
                   38
Match length
                   74
% identity
NCBI Description
                  (AF062894) putative transcription factor [Arabidopsis
                  thaliana]
                   418872
Seq. No.
Seq. ID
                   uC-osroM202037h06a1
Method
                   BLASTN
                   g20094
NCBI GI
BLAST score
                   310
E value
                   1.0e-174
Match length
                   390
% identity
                   95
NCBI Description O.sativa RSs2 gene for sucrose-UDP glucosyltransferase
                   (isozyme 2)
Seq. No.
                   418873
Seq. ID
                   uC-osroM202037h06b1
Method
                   BLASTX
NCBI GI
                   q586078
BLAST score
                   687
                   2.0e-72
E value
Match length
                   128
% identity
NCBI Description
                  TUBULIN BETA CHAIN >gi 1076736 pir JC2518 beta-tubulin
                   pTUB22 - rice >gi_303842_dbj_BAA02505_ (D13224)
                  beta-tubulin [Oryza sativa]
```

Seq. No. 418874 Seq. ID uC-osroM202037h07a1 Method BLASTN NCBI GI g167099 BLAST score 143 E value 2.0e-74 Match length 358 % identity 88 NCBI Description Hordeum vulgare seed imbitition protein (Sip1) gene, complete cds Seq. No. 418875 Seq. ID uC-osroM202037h08a1 Method BLASTN NCBI GI q5042437 BLAST score 40 E value 6.0e-13 Match length 64 % identity 91 NCBI Description Oryza sativa BAC T49B20 genomic sequence, complete sequence Seq. No. 418876 Seq. ID uC-osroM202037h09a1 Method BLASTX NCBI GI g3123130 BLAST score 309 E value 4.0e-28 Match length 90 % identity 61 HYPOTHETICAL 61.8 KD TRP-ASP REPEATS CONTAINING PROTEIN NCBI Description T32G6.2 IN CHROMOSOME II >gi 2618685 (AC002510) putative small nuclear ribonucleoprotein Prp4p [Arabidopsis thaliana] >gi 3241948 (AC004625) putative small nuclear ribonucleoprotein Prp4p [Arabidopsis thaliana] Seq. No. 418877 Seq. ID uC-osroM202037h11a1 Method BLASTN NCBI GI g303841 BLAST score 382 E value 0.0e + 00Match length 389 100 % identity NCBI Description Rice mRNA for beta-tubulin, complete cds Seq. No. 418878 Seq. ID uC-osroM202037h11b1 Method BLASTX

Method BLASTX
NCBI GI g1657843
BLAST score 231
E value 5.0e-19
Match length 130
% identity 45

NCBI Description (U73210) cold acclimation protein WCOR410b [Triticum

aestivum]

Seq. No. 418879 Seq. ID uC-osroM202037h12b1 Method BLASTX NCBI GI g401140 BLAST score 893 E value 1.0e-96 171 Match length % identity SUCROSE SYNTHASE 2 (SUCROSE-UDP GLUCOSYLTRANSFERASE 2) NCBI Description >gi 20095 emb CAA41774 (X59046) sucrose-UDP glucosyltransferase (isoenzyme 2) [Oryza sativa] >gi 1587662 prf 2207194A sucrose synthase:ISOTYPE=2 [Oryza sativa] 418880 Seq. No. Seq. ID uC-osroM202038a01b1 Method BLASTX NCBI GI g1502430 BLAST score 498 E value 2.0e-50 Match length 120 % identity NCBI Description (U62331) phosphate transporter [Arabidopsis thaliana] >gi 2564661 (AF022872) phosphate transporter [Arabidopsis thaliana] >gi 3869206 dbj BAA34398 (AB016166) Phosphate Transporter 4 [Arabidopsis thaliana] >gi 3928081 (AC005770) phosphate transporter, AtPT2 [Arabidopsis thaliana] Seq. No. 418881 Seq. ID uC-osroM202038a02b1 Method BLASTX NCBI GI q3738331 BLAST score 206 E value 4.0e-16 Match length 51 % identity NCBI Description (AC005170) unknown protein [Arabidopsis thaliana] Seq. No. 418882 Seq. ID uC-osroM202038a03a1 Method BLASTX NCBI GI g3913426 379 BLAST score 2.0e-36 E value Match length 73 % identity 96 NCBI Description S-ADENOSYLMETHIONINE DECARBOXYLASE PROENZYME (ADOMETDC) (SAMDC) >gi 1532048 emb CAA69074 (Y07766) S-adenosylmethionine decarboxylase [Oryza sativa]

Seq. No. 418883

Seq. ID uC-osroM202038a03b1

Method BLASTX
NCBI GI g2129921
BLAST score 179
E value 6.0e-13
Match length 51

```
% identity
                  67
                  hypothetical protein 1 - Madagascar periwinkle >gi_758694
NCBI Description
                   (U12573) putative [Catharanthus roseus]
                  418884
Seq. No.
                  uC-osroM202038a04a1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4008156
BLAST score
                  279
                  1.0e-24
E value
                  56
Match length
% identity
                  98
NCBI Description (AB008845) NADH dependent Glutamate Synthase [Oryza sativa]
Seq. No.
                  418885
Seq. ID
                  uC-osroM202038a04b1
Method
                  BLASTX
NCBI GI
                  q4008156
BLAST score
                  534
                  6.0e-67
E value
Match length
                  157
% identity
                  87
NCBI Description (AB008845) NADH dependent Glutamate Synthase [Oryza sativa]
                  418886
Seq. No.
                  uC-osroM202038a07b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2708737
BLAST score
                  332
                  7.0e-31
E value
                  84
Match length
                  67
% identity
NCBI Description (AC003952) putative nuclear protein [Arabidopsis thaliana]
                  418887
Seq. No.
                  uC-osroM202038a08a1
Seq. ID
Method
                  BLASTX
                  g1651459
NCBI GI
BLAST score
                  179
E value
                  5.0e-13
Match length
                  81
                  48
% identity
NCBI Description (D90732) Aminopeptidase n (EC 3.4.11.2)
                  (alpha-aminoacylpeptide hydrolase). [Escherichia coli]
Seq. No.
                  418888
Seq. ID
                  uC-osroM202038a09b1
Method
                  BLASTX
NCBI GI
                  q731718
BLAST score
                  162
E value
                  6.0e-11
Match length
                  108
% identity
NCBI Description
                  HYPOTHETICAL 30.6 KD PROTEIN IN ACT5-YCK1 INTERGENIC REGION
                  >gi_626657_pir__S48978 hypothetical protein YHR134w - yeast
```

[Saccharomyces cerevisiae]

(Saccharomyces cerevisiae) >gi 500671 (U10398) Yhr134wp

```
418889
Seq. No.
                  uC-osroM202038b01b1
Seq. ID
Method
                  BLASTX
                  g2208908
NCBI GI
                  353
BLAST score
E value
                  2.0e-33
                  105
Match length
% identity
                  68
NCBI Description (AB004809) phosphate transporter [Catharanthus roseus]
Seq. No.
                  418890
                  uC-osroM202038b04a1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g474011
BLAST score
                  159
E value
                  4.0e-84
Match length
                  298
% identity
                  92
NCBI Description Rice mRNA, partial homologous to sucrose phosphate synthase
Seq. No.
                  418891
                  uC-osroM202038b04b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g283008
BLAST score
                  363
E value
                  1.0e-34
Match length
                  129
% identity
                  64
                  sucrose synthase (EC 2.4.1.13) - rice
NCBI Description
                  >gi 20366 emb CAA46017 (X64770) sucrose synthase [Oryza
                   sativa]
                   418892
Seq. No.
                  uC-osroM202038b07b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1762309
BLAST score
                  153
                  4.0e-10
E value
                  44
Match length
                  80
% identity
NCBI Description
                  (U53345) AP-1 Golgi-related complex component; clathrin
                  coated vesicles; clathrin assembly protein [Camptotheca
                  acuminata]
                   418893
Seq. No.
Seq. ID
                  uC-osroM202038b08a1
Method
                  BLASTX
                  g1142614
NCBI GI
BLAST score
                   312
E value
                  1.0e-28
Match length
                  83
% identity
                   72
NCBI Description
                  (U17250) ubiquitin conjugating enzyme, E2 [Brassica
```

oleracea]

BLAST score

449

```
Seq. No.
                  418894
                  uC-osroM202038b08b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q5762457
BLAST score
                  688
E value
                  1.0e-72
                  131
Match length
                  96
% identity
                  (AF176040) ubiquitin-conjugating enzyme UBC2
NCBI Description
                   [Mesembryanthemum crystallinum]
                  418895
Seq. No.
                  uC-osroM202038b09b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g5824531
BLAST score
                  153
E value
                  6.0e-10
Match length
                  118
                  32
% identity
NCBI Description (AL024499) cDNA EST EMBL: C10123 comes from this gene
                  [Caenorhabditis elegans]
Seq. No.
                  418896
                  uC-osroM202038b10b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g5668608
BLAST score
                  162
E value
                  4.0e-11
Match length
                  67
                  45
% identity
NCBI Description (AF115334) MenG [Pseudomonas fluorescens]
Seq. No.
                  418897
                  uC-osroM202038b11a1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3746581
BLAST score
                  364
E value
                  1.0e-34
                  69
Match length
                  99
% identity
NCBI Description (AF062403) glutathione S-transferase II [Oryza sativa]
                  418898
Seq. No.
                  uC-osroM202038b11b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3746581
BLAST score
                  695
E value
                  2.0e-73
Match length
                  141
% identity
                  96
NCBI Description (AF062403) glutathione S-transferase II [Oryza sativa]
Seq. No.
                  418899
Seq. ID
                  uC-osroM202038c01b1
Method
                  BLASTX
NCBI GI
                  q2102691
```

```
E value
                   1.0e-44
Match length
                   155
% identity
                   58
NCBI Description
                  (U64817) fructokinase [Lycopersicon esculentum]
                   418900
Seq. No.
Seq. ID
                   uC-osroM202038c02b1
Method
                   BLASTX
NCBI GI
                   g4678364
BLAST score
                   144
E value
                   8.0e-09
Match length
                   39
                   72
% identity
NCBI Description
                  (AL049659) putative protein [Arabidopsis thaliana]
Seq. No.
                   418901
Seq. ID
                   uC-osroM202038c03a1
Method
                   BLASTX
NCBI GI
                   g1743354
BLAST score
                   238
E value
                   8.0e-23
                   96
Match length
                   55
% identity
NCBI Description
                  (Y09876) aldehyde dehydrogenase (NAD+) [Nicotiana tabacum]
Seq. No.
                   418902
Seq. ID
                   uC-osroM202038c03b1
Method
                   BLASTX
NCBI GI
                   g4678328
BLAST score
                   321
E value
                   7.0e-35
Match length
                   129
                   60
% identity
NCBI Description
                  (AL049658) aldehyde dehydrogenase (NAD+)-like protein
                   [Arabidopsis thaliana]
Seq. No.
                   418903
                   uC-osroM202038c04b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   q3928543
BLAST score
                   285
                   2.0e-33
E value
Match length
                   166
% identity
                   47
NCBI Description
                  (AB016819) UDP-glucose glucosyltransferase [Arabidopsis
                   thaliana]
Seq. No.
                   418904
Seq. ID
                   uC-osroM202038c08b1
Method
                   BLASTX
NCBI GI
                   q3868758
BLAST score
                   585
E value
                   1.0e-60
Match length
                   118
% identity
                   94
```

NCBI Description (D89802) elongation factor 1B gamma [Oryza sativa]

Seq. No. 418905 Seq. ID uC-osroM202038c09b1 Method BLASTX NCBI GI g1717779 BLAST score 246 E value 1.0e-22 Match length 74 % identity 77 NCBI Description THIOREDOXIN REDUCTASE >gi_757510 dbj BAA08090 (D45049) Thioredoxin Reductase (NADPH) [Neurospora crassa] Seq. No. 418906 Seq. ID uC-osroM202038c10a1 Method BLASTX NCBI GI g2792155 BLAST score 274 E value 5.0e-24 Match length 91 % identity 52 Seq. No. 418907

NCBI Description (AJ223291) chalcone reductase [Sesbania rostrata]

Seq. ID uC-osroM202038c10b1

Method BLASTX NCBI GI g5080826 BLAST score 336 E value 3.0e-36 Match length 145 % identity 49

NCBI Description (AC007258) Putative Aldo/keto reductase [Arabidopsis

thaliana]

Seq. No. 418908

Seq. ID uC-osroM202038d02b1

Method BLASTX NCBI GI q6006895 BLAST score 440 E value 2.0e-43 Match length 156 % identity 47

NCBI Description (AC008153) hypothetical protein [Arabidopsis thaliana]

Seq. No. 418909

Seq. ID uC-osroM202038d03b1

Method BLASTX NCBI GI g2641211 BLAST score 292 E value 3.0e-26 Match length 74 % identity

NCBI Description (AF031547) histone-like protein [Fritillaria agrestis]

Seq. No. 418910

Seq. ID uC-osroM202038d04b1

Method BLASTX NCBI GI g483410 BLAST score 210

```
E value
                   1.0e-16
Match length
                   74
% identity
                   61
NCBI Description (L01496) calmodulin-binding protein [Zea mays]
Seq. No.
                   418911
Seq. ID
                   uC-osroM202038d06a1
Method
                   BLASTN
NCBI GI
                   g2331130
BLAST score
                   205
E value
                   1.0e-111
Match length
                   261
% identity
                   99
NCBI Description Oryza sativa glycine-rich protein (OSGRP1) mRNA, complete
Seq. No.
                   418912
Seq. ID
                   uC-osroM202038d06b1
Method
                   BLASTX
NCBI GI
                  g2624326
BLAST score
                   451
E value
                   5.0e-45
Match length
                  91
% identity
                  96
NCBI Description (AJ002893) OsGRP1 [Oryza sativa]
Seq. No.
                  418913
Seq. ID
                  uC-osroM202038d08a1
Method
                  BLASTX
NCBI GI
                  q282994
BLAST score
                  729
E value
                  2.0e-77
Match length
                  170
% identity
                  76
NCBI Description Sip1 protein - barley >gi 167100 (M77475) seed imbibition
                  protein [Hordeum vulgare]
Seq. No.
                  418914
Seq. ID
                  uC-osroM202038d08b1
Method
                  BLASTX
NCBI GI
                  g282994
BLAST score
                  151
E value
                  9.0e-10
Match length
                  60
% identity
                  48
NCBI Description Sip1 protein - barley >gi 167100 (M77475) seed imbibition
                  protein [Hordeum vulgare]
Seq. No.
                  418915
Seq. ID
                  uC-osroM202038d09b1
Method
                  BLASTX
NCBI GI
                  q132983
BLAST score
                  504
E value
                  4.0e-51
Match length
                  133
% identity
                  68
NCBI Description 60S RIBOSOMAL PROTEIN L5A >gi_85843_pir__A33823 ribosomal
```

protein L5a - African clawed frog >gi_214754 (M29032) L5a
ribosomal protein [Xenopus laevis]

Seq. No. 418916

Seq. ID uC-osroM202038d12b1

Method BLASTX
NCBI GI g5596622
BLAST score 647
E value 8.0e-68
Match length 141
% identity 87

NCBI Description (AF160729) isovaleryl-CoA-dehydrogenase precursor

[Arabidopsis thaliana]

Seq. No. 418917

Seq. ID uC-osroM202038e01b1

Method BLASTX
NCBI GI g4538968
BLAST score 203
E value 9.0e-16
Match length 108
% identity 43

NCBI Description (AL049488) putative protein kinase [Arabidopsis thaliana]

Seq. No. 418918

Seq. ID uC-osroM202038e02b1

Method BLASTX
NCBI GI g4587571
BLAST score 182
E value 3.0e-13
Match length 106
% identity 40

NCBI Description (AC006550) Belongs to the PF_01027 Uncharacterized protein

family UPF0005 with 7 transmembrane domains. [Arabidopsis

thaliana]

Seq. No. 418919

Seq. ID uC-osroM202038e03b1

Method BLASTX
NCBI GI g2494034
BLAST score 563
E value 6.0e-58
Match length 162
% identity 65

NCBI Description DIACYLGLYCEROL KINASE 1 (DIGLYCERIDE KINASE) (DGK 1) (DAG

KINASE 1) >gi_2129573_pir__S71467 diacylglycerol kinase - Arabidopsis thaliana >gi_1374772_dbj_BAA09856_ (D63787)

diacylglycerol kinase [Arabidopsis thaliana]

Seq. No. 418920

Seq. ID uC-osroM202038e04a1

Method BLASTN
NCBI GI g639685
BLAST score 209
E value 1.0e-114
Match length 360
% identity 93

BLAST score

```
NCBI Description Rice mRNA for phosphoglucose isomerase (Pgi-b), complete
                   418921
Seq. No.
Seq. ID
                   uC-osroM202038e04b1
Method
                   BLASTX
NCBI GI
                   q1169798
BLAST score
                   681
E value
                   9.0e-72
Match length
                   153
% identity
                   88
NCBI Description
                   GLUCOSE-6-PHOSPHATE ISOMERASE, CYTOSOLIC B (GPI-B)
                   (PHOSPHOGLUCOSE ISOMERASE B) (PGI-B) (PHOSPHOHEXOSE
                   ISOMERASE B) (PHI-B) >gi_639686_dbj_BAA08149_ (D45218)
                   phosphoglucose isomerase (Pgi-b) [Oryza sativa]
Seq. No.
                   418922
Seq. ID
                   uC-osroM202038e05b1
Method
                   BLASTX
NCBI GI
                   g4467122
BLAST score
                   308
E value
                   4.0e-28
Match length
                   110
% identity
                   52
NCBI Description (AL035538) putative protein [Arabidopsis thaliana]
Seq. No.
                   418923
Seq. ID
                   uC-osroM202038e06a1
Method
                   BLASTX
NCBI GI
                   g2499613
BLAST score
                   360
E value
                   4.0e-34
Match length
                   85
% identity
                   78
NCBI Description
                  MITOGEN-ACTIVATED PROTEIN KINASE HOMOLOG MMK2
                  >gi 1204129 emb_CAA57719 (X82268) protein kinase [Medicago
                   sativa]
Seq. No.
                   418924
Seq. ID
                  uC-osroM202038e06b1
Method
                  BLASTX
NCBI GI
                  g2499608
BLAST score
                  547
E value
                  5.0e-56
Match length
                  122
% identity
NCBI Description MITOGEN-ACTIVATED PROTEIN KINASE HOMOLOG 4 (MAP KINASE 4)
                   (ATMPK4) >gi_2129645_pir__S40470 mitogen-activated protein
                  kinase 4 (EC 2.7.1.-) - Arabidopsis thaliana
                  >gi_457400_dbj_BAA04867_ (D21840) MAP kinase [Arabidopsis
                  thaliana]
Seq. No.
                  418925
Seq. ID
                  uC-osroM202038e07b1
Method
                  BLASTX
NCBI GI
                  g2781433
```

E value 5.0e-76 Match length 134 % identity 99 NCBI Description (AF030052) RSW1-like cellulose synthase catalytic subunit [Oryza sativa subsp. japonica] Seq. No. 418926 uC-osroM202038e08b1 Seq. ID BLASTX Method g2494034 NCBI GI BLAST score 498 E value 2.0e-50 Match length 153 % identity 60 DIACYLGLYCEROL KINASE 1 (DIGLYCERIDE KINASE) (DGK 1) (DAG NCBI Description KINASE 1) >gi_2129573_pir__S71467 diacylglycerol kinase -Arabidopsis thaliana >gi_1374772_dbj_BAA09856_ (D63787) diacylglycerol kinase [Arabidopsis thaliana] Seq. No. Seq. ID uC-osroM202038e11a1 Method BLASTX NCBI GI g3212879 BLAST score 431 2.0e-42 E value Match length 104 75 % identity NCBI Description (AC004005) putative ribosomal protein L7 [Arabidopsis thaliana] Seq. No. 418928 Seq. ID uC-osroM202038e11b1 Method BLASTX NCBI GI q3212879 BLAST score 348 E value 1.0e-32 Match length 145 % identity 52 NCBI Description (AC004005) putative ribosomal protein L7 [Arabidopsis thaliana] Seq. No. 418929 Seq. ID uC-osroM202038f04a1 Method BLASTX NCBI GI q2708745 BLAST score 167 E value 2.0e-11 Match length 122 % identity NCBI Description (AC003952) putative calcium-dependent ser/thr protein kinase [Arabidopsis thaliana]

Seq. No. 418930

Seq. ID uC-osroM202038f05a1

Method BLASTN NCBI GI g2801537 BLAST score 482

```
E value
                    0.0e+00
 Match length
                    486
 % identity
                    100
 NCBI Description Oryza sativa harpin induced gene 1 homolog (Hinl) mRNA,
                   complete cds
 Seq. No.
                   418931
 Seq. ID
                   uC-osroM202038f05b1
 Method
                   BLASTX
 NCBI GI
                   g2801538
 BLAST score
                   413
 E value
                   7.0e-41
 Match length
                   114
 % identity
                   78
NCBI Description (AF039532) harpin induced gene 1 homolog [Oryza sativa]
 Seq. No.
                   418932
 Seq. ID
                   uC-osroM202038f06a1
Method
                   BLASTN
NCBI GI
                   g2801537
BLAST score
                   402
E value
                   0.0e+00
Match length
                   402
% identity
                   100
NCBI Description Oryza sativa harpin induced gene 1 homolog (Hin1) mRNA,
                   complete cds
Seq. No.
                   418933
Seq. ID
                   uC-osroM202038f06b1
Method
                   BLASTX
NCBI GI
                   g2801538
BLAST score
                   554
E value
                   7.0e-57
Match length
                   128
% identity
NCBI Description (AF039532) harpin induced gene 1 homolog [Oryza sativa]
Seq. No.
                   418934
Seq. ID
                   uC-osroM202038f08b1
Method
                   BLASTX
NCBI GI
                   g2984709
BLAST score
                   464
E value
                   2.0e-46
Match length
                  88
% identity
                   99
NCBI Description (AF053468) DnaJ-related protein ZMDJ1 [Zea mays]
Seq. No.
                   418935
Seq. ID
                  uC-osroM202038f09a1
Method
                  BLASTX
NCBI GI
                  g3075391
BLAST score
                  303
E value
                  1.0e-27
Match length
                  103
% identity
                  62
                 (AC004484) unknown protein [Arabidopsis thaliana]
NCBI Description
```

```
418936
Seq. No.
Seq. ID
                  uC-osroM202038f10b1
Method
                  BLASTX
NCBI GI
                  q4455169
                  473
BLAST score
E value
                  2.0e-47
Match length
                  163
% identity
NCBI Description
                  (AL035521) putative aldehyde dehydrogenase [Arabidopsis
                  thaliana]
Seq. No.
                  418937
Seq. ID
                  uC-osroM202038f11a1
Method
                  BLASTN
NCBI GI
                   q2773153
BLAST score
                   34
                  2.0e-09
E value
                  50
Match length
                  92
% identity
NCBI Description Oryza sativa abscisic acid- and stress-inducible protein
                  (Asr1) mRNA, complete cds
Seq. No.
                  418938
Seq. ID
                  uC-osroM202038f11b1
Method
                  BLASTN
                  q2773153
NCBI GI
BLAST score
                  35
                   6.0e-10
E value
Match length
                  95
% identity
                  84
NCBI Description Oryza sativa abscisic acid- and stress-inducible protein
                  (Asr1) mRNA, complete cds
                  418939
Seq. No.
                  uC-osroM202038f12b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g6041837
BLAST score
                  246
E value
                  9.0e-21
Match length
                  68
% identity
                  62
NCBI Description (AC009853) hypothetical protein [Arabidopsis thaliana]
                  418940
Seq. No.
Seq. ID
                  uC-osroM202038g01a1
Method
                  BLASTX
NCBI GI
                  g283008
BLAST score
                  264
E value
                  2.0e-24
                  70
Match length
% identity
                  90
                  sucrose synthase (EC 2.4.1.13) - rice
NCBI Description
                  >gi 20366 emb CAA46017 (X64770) sucrose synthase [Oryza
                  sativa]
                  418941
Seq. No.
Seq. ID
                  uC-osroM202038q01b1
```

Seq. No.

418946

```
Method
                   BLASTN
NCBI GI
                   q20373
BLAST score
                   72
                   2.0e-32
E value
Match length
                   88
                   95
% identity
NCBI Description O.sativa mRNA for sucrose synthase
                   418942
Seq. No.
                   uC-osroM202038g02a1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3218550
                   169
BLAST score
E value
                   2.0e-13
Match length
                   129
% identity
NCBI Description
                   (AB009399) Cdk-activating kinase 1At [Arabidopsis thaliana]
                   >gi_4972044_emb_CAB43912.1_ (AL078470) Cdk-activating
                   kinase CAK1At [Arabidopsis thaliana]
Seq. No.
                   418943
Seq. ID
                   uC-osroM202038g03b1
Method
                   BLASTX
NCBI GI
                   q4510403
BLAST score
                   244
                   3.0e-23
E value
Match length
                   132
% identity
NCBI Description
                  (AC006587) putative DNA repair protein [Arabidopsis
                   thaliana]
Seq. No.
                   418944
                   uC-osroM202038q04a1
Seq. ID
Method
                   BLASTX
NCBI GI
                   q585551
BLAST score
                   215
E value
                   2.0e-17
Match length
                   46
% identity
                   80
NCBI Description
                   NUCLEOSIDE DIPHOSPHATE KINASE I (NDK I) (NDP KINASE I)
                   >gi_629798_pir__S43330 nucleoside-diphosphate kinase (EC
2.7.4.6) - rice >gi_303849_dbj_BAA03798_ (D16292)
                   nucleoside diphosphate kinase [Oryza sativa]
Seq. No.
                   418945
Seq. ID
                   uC-osroM202038g04b1
Method
                   BLASTX
NCBI GI
                   g2498077
BLAST score
                   684
E value
                   4.0e-72
                   146
Match length
% identity
                   84
NCBI Description NUCLEOSIDE DIPHOSPHATE KINASE I (NDK I) (NDP KINASE I)
                   (PP18) >gi_1777930 (U55019) nucleoside diphosphate kinase
                   [Saccharum officinarum]
```

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uC-osroM202038g06a1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3913426
BLAST score
                   433
E value
                   1.0e-42
Match length
                   80
                   100
% identity
NCBI Description S-ADENOSYLMETHIONINE DECARBOXYLASE PROENZYME (ADOMETDC)
                   (SAMDC) >gi 1532048 emb CAA69074 (Y07766)
                   S-adenosylmethionine decarboxylase [Oryza sativa]
Seq. No.
                   418947
Seq. ID
                   uC-osroM202038g06b1
Method
                   BLASTX
NCBI GI
                   q2129921
BLAST score
                   179
E value
                   6.0e-13
Match length
                   51
% identity
                   67
NCBI Description hypothetical protein 1 - Madagascar periwinkle >gi 758694
                   (U12573) putative [Catharanthus roseus]
Seq. No.
                   418948
Seq. ID
                   uC-osroM202038g07a1
Method
                   BLASTN
                   g1778820
NCBI GI
BLAST score
                   194
E value
                   1.0e-105
Match length
                   354
% identity
                   95
NCBI Description Oryza sativa S-adenosyl-L-methionine synthetase (pOS-SAMS2)
                   mRNA, complete cds
Seq. No.
                   418949
Seq. ID
                   uC-osroM202038g07b1
Method
                   BLASTX
NCBI GI
                   g1709000
BLAST score
                   363
                   8.0e-35
E value
Match length
                   73
% identity
NCBI Description
                  S-ADENOSYLMETHIONINE SYNTHETASE 1 (METHIONINE
                   ADENOSYLTRANSFERASE 1) (ADOMET SYNTHETASE 1) >gi_960357_dbj_BAA09895_ (D63835) S-adenosylmethionine
                   synthetase [Hordeum vulgare]
Seq. No.
                   418950
Seq. ID
                   uC-osroM202038g08a1
Method
                   BLASTX
NCBI GI
                   q3738302
BLAST score
                   348
E value
                   6.0e-40
Match length
                   150
% identity
NCBI Description
                  (AC005309) tubby-like protein [Arabidopsis thaliana]
                   >gi 4249398 (AC006072) putative tubby protein [Arabidopsis
                   thaliana1
```

```
Seq. No.
                  418951
                  uC-osroM202038g10a1
Seq. ID
Method
                  BLASTX
                  g2244866
NCBI GI
BLAST score
                  315
E value
                  7.0e-29
Match length
                  108
% identity
                  53
NCBI Description (Z97337) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  418952
Seq. ID
                  uC-osroM202038h01b1
Method
                  BLASTX
NCBI GI
                  q6015065
BLAST score
                  750
E value
                  7.0e-80
Match length
                  163
% identity
                  89
NCBI Description ELONGATION FACTOR 2 (EF-2) >gi 2369714 emb CAB09900
                  (Z97178) elongation factor 2 [Beta vulgaris]
Seq. No.
                  418953
Seq. ID
                  uC-osroM202038h02b1
                  BLASTX
Method
                  g1747296
NCBI GI
                  751
BLAST score
E value
                  5.0e-80
Match length
                  158
% identity
                  96
NCBI Description (D45384) vacuolar H+-pyrophosphatase [Oryza sativa]
                  >gi_3298476_dbj_BAA31524_ (AB012766) ovp2 [Oryza sativa]
Seq. No.
                  418954
                  uC-osroM202038h03a1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4803924
BLAST score
                  188
E value
                  3.0e-14
                  80
Match length
% identity
                  53
NCBI Description (AC006264) putative ER lumen protein retaining receptor
                   [Arabidopsis thaliana]
                  418955
Seq. No.
                  uC-osroM202038h05b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q6041850
BLAST score
                  378
E value
                  3.0e-36
Match length
                  160
% identity
                  45
NCBI Description (AC009853) unknown protein [Arabidopsis thaliana]
Seq. No.
                  418956
Seq. ID
                  uC-osroM202038h06b1
Method
                  BLASTX
```

% identity

```
NCBI GI
                  g6041850
BLAST score
                  338
E value
                  1.0e-31
Match length
                  139
% identity
                  47
NCBI Description (AC009853) unknown protein [Arabidopsis thaliana]
Seq. No.
                  418957
                  uC-osroM202038h09a1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2746086
BLAST score
                  188
E value
                  4.0e-14
Match length
                  43
% identity
                  84
NCBI Description (AF025292) putative high-affinity potassium transporter
                  [Hordeum vulgare]
Seq. No.
                  418958
Seq. ID
                  uC-osroM202038h10b1
Method
                  BLASTX
NCBI GI
                  q4220518
BLAST score
                  320
                  2.0e-29
E value
                  135
Match length
% identity
                  46
NCBI Description (AL035356) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  418959
Seq. ID
                  uC-osroM202039a01b1
Method
                  BLASTX
NCBI GI
                  g1420871
BLAST score
                  497
E value
                  3.0e-50
Match length
                  150
% identity
                  65
NCBI Description (X98890) inorganic phosphate transporter 1 [Solanum
                  tuberosum]
Seq. No.
                  418960
Seq. ID
                  uC-osroM202039a05b1
Method
                  BLASTX
NCBI GI
                  g4996640
BLAST score
                  295
E value
                  1.0e-26
Match length
                  104
% identity
                  57
NCBI Description (AB028129) Dof zinc finger protein [Oryza sativa]
Seq. No.
                  418961
Seq. ID
                  uC-osroM202039a06b1
Method
                  BLASTX
NCBI GI
                  g3264767
BLAST score
                  154
E value
                  9.0e-13
Match length
                  41
```

```
NCBI Description (AF071893) AP2 domain containing protein [Prunus armeniaca]
                  418962
Seq. No.
Seq. ID
                  uC-osroM202039a07a1
Method
                  BLASTX
NCBI GI
                  q283008
BLAST score
                  253
                  1.0e-21
E value
Match length
                  52
                  96
% identity
NCBI Description
                  sucrose synthase (EC 2.4.1.13) - rice
                  >gi 20366 emb CAA46017 (X64770) sucrose synthase [Oryza
                  418963
Seq. No.
                  uC-osroM202039a07b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q283008
BLAST score
                  439
E value
                  1.0e-43
Match length
                  98
% identity
                  88
                  sucrose synthase (EC 2.4.1.13) - rice
NCBI Description
                  >gi 20366 emb CAA46017 (X64770) sucrose synthase [Oryza
                  sativa] ...
                  418964
Seq. No.
Seq. ID
                  uC-osroM202039a08b1
Method
                  BLASTX
NCBI GI
                  q5919185
BLAST score
                  228
                  2.0e-20
E value
Match length
                  108
% identity
                  57
NCBI Description (AF183809) arabinogalactan protein Pop14A9 [Populus alba x
                  Populus tremula]
Seq. No.
                  418965
                  uC-osroM202039a10a1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4914414
BLAST score
                  146
E value
                  5.0e-09
Match length
                  41
% identity
NCBI Description (AL050352) Ca2+-transporting ATPase-like protein
                  [Arabidopsis thaliana]
                  418966
Seq. No.
                  uC-osroM202039a10b1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g4996639
BLAST score
                  129
E value
                  3.0e-66
Match length
                  177
% identity
                  93
NCBI Description Oryza sativa mRNA for Dof zinc finger protein, complete cds
```

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418967
Seq. No.
                  uC-osroM202039b02b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4678356
BLAST score
                  185
                  1.0e-13
E value
Match length
                  91
% identity
                  46
NCBI Description
                  (ALO49659) cytochrome P450-like protein [Arabidopsis
                  thaliana]
Seq. No.
                  418968
Seq. ID
                  uC-osroM202039b04a1
Method
                  BLASTX
NCBI GI
                  g5257275
                  398
BLAST score
                  1.0e-38
E value
                  78
Match length
                  99
% identity
NCBI Description
                  (AP000364) ESTs AU030740(E60171), AU030739(E60171)
                  correspond to a region of the predicted gene.; Similar to
                  Populus tremuloides caffeoyl-CoA 3-O-methyltransferase.
                   (U27116) [Oryza sativa]
                  418969
Seq. No.
Seq. ID
                  uC-osroM202039b04b1
Method
                  BLASTX
NCBI GI
                  q4506221
BLAST score
                  187
E value
                  6.0e-14
Match length
                  95
% identity
                  40
NCBI Description
                  proteasome (prosome, macropain) 26S subunit, non-ATPase, 12
                  >gi 1945611 dbj BAA19749 (AB003103) 26S proteasome subunit
                  p55 [Homo sapiens]
Seq. No.
                  418970
                  uC-osroM202039b05a1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4506221
BLAST score
                  234
E value
                  2.0e-19
Match length
                  92
                  48
% identity
NCBI Description
                  proteasome (prosome, macropain) 26S subunit, non-ATPase, 12
                  >gi_1945611_dbj_BAA19749_ (AB003103) 26S proteasome subunit
                  p55 [Homo sapiens]
Seq. No.
                  418971
Seq. ID
                  uC-osroM202039b09b1
Method
                  BLASTX
NCBI GI
                  g4914414
BLAST score
                  487
E value
                  5.0e-49
Match length
                  156
% identity
                  65
```

```
NCBI Description (AL050352) Ca2+-transporting ATPase-like protein
                  [Arabidopsis thaliana]
Seq. No.
                  418972
                  uC-osroM202039b11b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2062175
BLAST score
                  361
E value
                  3.0e-34
Match length
                  157
% identity
                  47
NCBI Description (AC001645) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  418973
Seq. ID
                  uC-osroM202039b12b1
Method
                  BLASTX
NCBI GI
                  g2257756
BLAST score
                  144
E value
                  7.0e-09
Match length
                  40
                  75
% identity
                  (U82815) nucleolar histone deacetylase HD2-p39 [Zea mays]
NCBI Description
                  >gi 3650466 (AF026917) histone deacetylase HD2-p39 [Zea
                  mays]
                  418974
Seq. No.
Seq. ID
                  uC-osroM202039c01a1
Method
                  BLASTN
NCBI GI
                  q1777454
BLAST score
                  168
E value
                  9.0e-90
Match length
                  196
% identity
                  98
NCBI Description Oryza sativa pyruvate decarboxylase 2 (pdc2) gene, complete
Seq. No.
                  418975
Seq. ID
                  uC-osroM202039c01b1
Method
                  BLASTX
                  g1706328
NCBI GI
BLAST score
                  786
E value
                  4.0e-84
Match length
                  163
% identity
                  95
NCBI Description PYRUVATE DECARBOXYLASE ISOZYME 2 (PDC) >gi 1009710 (U27350)
                  pyruvate decarboxylase 2 [Oryza sativa] >gi 1777455
                  (U38199) pyruvate decarboxylase 2 [Oryza sativa]
Seq. No.
                  418976
Seq. ID
                  uC-osroM202039c02a1
Method
                  BLASTX
NCBI GI
                  g3522950
BLAST score
                  145
E value
                  3.0e-09
Match length
                  48
% identity
NCBI Description (AC004411) hypothetical protein [Arabidopsis thaliana]
```

```
Seq. No.
                   418977
Seq. ID
                  uC-osroM202039c02b1
Method
                  BLASTX
NCBI GI
                   g3522950
BLAST score
                  236
E value
                  1.0e-19
Match length
                  73
% identity
                  55
NCBI Description (AC004411) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  418978
Seq. ID
                  uC-osroM202039c03b1
                  BLASTX
Method
NCBI GI
                  g4335864
BLAST score
                  197
                  5.0e-15
E value
Match length
                  47
% identity
                  68
NCBI Description (AF052040) calreticulin [Berberis stolonifera]
                  418979
Seq. No.
Seq. ID
                  uC-osroM202039c04a1
Method
                  BLASTX
NCBI GI
                  g3511285
BLAST score
                  151
                  1.0e-09
E value
Match length
                  37
% identity
                  65
NCBI Description
                  (AF081534) cellulose synthase [Populus alba x Populus
                  tremula]
Seq. No.
                  418980
                  uC-osroM202039c04b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4056568
BLAST score
                  315
E value
                  2.0e-29
Match length
                  78
                  77
% identity
NCBI Description (U90944) PDI-like protein [Zea mays]
Seq. No.
                  418981
Seq. ID
                  uC-osroM202039c05b1
Method
                  BLASTX
NCBI GI
                  g5257275
BLAST score
                  511
E value
                  2.0e-52
Match length
                  120
% identity
                  87
                  (AP000364) ESTs AU030740(E60171), AU030739(E60171)
NCBI Description
                  correspond to a region of the predicted gene.; Similar to
                  Populus tremuloides caffeoyl-CoA 3-O-methyltransferase.
                   (U27116) [Oryza sativa]
Seq. No.
                  418982
Seq. ID
                  uC-osroM202039c06a1
```

```
Method
                  BLASTX
NCBI GI
                  g5257275
BLAST score
                  351
E value
                   4.0e-33
Match length
                  68
                  100
% identity
                  (AP000364) ESTs AU030740(E60171), AU030739(E60171)
NCBI Description
                  correspond to a region of the predicted gene.; Similar to
                  Populus tremuloides caffeoyl-CoA 3-O-methyltransferase.
                   (U27116) [Oryza sativa]
Seq. No.
                  418983
                  uC-osroM202039c06b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q5257275
BLAST score
                  610
E value
                  1.0e-63
Match length
                  122
% identity
                  98
NCBI Description
                  (AP000364) ESTs AU030740(E60171), AU030739(E60171)
                  correspond to a region of the predicted gene.; Similar to
                  Populus tremuloides caffeoyl-CoA 3-O-methyltransferase.
                   (U27116) [Oryza sativa]
Seq. No.
                  418984
                  uC-osroM202039c09a1
Seq. ID
Method
                  BLASTX
                  g1197587
NCBI GI
BLAST score
                  348
E value
                  9.0e-33
Match length
                  74
% identity
NCBI Description
                  (U46758) potassium channel beta subunit protein [Oryza
                  sativa]
Seq. No.
                  418985
                  uC-osroM202039c09b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2832783
BLAST score
                  557
E value
                  3.0e-57
Match length
                  116
% identity
NCBI Description (AJ225806) potassium channel beta subunit [Egeria densa]
Seq. No.
                  418986
Seq. ID
                  uC-osroM202039c11a1
Method
                  BLASTN
NCBI GI
                  g1519250
BLAST score
                  307
E value
                  1.0e-172
                  311
Match length
% identity
                  100
```

Seq. No. 418987

Seq. ID uC-osroM202039c11b1

NCBI Description Oryza sativa GF14-c protein mRNA, complete cds

```
Method
                 BLASTX
NCBI GI
                 g1519251
BLAST score
                 591
E value
                 6.0e-68
Match length
                 143
% identity
                 98
NCBI Description (U65957) GF14-c protein [Oryza sativa]
Seq. No.
                 418988
Seq. ID
                 uC-osroM202039c12a1
Method
                 BLASTN
NCBI GI
                 g1519250
BLAST score
                 261
E value
                 1.0e-145
Match length
                 393
                92
% identity
NCBI Description Oryza sativa GF14-c protein mRNA, complete cds
Seq. No.
                 418989
Seq. ID
                 uC-osroM202039c12b1
Method
                BLASTX
NCBI GI
                 q3766535
BLAST score
                144
E value
                4.0e-09
Match length
                78
% identity
NCBI Description (Y11687) 14-3-3 protein [Solanum tuberosum]
Seq. No.
                 418990
               uC-osroM202039d04b1
Seq. ID
Method
                BLASTX
               g1588281
NCBI GI
BLAST score
                181
E value
                3.0e-13
               125
Match length
% identity
                 34
NCBI Description RING3 protein [Homo sapiens]
Seq. No.
                 418991
Seq. ID
                 uC-osroM202039d06a1
Method
                 BLASTN
                g5257255
288
NCBI GI
BLAST score
E value
                 1.0e-161
                376
Match length
                94
% identity
NCBI Description Oryza sativa genomic DNA, chromosome 8, clone:P0026F07
Seq. No.
                 418992
Seq. ID
                 uC-osroM202039d07a1
Method
                 BLASTX
NCBI GI
                 g2190551
BLAST score
                146
E value
                4.0e-09
Match length
                 32
% identity
NCBI Description (AC001229) Similar to C. elegans hypothetical protein
```

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K07C5.6 (gb_Z71181). ESTs gb_H36844,gb_AA394956 come from this gene. [Arabidopsis thaliana]

Seq. No. 418993

Seq. ID uC-osroM202039d08b1

Method BLASTX
NCBI GI g133961
BLAST score 274
E value 3.0e-24
Match length 73
% identity 77

NCBI Description 40S RIBOSOMAL PROTEIN S2 (S4) (YS5) (RP12) (OMNIPOTENT

SUPRESSOR PROTEIN SUP44) >gi_70888_pir__R3BYS2 ribosomal protein S2.e - yeast (Saccharomyces cerevisiae) >gi_172793 (M59375) ribosomal protein S4 [Saccharomyces cerevisiae]

>gi_1322683_emb_CAA96831 (Z72645) ORF YGL123w
[Saccharomyces cerevisiae] >gi_1628451_emb_CAA63835

(X94106) SUP44 [Saccharomyces cerevisiae]

Seq. No. 418994

Seq. ID uC-osroM202039d09b1

Method BLASTX
NCBI GI g1763063
BLAST score 220
E value 9.0e-18
Match length 135
% identity 40

NCBI Description (U68763) SCOF-1 [Glycine max]

Seq. No. 418995

Seq. ID uC-osroM202039d10b1

Method BLASTX
NCBI GI 94680207
BLAST score 194
E value 1.0e-14
Match length 102
% identity 42

NCBI Description (AF114171) disease resistance protein RPM1 homolog [Sorghum

bicolor]

Seq. No. 418996

Seq. ID uC-osroM202039d11a1

Method BLASTX
NCBI GI g1519251
BLAST score 250
E value 3.0e-21
Match length 54
% identity 93

NCBI Description (U65957) GF14-c protein [Oryza sativa]

Seq. No. 418997

Seq. ID uC-osroM202039d11b1

Method BLASTX
NCBI GI g1519251
BLAST score 629
E value 4.0e-71
Match length 141

% identity NCBI Description (U65957) GF14-c protein [Oryza sativa] 418998 Seq. No. Seq. ID uC-osroM202039e01b1 BLASTX Method g5107819 NCBI GI BLAST score 361 E value 2.0e-34 139 Match length 53 % identity NCBI Description (AF149413) contains similarity to arabinosidase [Arabidopsis thaliana] 418999 Seq. No. Seq. ID uC-osroM202039e02b1 Method BLASTX NCBI GI q5107819 BLAST score 378 E value 3.0e - 36Match length 145 % identity 52 NCBI Description (AF149413) contains similarity to arabinosidase [Arabidopsis thaliana] 419000 Seq. No. Seq. ID uC-osroM202039e03b1 Method BLASTX g1071913 NCBI GI BLAST score 198 E value 2.0e-15 Match length 77 53 % identity cysteine synthase (EC 4.2.99.8) C precursor, mitochondrial NCBI Description - spinach >gi_1066153_dbj_BAA07177_ (D37963) cysteine synthase [Spinacia oleracea] 419001 Seq. No. Seq. ID uC-osroM202039e04b1 Method BLASTX NCBI GI q4585991 396 BLAST score E value 9.0e-39 89 Match length % identity NCBI Description (AC005287) very similar to mouse Dhm1 and Dhm2 [Arabidopsis thaliana] Seq. No. 419002 Seq. ID uC-osroM202039e05a1 Method BLASTX NCBI GI g1747296 BLAST score 306 E value 8.0e-28 Match length 90 % identity 74

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NCBI Description (D45384) vacuolar H+-pyrophosphatase [Oryza sativa]

NCBI GI

```
>gi 3298476 dbj BAA31524 (AB012766) ovp2 [Oryza sativa]
Seq. No.
                   419003
Seq. ID
                  uC-osroM202039e05b1
Method
                  BLASTX
NCBI GI
                  q5926740
BLAST score
                  566
E value
                  1.0e-58
                  107
Match length
                   97
% identity
NCBI Description (AB025310) asparaginyl endopeptidase [Oryza sativa]
                   419004
Seq. No.
                  uC-osroM202039e06a1
Seq. ID
                  BLASTX
Method
NCBI GI
                   q5926740
BLAST score
                   320
                   2.0e-29
E value
Match length
                   61
                  100
% identity
NCBI Description (AB025310) asparaginyl endopeptidase [Oryza sativa]
                   419005
Seq. No.
                   uC-osroM202039e09a1
Seq. ID
                   BLASTX
Method
NCBI GI
                   q3548808
BLAST score
                   230
                   6.0e-19
E value
Match length
                   96
% identity
                   46
NCBI Description (AC005313) unknown protein [Arabidopsis thaliana]
                   419006
Seq. No.
                   uC-osroM202039e10a1
Seq. ID
                   BLASTX
Method
                   g3548808
NCBI GI
                   341
BLAST score
                   7.0e-32
E value
                  130
Match length
% identity
                   49
NCBI Description (AC005313) unknown protein [Arabidopsis thaliana]
                   419007
Seq. No.
                   uC-osroM202039e11a1
Seq. ID
                   BLASTX
Method
                   q1747296
NCBI GI
                   729
BLAST score
                   2.0e-77
E value
                   143
Match length
                   100
% identity
                  (D45384) vacuolar H+-pyrophosphatase [Oryza sativa]
NCBI Description
                   >gi 3298476 dbj BAA31524 (AB012766) ovp2 [Oryza sativa]
                   419008
Seq. No.
                   uC-osroM202039e11b1
Seq. ID
Method
                   BLASTX
```

54931

g1747296

```
BLAST score
                  204
                  8.0e-27
E value
Match length
                  65
% identity
                  93
NCBI Description
                  (D45384) vacuolar H+-pyrophosphatase [Oryza sativa]
                  >gi 3298476 dbj BAA31524 (AB012766) ovp2 [Oryza sativa]
Seq. No.
                  419009
                  uC-osroM202039e12b1
Seq. ID
                  BLASTX
Method
NCBI GI
                  g1588281
BLAST score
                  247
E value
                  7.0e-21
                  165
Match length
                  23
% identity
NCBI Description RING3 protein [Homo sapiens]
                   419010
Seq. No.
Seq. ID
                  uC-osroM202039f01b1
                  BLASTX
Method
                  q3395441
NCBI GI
BLAST score
                   211
                   1.0e-16
E value
Match length
                   66
                   61
% identity
NCBI Description (AC004683) unknown protein [Arabidopsis thaliana]
                   419011
Seq. No.
Seq. ID
                   uC-osroM202039f02b1
Method
                   BLASTX
                   q4733891
NCBI GI
                   158
BLAST score
                   1.0e-10
E value
                   55
Match length
                   58
% identity
NCBI Description (AF104924) unconventional myosin heavy chain [Zea mays]
                   419012
Seq. No.
                   uC-osroM202039f05b1
Seq. ID
                   BLASTX
Method
                   g4263704
NCBI GI
                   258
BLAST score
E value
                   3.0e-22
                   138
Match length
                   41
% identity
NCBI Description (AC006223) putative sugar starvation-induced protein
                   [Arabidopsis thaliana]
                   419013
Seq. No.
                   uC-osroM202039f06b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   q4263704
BLAST score
                   217
E value
                   2.0e-17
                   141
Match length
% identity
                   36
                  (AC006223) putative sugar starvation-induced protein
NCBI Description
```

[Arabidopsis thaliana]

Seq. No. 419014 uC-osroM202039f07a1 Seq. ID BLASTX Method NCBI GI q4914402 267 BLAST score E value 2.0e-24 Match length 84 70 % identity NCBI Description (AL050352) hypothetical protein [Arabidopsis thaliana] 419015 Seq. No. Seq. ID uC-osroM202039f08a1 BLASTX Method NCBI GI g114682 193 BLAST score E value 1.0e-14 Match length 53 % identity 66 NCBI Description ATP SYNTHASE DELTA CHAIN, MITOCHONDRIAL PRECURSOR (OLIGOMYCIN SENSITIVITY CONFERRAL PROTEIN) (OSCP) >qi 100471 pir A35227 H+-transporting ATP synthase (EC 3.6.1.34) gamma chain precursor, mitochondrial - sweet potato >gi 168270 (J05397) F-1-ATPase delta subunit precursor (EC 3.6.1.3) [Ipomoea batatas] 419016 Seq. No. Seq. ID uC-osroM202039f09a1 Method BLASTN q450548 NCBI GI 104 BLAST score 1.0e-51 E value Match length 120 % identity 97 NCBI Description O.sativa (pRSAM-1) gene for S-adenosyl methionine synthetase Seq. No. 419017 uC-osroM202039f09b1 Seq. ID Method BLASTX NCBI GI g1170937 BLAST score 408 E value 4.0e-40 Match length 79 % identity 96 S-ADENOSYLMETHIONINE SYNTHETASE 1 (METHIONINE NCBI Description ADENOSYLTRANSFERASE 1) (ADOMET SYNTHETASE 1) >gi 450549 emb CAA81481 (Z26867) S-adenosyl methionine synthetase [Oryza sativa] 419018 Seq. No. uC-osroM202039f10b1 Seq. ID

Seq. ID uC-osroM202039f1
Method BLASTN
NCBI GI g1159876
BLAST score 48

E value

9.0e-18

Match length 56 96 % identity NCBI Description A.fatua mRNA for DNA-binding protein (clone ABF1) 419019 Seq. No. uC-osroM202039g01a1 Seq. ID BLASTN Method NCBI GI g1574943 BLAST score 86 E value 1.0e-40 114 Match length % identity NCBI Description Oryza sativa polyubiquitin (Rubq1) mRNA, complete cds 419020 Seq. No. Seq. ID uC-osroM202039g01b1 BLASTX Method NCBI GI q82734 BLAST score 599 E value 3.0e-62 126 Match length 29 % identity NCBI Description ubiquitin precursor - maize (fragment) >gi 226763 prf 1604470A poly-ubiquitin [Zea mays] 419021 Seq. No. Seq. ID uC-osroM202039g02b1 BLASTX Method NCBI GI g3334320 BLAST score 643 3.0e-67 E value 140 Match length 90 % identity NCBI Description 40S RIBOSOMAL PROTEIN SA (P40) >gi 2444420 (AF020553) ribosome-associated protein p40 [Glycine max] Seq. No. 419022 Seq. ID uC-osroM202039q03b1 BLASTX Method NCBI GI q3786016 BLAST score 446 E value 3.0e-44Match length 149 % identity NCBI Description (AC005499) putative elongation factor [Arabidopsis thaliana] 419023 Seq. No. uC-osroM202039g04a1 Seq. ID Method BLASTX NCBI GI g1706260 BLAST score 217 E value 2.0e-17 43 Match length 88 % identity NCBI Description CYSTEINE PROTEINASE 1 PRECURSOR >gi 2118131 pir S59597

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cysteine proteinase 1 precursor - maize

```
>gi 643597 dbj BAA08244 (D45402) cysteine proteinase [Zea
                  mays]
                  419024
Seq. No.
                  uC-osroM202039g04b1
Seq. ID
                  BLASTX
Method
NCBI GI
                  g2129921
BLAST score
                  188
                  3.0e-14
E value
                  51
Match length
                  71
% identity
NCBI Description hypothetical protein 1 - Madagascar periwinkle >gi_758694
                  (U12573) putative [Catharanthus roseus]
Seq. No.
                  419025
                  uC-osroM202039g05a1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g5263324
BLAST score
                  264
                  4.0e-23
E value
                  61
Match length
                  80
% identity
                  (AC007727) Identical to gb Y13173 Arabidopsis thaliana mRNA
NCBI Description
                  for proteasome subunit. EST gb_T76747 comes from this gene
                  419026
Seq. No.
                  uC-osroM202039q05b1
Seq. ID
Method
                  BLASTX
                  g2662341
NCBI GI
                  792
BLAST score
                  2.0e-88
E value
Match length
                  166
% identity
                  97
                  (D63580) EF-1 alpha [Oryza sativa]
NCBI Description
                  >gi_2662345_dbj_BAA23659_ (D63582) EF-1 alpha [Oryza
                  satīva] >gi_2662347_dbj_BAA23660_ (D63583) EF-1 alpha
                   [Oryza sativa]
                  419027
Seq. No.
                  uC-osroM202039g06a1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2662343
BLAST score
                  228
E value
                  1.0e-18
                  45
Match length
% identity
NCBI Description (D63581) EF-1 alpha [Oryza sativa]
Seq. No.
                  419028
Seq. ID
                  uC-osroM202039g09a1
Method
                  BLASTX
NCBI GI
                  q3914899
BLAST score
                  225
E value
                  2.0e-18
Match length
                  44
% identity
                  95
NCBI Description 40S RIBOSOMAL PROTEIN S4 >gi 2331301 (AF013487) ribosomal
```

protein S4 type I [Zea mays]

Seq. No. 419029 uC-osroM202039g09b1 Seq. ID Method BLASTX NCBI GI q3123270 BLAST score 641 4.0e-67 E value Match length 123 % identity 100 NCBI Description

40S RIBOSOMAL PROTEIN S4 (SCAR PROTEIN SS620)

>gi 2463335 emb CAA75242 (Y15009) ribosomal protein S4

[Oryza sativa]

419030 Seq. No.

Seq. ID uC-osroM202039g10a1

Method BLASTX NCBI GI g3914899 BLAST score 287 1.0e-25 E value Match length 56 % identity 95

NCBI Description 40S RIBOSOMAL PROTEIN S4 >gi_2331301 (AF013487) ribosomal

protein S4 type I [Zea mays]

Seq. No. 419031

uC-osroM202039g10b1 Seq. ID

Method BLASTX g3123270 NCBI GI 730 BLAST score 2.0e-77 E value Match length 142 98 % identity

NCBI Description 40S RIBOSOMAL PROTEIN S4 (SCAR PROTEIN SS620)

>gi 2463335 emb CAA75242 (Y15009) ribosomal protein S4

[Oryza sativa]

Seq. No. 419032

uC-osroM202039h01b1 Seq. ID

Method BLASTX g3786016 NCBI GI BLAST score 246 E value 9.0e-21 143 Match length % identity 42

NCBI Description (AC005499) putative elongation factor [Arabidopsis

thaliana]

Seq. No. 419033

uC-osroM202039h02a1 Seq. ID

Method BLASTN NCBI GI q218182 BLAST score 266 1.0e-148 E value Match length 286 99 % identity

NCBI Description Rice mRNA for oryzain beta (EC 3.4.22)

E value Match length

82

Seq. No. 419034 uC-osroM202039h02b1 Seq. ID Method BLASTX NCBI GI q129232 BLAST score 466 1.0e-46 E value Match length 89 98 % identity ORYZAIN BETA CHAIN PRECURSOR >gi_67645_pir__KHRZOB oryzain NCBI Description (EC 3.4.22.-) beta precursor - rice >gi 218183_dbj_BAA14403 (D90407) oryzain beta precursor [Oryza sativa] 419035 Seq. No. uC-osroM202039h03b1 Seq. ID Method BLASTX q1839188 NCBI GI BLAST score 568 2.0e-58 E value 133 Match length % identity (U86081) root hair defective 3 [Arabidopsis thaliana] NCBI Description 419036 Seq. No. uC-osroM202039h05b1 Seq. ID BLASTX Method q1076641 NCBI GI BLAST score 638 E value 1.0e-66 Match length 160 % identity 76 tau-protein kinase (EC 2.7.1.135) homolog - common tobacco NCBI Description >gi 456356 emb_CAA54803_ (X77763) shaggy like protein kinase [Nicotiana tabacum] >gi_1094395_prf__2106142A Ser/Thr protein kinase [Nicotiana tabacum] 419037 Seq. No. Seq. ID uC-osroM202039h06b1 Method BLASTX g1706260 NCBI GI BLAST score 616 4.0e-64 E value Match length 133 89 % identity CYSTEINE PROTEINASE 1 PRECURSOR >gi_2118131_pir__S59597 NCBI Description cysteine proteinase 1 precursor - maize >gi 643597 dbj_BAA08244_ (D45402) cysteine proteinase [Zea mays] 419038 Seq. No. uC-osroM202039h07a1 Seq. ID Method BLASTX NCBI GI q4773917 243 BLAST score 9.0e-21

```
% identity
                  (AF147259) similar to human prostate-specific membrane
NCBI Description
                  antigen (PSM) (SP:Q04609) [Arabidopsis thaliana]
Seq. No.
                  419039
Seq. ID
                  uC-osroM202039h08b1
                  BLASTX
Method
                  q1946367
NCBI GI
                  142
BLAST score
                  5.0e-09
E value
                  72
Match length
                  32
% identity
                  (U93215) unknown protein [Arabidopsis thaliana]
NCBI Description
                  419040
Seq. No.
Seq. ID
                  uC-osroM202039h09b1
                  BLASTX
Method
NCBI GI
                  q6017104
BLAST score
                  143
                  1.0e-08
E value
                  122
Match length
                  38
% identity
                  (AC009895) putative hypersensitivity-related gene
NCBI Description
                   [Arabidopsis thaliana]
                   419041
Seq. No.
Seq. ID
                  uC-osroM202039h10a1
                  BLASTX
Method
NCBI GI
                  q3044218
BLAST score
                   192
                  1.0e-14
E value
                   41
Match length
% identity
                  80
NCBI Description (AF057144) signal peptidase [Arabidopsis thaliana]
Seq. No.
                   419042
                   uC-osroM202039h10b1
Seq. ID
Method
                  BLASTX
NCBI GI
                   q3044218
BLAST score
                   538
E value
                   5.0e-55
                   134
Match length
                   75
% identity
NCBI Description (AF057144) signal peptidase [Arabidopsis thaliana]
                   419043
Seq. No.
                   uC-osroM202039h11b1
Seq. ID
                   BLASTX
Method
                   g1706260
NCBI GI
BLAST score
                   379
                   1.0e-36
E value
Match length
                   95
                   80
% identity
NCBI Description CYSTEINE PROTEINASE 1 PRECURSOR >gi_2118131_pir__S59597
                   cysteine proteinase 1 precursor - maize
                   >gi_643597_dbj_BAA08244_ (D45402) cysteine proteinase [Zea
```

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mays]

```
Seq. No.
                  419044
                  uC-osroM202039h12a1
Seq. ID
                  BLASTX
Method
NCBI GI
                  q3913426
                  285
BLAST score
                  2.0e-25
E value
                  53
Match length
                  100
% identity
                  S-ADENOSYLMETHIONINE DECARBOXYLASE PROENZYME (ADOMETDC)
NCBI Description
                   (SAMDC) >gi 1532048_emb_CAA69074_ (Y07766)
                  S-adenosylmethionine decarboxylase [Oryza sativa]
                   419045
Seq. No.
Seq. ID
                  uC-osroM202039h12b1
Method
                  BLASTX
                  g2129921
NCBI GI
BLAST score
                  179
                  7.0e-13
E value
Match length
                  51
% identity
                   67
                  hypothetical protein 1 - Madagascar periwinkle >gi_758694
NCBI Description
                   (U12573) putative [Catharanthus roseus]
                   419046
Seq. No.
                   uC-osroM202040a04b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g294845
BLAST score
                   285
                   2.0e-43
E value
                   114
Match length
                   78
% identity
                  (L13655) membrane protein [Saccharum hybrid cultivar
NCBI Description
                   H65-7052]
                   419047
Seq. No.
                   uC-osroM202040a05b1
Seq. ID
Method
                   BLASTX
                   g2911042
NCBI GI
BLAST score
                   200
                   2.0e-15
E value
                   74
Match length
                   58
% identity
                  (AL021961) Phosphoglycerate dehydrogenase - like protein
NCBI Description
                   [Arabidopsis thaliana]
                   419048
Seq. No.
Seq. ID
                   uC-osroM202040a10b1
Method
                   BLASTX
                   g1184776
NCBI GI
BLAST score
                   533
E value
                   1.0e-54
Match length
                   114
% identity
                   (U45857) cytosolic glyceroldehyde-3-phosphate dehydrogenase
NCBI Description
```

GAPC4 [Zea mays]

Seq. ID

```
419049
Seq. No.
                  uC-osroM202040b08b1
Seq. ID
Method
                  BLASTX
                  g2894599
NCBI GI
                  186
BLAST score
                  8.0e-14
E value
                  110
Match length
% identity
                  42
                 (AL021889) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  419050
                  uC-osroM202040b09b1
Seq. ID
                  BLASTX
Method
NCBI GI
                  q1184774
                  619
BLAST score
                  2.0e-64
E value
Match length
                  144
                  83
% identity
                 (U45856) cytosolic glyceroldehyde-3-phosphate dehydrogenase
NCBI Description
                  GAPC3 [Zea mays]
Seq. No.
                  419051
                  uC-osroM202040b10b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3023816
BLAST score
                  356
E value
                  9.0e-49
                  115
Match length
                  82
% identity
NCBI Description GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC
                  >gi_968996 (U31676) glyceraldehyde-3-phosphate
                  dehydrogenase [Oryza sativa]
                  419052
Seq. No.
                  uC-osroM202040b11b1
Seq. ID
Method
                  BLASTN
NCBI GI
                  a218146
                  98
BLAST score
                  8.0e-48
E value
                  125
Match length
                  96
% identity
NCBI Description Rice mRNA for mitochondrial F1-ATPase
                  419053
Seq. No.
                  uC-osroM202040c03b1
Seq. ID
                  BLASTX
Method
NCBI GI
                  q1706325
BLAST score
                  613
E value
                  9.0e-64
Match length
                  146
                  86
% identity
NCBI Description PYRUVATE DECARBOXYLASE ISOZYME 1 (PDC) >qi 476286 (U07339)
                  pyruvate decarboxylase 1 [Oryza sativa] >gi 1098559
                  (U26660) pyruvate decarboxylase [Oryza sativa]
Seq. No.
                  419054
```

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uC-osroM202040c05b1

Method BLASTX g2130089 NCBI GI BLAST score 447 2.0e-44 E value 130 Match length 74 % identity 2-oxoglutarate/malate translocator (clone OMT103), NCBI Description mitochondrial membrane - proso millet >gi 1100743 dbj BAA08105 (D45075) 2-oxoglutarate/malate translocator [Panicum miliaceum] Seq. No. 419055 uC-osroM202040c06b1 Seq. ID Method BLASTX q3695383 NCBI GI BLAST score 535 1.0e-54 E value Match length 113 86 % identity (AF096370) similar to inorganic pyrophosphatase (Pfam: NCBI Description PF00719 Pyrophosphatase, E-value: 2.7e-88) [Arabidopsis thaliana] 419056 Seq. No. uC-osroM202040c07b1 Seq. ID BLASTX Method g169757 NCBI GI BLAST score 789 2.0e-84 E value 171 Match length 88 % identity NCBI Description (M36469) alcohol dehydrogenase (adh2) [Oryza sativa] 419057 Seq. No. uC-osroM202040c08b1 Seq. ID BLASTX Method NCBI GI g113378 BLAST score 922 1.0e-100 E value 179 Match length 98 % identity ALCOHOL DEHYDROGENASE 2 >gi_65904_pir__DERZA2 alcohol dehydrogenase (EC 1.1.1.1) 2 - rice >gi_20169_emb_CAA34364_ NCBI Description (X16297) alcohol dehydrogenase 2 [Oryza sativa] 419058 Seq. No. Seq. ID uC-osroM202040c10b1 Method BLASTX NCBI GI q3413511 215 BLAST score

4.0e-17 E value 64 Match length % identity

(AJ000265) glucose-6-phosphate isomerase [Spinacia NCBI Description

oleracea]

Seq. No. 419059

```
uC-osroM202040d01b1
Seq. ID
                    BLASTX
Method
                    g1706328
NCBI GI
                    848
BLAST score
                    2.0e-91
E value
                    174
Match length
                    96
% identity
                    PYRUVATE DECARBOXYLASE ISOZYME 2 (PDC) >gi 1009710 (U27350)
NCBI Description
                    pyruvate decarboxylase 2 [Oryza sativa] >gi 1777455
                    (U38199) pyruvate decarboxylase 2 [Oryza sativa]
                    419060
Seq. No.
                    uC-osroM202040d02b1
Seq. ID
                    BLASTX
Method
                    q1706328
NCBI GI
                    824
BLAST score
                    2.0e-88
E value
                    171
Match length
                    95
% identity
NCBI Description PYRUVATE DECARBOXYLASE ISOZYME 2 (PDC) >gi 1009710 (U27350)
                    pyruvate decarboxylase 2 [Oryza sativa] >gi_1777455
                    (U38199) pyruvate decarboxylase 2 [Oryza sativa]
                    419061
Seq. No.
                    uC-osroM202040d03b1
Seq. ID
                    BLASTX
Method
                    g2499819
NCBI GI
                    563
BLAST score
                    7.0e-58
E value
                    163
Match length
                    71
% identity
NCBI Description ASPARTIC PROTEINASE ORYZASIN 1 PRECURSOR
                    >gi_2130068_pir__ S66516 aspartic proteinase 1 precursor -
rice >gi_1030715_dbj_BAA06876_ (D32165) aspartic protease
[Oryza sativa] >gi_1711289_dbj_BAA06875_ (D32144) aspartic
                    protease [Oryza sativa]
                    419062
Seq. No.
                    uC-osroM202040d04b1
Seq. ID
                    BLASTX
Method
NCBI GI
                    g2150002
BLAST score
                    516
                     2.0e-52
E value
Match length
                    97
                    86
% identity
NCBI Description (AF000940) ribonuclease [Hordeum vulgare]
Seq. No.
                     419063
Seq. ID
                     uC-osroM202040d06b1
Method
                    BLASTX
NCBI GI
                     q2497883
```

Method BLASTX
NCBI GI g2497883
BLAST score 226
E value 2.0e-18
Match length 56

Match length 56 % identity 75

NCBI Description METALLOTHIONEIN-LIKE PROTEIN TYPE 1 >gi_1362174_pir__S57768 metallothionein-like protein - rice >gi_687638 (U18404)

metallothionein-like protein [Oryza sativa] >gi_1815626 (U43529) metallothionein-like type 1 [Oryza sativa] >gi_4097154_gb_AAD10376.1_ (U46159) type 1 rice metallothionein-like gene; Method: conceptual translation supplied by author. [Oryza sativa]

Seq. No. 419064

Seq. ID uC-osroM202040d07b1

Method BLASTX
NCBI GI g1706956
BLAST score 800
E value 1.0e-85
Match length 167
% identity 88

NCBI Description (U58283) cellulose synthase [Gossypium hirsutum]

Seq. No. 419065

Seq. ID uC-osroM202040d10b1

Method BLASTX
NCBI GI g2832783
BLAST score 754
E value 3.0e-80
Match length 159
% identity 86

NCBI Description (AJ225806) potassium channel beta subunit [Egeria densa]

Seq. No. 419066

Seq. ID uC-osroM202040d11b1

Method BLASTX
NCBI GI g4559342
BLAST score 891
E value 2.0e-96
Match length 176
% identity 91

NCBI Description (AC007087) putative copper methylamine oxidase [Arabidopsis

thaliana]

Seq. No. 419067

Seq. ID uC-osroM202040d12b1

Method BLASTN
NCBI GI g6063530
BLAST score 36
E value 7.0e-11
Match length 122
% identity 84

NCBI Description Oryza sativa genomic DNA, chromosome 3, clone:P0043E01

Seq. No. 419068

Seq. ID uC-osroM202040e01b1

Method BLASTX
NCBI GI g1519251
BLAST score 666
E value 5.0e-70
Match length 133
% identity 100

NCBI Description (U65957) GF14-c protein [Oryza sativa]

Method

BLASTX

```
419069
Seq. No.
                  uC-osroM202040e02b1
Seq. ID
Method
                  BLASTX
                  g3132310
NCBI GI
BLAST score
                  369
                  2.0e-46
E value
                  110
Match length
                  92
% identity
                  (AB012228) phosphoenolpyruvate carboxylase [Zea mays]
NCBI Description
                  419070
Seq. No.
                  uC-osroM202040e03b1
Seq. ID
Method
                  BLASTX
                  q1709619
NCBI GI
                  258
BLAST score
                  3.0e-22
E value
                  69
Match length
                   68
% identity
                  PROTEIN DISULFIDE ISOMERASE PRECURSOR (PDI)
NCBI Description
                  >qi 2146814 pir S69181 protein disulfide isomerase (EC
                   5.3.4.1) precursor - maize >gi_625148 (L39014) protein
                  disulfide isomerase [Zea mays]
                   419071
Seq. No.
                  uC-osroM202040e05b1
Seq. ID
Method
                  BLASTX
NCBI GI
                   q3386621
                   598
BLAST score
                   5.0e-62
E value
                   146
Match length
                   76
% identity
NCBI Description (AC004665) unknown protein [Arabidopsis thaliana]
                   419072
Seq. No.
                   uC-osroM202040e07b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   a1084461
BLAST score
                   488
                   4.0e-49
E value
                   130
Match length
                   77
% identity
NCBI Description RCc3 protein - rice >gi_786132 (L27208) RCc3 [Oryza sativa]
                   419073
Seq. No.
                   uC-osroM202040e09b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3850816
BLAST score
                   591
E value
                   3.0e-61
Match length
                   108
% identity
                   100
                   (Y18348) U2 snRNP auxiliary factor, small subunit [Oryza
NCBI Description
                   sativa]
                   419074
Seq. No.
Seq. ID
                   uC-osroM202040e10b1
```

54944

```
g3850816
NCBI GI
BLAST score
                  683
                  5.0e-72
E value
                  127
Match length
                  99
% identity
                  (Y18348) U2 snRNP auxiliary factor, small subunit [Oryza
NCBI Description
                  sativa]
                  419075
Seq. No.
                  uC-osroM202040f01b1
Seq. ID
                  BLASTX
Method
                  g1362086
NCBI GI
                  801
BLAST score
                  9.0e-86
E value
                  173
Match length
                  87
% identity
                  5-methyltetrahydropteroyltriglutamate--homocysteine
NCBI Description
                  S-methyltransferase (EC 2.1.1.14) - Madagascar periwinkle
                  >qi 2129919 pir S65957
                   5-methyltetrahydropteroyltriglutamate--homocysteine
                  S-methyltransferase (EC 2.1.1.14) - Madagascar periwinkle
                  >gi_886471_emb_CAA58474_ (X83499) methionine synthase
                   [Catharanthus roseus]
                   419076
Seq. No.
                  uC-osroM202040f02b1
Seq. ID
                  BLASTX
Method
                  g2853076
NCBI GI
BLAST score
                   402
                   5.0e-39
E value
                  171
Match length
                   51
% identity
NCBI Description (AL021768) putative protein [Arabidopsis thaliana]
                   419077
Seq. No.
                   uC-osroM202040f03b1
Seq. ID
Method
                   BLASTX
                   g3643611
NCBI GI
                   317
BLAST score
                   5.0e-29
E value
                   77
Match length
% identity
                   75
NCBI Description (AC005395) putative casein kinase [Arabidopsis thaliana]
                   419078
Seq. No.
                   uC-osroM202040f04b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3551958
BLAST score
                   217
                   3.0e-17
E value
```

Match length 55 75 % identity

(AF082032) senescence-associated protein 12 [Hemerocallis NCBI Description

hybrid cultivar]

419079 Seq. No.

uC-osroM202040f05b1 Seq. ID

Method BLASTX NCBI GI g2285877 BLAST score 331 7.0e-58 E value Match length 167 70 % identity (D86337) pyruvate orthophosphate dikinase [Eleocharis NCBI Description vivipara] 419080 Seq. No. uC-osroM202040f06b1 Seq. ID Method BLASTX NCBI GI g4929621 BLAST score 450 E value 1.0e-44Match length 142 58 % identity (AF151834) CGI-76 protein [Homo sapiens] NCBI Description Seq. No. 419081 uC-osroM202040f08b1 Seq. ID Method BLASTX NCBI GI g1084461 BLAST score 464 2.0e-46 E value 133 Match length 71 % identity NCBI Description RCc3 protein - rice >gi 786132 (L27208) RCc3 [Oryza sativa] Seq. No. 419082 uC-osroM202040f09b1 Seq. ID Method BLASTN NCBI GI g4680488 BLAST score 87 5.0e-41 E value Match length 111 % identity 95 NCBI Description Oryza sativa BAC clone 1.H19, complete sequence 419083 Seq. No. uC-osroM202040f10b1 Seq. ID Method BLASTX NCBI GI q4001819 BLAST score 215 E value 5.0e-17 Match length 84 % identity 46 NCBI Description (AF046007) putative polypyrimidine tract-binding protein [Carassius auratus]

Seq. No. 419084

Seq. ID uC-osroM202040g01b1

Method BLASTX
NCBI GI g1651890
BLAST score 338
E value 2.0e-31
Match length 171

```
% identity
                   15
                   (D90900) mitochondrial outer membrane 72K protein
NCBI Description
                   [Synechocystis sp.]
                   419085
Seq. No.
                   uC-osroM202040g02b1
Seq. ID
                   BLASTX
Method
                   g1651890
NCBI GI
                   338
BLAST score
                   2.0e-31
E value
                   171
Match length
                   15
% identity
                  (D90900) mitochondrial outer membrane 72K protein
NCBI Description
                   [Synechocystis sp.]
                   419086
Seq. No.
                   uC-osroM202040g03b1
Seq. ID
Method
                   BLASTX
                   q5734634
NCBI GI
                   301
BLAST score
                   3.0e-27
E value
                   133
Match length
                   50
% identity
                  (AP000391) Similar to putative lipase (AC006232) [Oryza
NCBI Description
                   sativa]
Seq. No.
                   419087
                   uC\hbox{-}osroM202040g04b1
Seq. ID
                   BLASTX
Method
                   q542157
NCBI GI
                   207
BLAST score
                   1.0e-16
E value
                   64
Match length
                   66
% identity
NCBI Description ribosomal 5S RNA-binding protein - Rice
Seq. No.
                   419088
                   uC-osroM202040g05b1
Seq. ID
                   BLASTX
Method
                   q699623
NCBI GI
                   685
BLAST score
E value
                   2.0e-82
                   157
Match length
% identity
NCBI Description (D14579) glutamine synthetase [Zea mays]
Seq. No.
                   419089
                   uC-osroM202040g06b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   q4104220
BLAST score
                   314
E value
                   7.0e-52
Match length
                   161
                   72
% identity
                   (AF033538) caffeic acid O-methyltransferase; LPOMT1 [Lolium
NCBI Description
```

perenne]

```
Seq. No.
                  419090
                  uC-osroM202040g09b1
Seq. ID
Method
                  BLASTX
                  g2149127
NCBI GI
BLAST score
                  281
                  8.0e-25
E value
                  171
Match length
                  35
% identity
                  (U81293) UDP-glucose:indole-3-acetate
NCBI Description
                  beta-D-glucosyltransferase [Arabidopsis thaliana]
                  419091
Seq. No.
                  uC-osroM202040g10b1
Seq. ID
                  BLASTX
Method
                  g1361983
NCBI GI
BLAST score
                  358
E value
                  3.0e-36
                  138
Match length
                  51
% identity
                  ARP protein - Arabidopsis thaliana >gi_886434_emb_CAA89858
NCBI Description
                  (Z49776) ARP protein [Arabidopsis thaliana]
                  419092
Seq. No.
                  uC-osroM202040g12b1
Seq. ID
Method
                  BLASTX
                   g3122673
NCBI GI
BLAST score
                   687
E value
                   2.0e-72
                   165
Match length
                   78
% identity
                  60S RIBOSOMAL PROTEIN L15 >gi 2245027 emb CAB10447.1
NCBI Description
                   (Z97341) ribosomal protein [Arabidopsis thaliana]
                   419093
Seq. No.
                   uC-osroM202040h01b1
Seq. ID
Method
                  BLASTX
NCBI GI
                   q1872521
BLAST score
                   171
E value
                   5.0e-12
Match length
                   68
                   50
% identity
NCBI Description
                  (U87833) zinc-finger protein Lsd1 [Arabidopsis thaliana]
                   >gi 1872523 (U87834) zinc-finger protein Lsd1 [Arabidopsis
                   thaliana] >gi_5262161_emb_CAB45804.1_ (AL080253)
                   zinc-finger protein Lsd1 [Arabidopsis thaliana]
Seq. No.
                   419094
                   uC-osroM202040h02b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g1872521
BLAST score
                   188
E value
                   6.0e-14
Match length
                   71
% identity
                  (U87833) zinc-finger protein Lsd1 [Arabidopsis thaliana]
NCBI Description
                   >gi_1872523 (U87834) zinc-finger protein Lsd1 [Arabidopsis
```

54948

thaliana] >gi 5262161 emb_CAB45804.1_ (AL080253)

zinc-finger protein Lsdl [Arabidopsis thaliana]

419095 Seq. No. uC-osroM202040h03b1 Seq. ID BLASTX Method g1323748 NCBI GI 234 BLAST score 2.0e-19 E value 105 Match length 50 % identity (U32430) thiol protease [Triticum aestivum] NCBI Description 419096 Seq. No. uC-osroM202040h05b1 Seq. ID BLASTX Method g4531446 NCBI GI BLAST score 242 3.0e-20 E value 87 Match length 55 % identity (AC006224) hypothetical protein [Arabidopsis thaliana] NCBI Description 419097 Seq. No. uC-osroM202040h06b1 Seq. ID BLASTX Method g4531446 NCBI GI BLAST score 241 4.0e-20 E value 89 Match length 54 % identity (AC006224) hypothetical protein [Arabidopsis thaliana] NCBI Description 419098 Seq. No. uC-osroM202040h07b1 Seq. ID Method BLASTX NCBI GI q5734618 BLAST score 378 3.0e-36 E value 165 Match length % identity 45 (AP000391) Similar to Arabidopsis thaliana chromosome II NCBI Description BAC F5H14 genomic sequence; unknown protein (AC006234) [Oryza sativa] 419099 Seq. No. uC-osroM202040h08b1 Seq. ID Method BLASTX NCBI GI g5734618 BLAST score 387 E value 3.0e-37 Match length 163 % identity 45 (APO00391) Similar to Arabidopsis thaliana chromosome II NCBI Description BAC F5H14 genomic sequence; unknown protein (AC006234)

Seq. No. 419100

[Oryza sativa]

```
uC-osroM202040h09b1
Seq. ID
                  BLASTX
Method
                  q401237
NCBI GI
                  424
BLAST score
                  9.0e-42
E value
                  133
Match length
                  64
% identity
                  UBIQUITIN-ACTIVATING ENZYME E1 2 >gi_170684 (M90663)
NCBI Description
                  ubiquitin activating enyme [Triticum aestivum]
Seq. No.
                  419101
                  uC-osroM202040h10b1
Seq. ID
                  BLASTX
Method
                  g3914899
NCBI GI
                  669
BLAST score
                  8.0e-77
E value
                  149
Match length
                  90
% identity
                 40S RIBOSOMAL PROTEIN S4 >gi 2331301 (AF013487) ribosomal
NCBI Description
                  protein S4 type I [Zea mays]
Seq. No.
                  419102
                  uC-osroM202040h11b1
Seq. ID
                  BLASTX
Method
                  g1747296
NCBI GI
BLAST score
                  572
E value
                  1.0e-76
                  166
Match length
                  90
% identity
NCBI Description (D45384) vacuolar H+-pyrophosphatase [Oryza sativa]
                  >gi_3298476_dbj_BAA31524 (AB012766) ovp2 [Oryza sativa]
                   419103
Seq. No.
                  uC-osroM202041a02b1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g2352918
BLAST score
                   37
E value
                   1.0e-11
                   57
Match length
                   91
% identity
NCBI Description Petroselinum crispum plastidic glucose-6-phosphate
                   dehydrogenase (pG6PDH) mRNA, nuclear gene encoding plastid
                   protein, complete cds
                   419104
Seq. No.
                   uC-osroM202041a03b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g4099408
BLAST score
                   497
E value
                   2.0e-50
Match length
                   109
                   84
% identity
                  (U86763) delta-type tonoplast intrinsic protein [Triticum
NCBI Description
                   aestivum]
```

Seq. ID uC-osroM202041a04b1

Seq. No.

419105

Method BLASTX q5007084 NCBI GI 597 BLAST score 5.0e-62 E value 114 Match length 100 % identity (AF155333) NADP-specific isocitrate dehydrogenase [Oryza NCBI Description sativa] 419106 Seq. No. uC-osroM202041a05b1 Seq. ID Method BLASTN g6013290 NCBI GI 140 BLAST score 5.0e-73 E value Match length 200 93 % identity NCBI Description Oryza sativa polyubiquitin (RUBQ2) gene, complete cds 419107 Seq. No. uC-osroM202041a08b1 Seq. ID BLASTX Method g547712 NCBI GI 224 BLAST score 1.0e-18 E value 44 Match length 95 % identity EUKARYOTIC INITIATION FACTOR 4A (EIF-4A) NCBI Description >gi_542153_pir__S38358 translation initiation factor eIF-4A - rice >gi_303844_dbj_BAA02152_ (D12627) eukaryotic initiation factor 4A [Oryza sativa] 419108 Seq. No. uC-osroM202041a11b1 Seq. ID BLASTX Method NCBI GI g5031275 BLAST score 202 6.0e-16 E value 81 Match length % identity 56 NCBI Description (AF139496) unknown [Prunus armeniaca] Seq. No. 419109 uC-osroM202041a12b1 Seq. ID BLASTN Method q20369 NCBI GI BLAST score 361 E value 0.0e + 00Match length 361

100 % identity

Oryza sativa shoot GS2 mRNA for chloroplastic glutamine NCBI Description

synthetase (EC 6.3.1.2) (clone lambda-GS31)

>gi_2170909_dbj_E02681_E02681 cDNA encoding precursor of

chloroplast localising glutamine synthetase

Seq. No. 419110

Seq. ID uC-osroM202041b01b1

```
BLASTX
Method
                   g2956711
NCBI GI
                   199
BLAST score
                   1.0e-15
E value
Match length
                   53
                   66
% identity
                   (Y16776) peroxidase [Spinacia oleracea]
NCBI Description
                   419111
Seq. No.
                   uC-osroM202041b02b1
Seq. ID
                   BLASTX
Method
                   q2773154
NCBI GI
                   328
BLAST score
                   2.0e-30
E value
                   136
Match length
                    50
% identity
                   (AF039573) abscisic acid- and stress-inducible protein
NCBI Description
                    [Oryza sativa]
                    419112
Seq. No.
                    uC-osroM202041b04b1
Seq. ID
                    BLASTX
Method
                    g4406783
NCBI GI
                    461
BLAST score
                    4.0e-46
E value
Match length
                    103
                    87
% identity
                   (AC006532) putative glutamate decarboxylase [Arabidopsis
NCBI Description
                    thaliana]
                    419113
Seq. No.
                    uC-osroM202041b05b1
Seq. ID
                    BLASTX
Method
                    g1351974
NCBI GI
                    622
BLAST score
                    7.0e-65
E value
Match length
                    124
% identity
                    98
NCBI Description ADP-RIBOSYLATION FACTOR >gi_1076788_pir__S49325
                    ADP-ribosylation factor - maize >gi_1076789_pir__S53486
ADP-ribosylation factor - maize >gi_556686_emb_CAA56351_
                    (X80042) ADP-ribosylation factor [Zea mays]
                    419114
Seq. No.
                    uC-osroM202041b06b1
Seq. ID
                    BLASTX
Method
NCBI GI
                    q2341042
BLAST score
                    431
E value
                    1.0e-42
                    109
Match length
                    75
% identity
NCBI Description (AC000104) F19P19.26 [Arabidopsis thaliana]
```

Seq. No. 419115

Seq. ID uC-osroM202041b08b1

Method BLASTX NCBI GI g1076738 BLAST score 661 E value 2.0e-69 Match length 124 % identity 99

NCBI Description beta-tubulin R2242 - rice

Seq. No. 419116

Seq. ID uC-osroM202041b11b1

Method BLASTX
NCBI GI g4512651
BLAST score 202
E value 1.0e-15
Match length 110
% identity 41

NCBI Description (AC007048) putative tyrosine transaminase [Arabidopsis

thaliana]

Seq. No. 419117

Seq. ID uC-osroM202041b12b1

Method BLASTX
NCBI GI g5734634
BLAST score 424
E value 1.0e-41
Match length 121
% identity 64

NCBI Description (AP000391) Similar to putative lipase (AC006232) [Oryza

sativa]

Seq. No. 419118

Seq. ID uC-osroM202041c05b1

Method BLASTX
NCBI GI g3377509
BLAST score 422
E value 1.0e-41
Match length 83
% identity 98

NCBI Description (AF056027) auxin transport protein REH1 [Oryza sativa]

Seq. No. 419119

Seq. ID uC-osroM202041c06b1

Method BLASTX
NCBI GI g2435519
BLAST score 524
E value 2.0e-53
Match length 162
% identity 69

NCBI Description (AF024504) similar to mouse MEM3 (GB:U47024 and S.

cerevisiae vacuolar sorting protein 35 (SW; P34110)

[Arabidopsis thaliana]

Seq. No. 419120

Seq. ID uC-osroM202041c07b1

Method BLASTX
NCBI GI g129232
BLAST score 539
E value 4.0e-55
Match length 105

```
% identity
NCBI Description
                  ORYZAIN BETA CHAIN PRECURSOR >gi 67645 pir KHRZOB oryzain
                  (EC 3.4.22.-) beta precursor - rice
                  >gi_218183_dbj_BAA14403_ (D90407) oryzain beta precursor
                  [Oryza sativa]
                  419121
Seq. No.
                  uC-osroM202041c09b1
Seq. ID
                  BLASTX
Method
NCBI GI
                  g1203832
                  707
BLAST score
                  8.0e-75
E value
                  160
Match length
                  84
% identity
                  (U46003) beta-D-glucan exohydrolase, isoenzyme ExoII
NCBI Description
                   [Hordeum vulgare] >gi_1588407_prf__2208395A beta-D-glucan
                  exohydrolase [Hordeum vulgare]
                  419122
Seq. No.
                  uC-osroM202041c10b1
Seq. ID
Method
                  BLASTX
                  g1203832
NCBI GI
                  734
BLAST score
                  5.0e-78
E value
                  163
Match length
                  85
% identity
                  (U46003) beta-D-glucan exohydrolase, isoenzyme ExoII
NCBI Description
                   [Hordeum vulgare] >gi_1588407_prf__2208395A beta-D-glucan
                  exohydrolase [Hordeum vulgare]
                   419123
Seq. No.
                   uC-osroM202041c11b1
Seq. ID
Method
                  BLASTX
                   q5734634
NCBI GI
                   446
BLAST score
E value
                   3.0e-44
Match length
                   128
% identity
                  (AP000391) Similar to putative lipase (AC006232) [Oryza
NCBI Description
                   sativa]
Seq. No.
                   419124
                   uC-osroM202041c12b1
Seq. ID
                   BLASTX
Method
NCBI GI
                   g5734634
BLAST score
                   305
E value
                   7.0e-28
                   90
Match length
% identity
                   67
                  (AP000391) Similar to putative lipase (AC006232) [Oryza
NCBI Description
                   sativa]
                   419125
Seq. No.
                   uC-osroM202041d01b1
Seq. ID
```

54954

BLASTX

546

g5091623

Method

NCBI GI

BLAST score

E value 6.0e-56
Match length 110
% identity 92

NCBI Description (AC007454) Similar to gb_U93048 somatic embryogenesis

receptor-like kinase from Daucus carota, contains 4 PF_00560 Leucine Rich Repeat domains and a PF_00069 Eukaryotic protein kinase domain. [Arabidopsis thaliana]

Seq. No. 419126

Seq. ID uC-osroM202041d02b1

Method BLASTX
NCBI GI g4836950
BLAST score 285
E value 2.0e-25
Match length 102
% identity 58

NCBI Description (AC006085) Hypothetical protein [Arabidopsis thaliana]

Seq. No. 419127

Seq. ID uC-osroM202041d08b1

Method BLASTX
NCBI GI g129916
BLAST score 627
E value 2.0e-65
Match length 134
% identity 92

NCBI Description PHOSPHOGLYCERATE KINASE, CYTOSOLIC >gi_66911_pir__TVWTGY

phosphoglycerate kinase (EC 2.7.2.3), cytosolic - wheat
>gi_21835_emb_CAA33302_ (X15232) phosphoglycerate kinase

(AA 1 - 401) [Triticum aestivum]

Seq. No. 419128

Seq. ID uC-osroM202041e01b1

Method BLASTX
NCBI GI 94006882
BLAST score 283
E value 2.0e-26
Match length 91
% identity 64

NCBI Description (Z99707) UDP-glucuronyltransferase-like protein

[Arabidopsis thaliana]

Seq. No. 419129

Seq. ID uC-osroM202041e06b1

Method BLASTX
NCBI GI g3024432
BLAST score 587
E value 7.0e-61
Match length 121
% identity 97

NCBI Description PROTEASOME ALPHA SUBUNIT (MULTICATALYTIC ENDOPEPTIDASE

COMPLEX ALPHA SUBUNIT) >qi 1930070 (U92540) proteasome

alpha subunit [Oryza sativa]

Seq. No. 419130

Seq. ID uC-osroM202041e08b1

Method BLASTX

NCBI GI g231536 BLAST score 223 4.0e-18 E value Match length 80 % identity 51 CYTOSOL AMINOPEPTIDASE (LEUCINE AMINOPEPTIDASE) (LAP) NCBI Description (LEUCYL AMINOPEPTIDASE) (PROLINE AMINOPEPTIDASE) (PROLYL AMINOPEPTIDASE) >gi_99683_pir__S22399 leucyl aminopeptidase (EC 3.4.11.1) - Arabidopsis thaliana >gi_16394_emb_CAA45040_ (X63444) leucine aminopeptidase
[Arabidopsis thaliana] >gi_4115380 (AC005967) putative leucine aminopeptidase [Arabidopsis thaliana] 419131 Seq. No. Seq. ID uC-osroM202041e09b1 BLASTX Method NCBI GI q129591 BLAST score 418 E value 4.0e-41Match length 101 81 % identity PHENYLALANINE AMMONIA-LYASE >gi 295824_emb_CAA34226_ NCBI Description (X16099) phenylalanine ammonia-Tyase [Oryza sativa] 419132 Seq. No. uC-osroM202041f01b1 Seq. ID Method BLASTX NCBI GI q1362086 BLAST score 198 3.0e-15 E value 91 Match length 51 % identity 5-methyltetrahydropteroyltriglutamate--homocysteine NCBI Description S-methyltransferase (EC 2.1.1.14) - Madagascar periwinkle >gi 2129919 pir S65957 5-methyltetrahydropteroyltriglutamate--homocysteine S-methyltransferase (EC 2.1.1.14) - Madagascar periwinkle >gi_886471_emb_CAA58474_ (X83499) methionine synthase [Catharanthus roseus] 419133 Seq. No. uC-osroM202041f03b1 Seq. ID Method BLASTX g129916 NCBI GI

Method BLASTX
NCBI GI g129916
BLAST score 580
E value 6.0e-60
Match length 132
% identity 86

NCBI Description PHOSPHOGLYCERATE KINASE, CYTOSOLIC >gi_66911_pir__TVWTGY

phosphoglycerate kinase (EC 2.7.2.3), cytosolic - wheat >gi_21835 emb CAA33302 (X15232) phosphoglycerate kinase

(AA 1 - 401) [Triticum aestivum]

Seq. No. 419134

Seq. ID uC-osroM202041f05b1

Method BLASTX NCBI GI g3913193

```
BLAST score
                  454
                  4.0e-45
E value
Match length
                  139
                  59
% identity
                  CINNAMYL-ALCOHOL DEHYDROGENASE 1 (CAD) >gi 556422 (L36823)
NCBI Description
                  cinnamyl-alcohol dehydrogenase [Stylosanthes humilis]
                  419135
Seq. No.
                  uC-osroM202041f08b1
Seq. ID
                  BLASTX
Method
NCBI GI
                  g82496
BLAST score
                  803
                  4.0e-86
E value
Match length
                  161
                  100
% identity
NCBI Description phenylalanine ammonia-lyase (EC 4.3.1.5) - rice
                  419136
Seq. No.
                  uC-osroM202041f09b1
Seq. ID
Method
                  BLASTX
                  g1173187
NCBI GI
                  709
BLAST score
                  5.0e-75
E value
Match length
                  142
                  95
% identity
                  40S RIBOSOMAL PROTEIN S23 (S12) >gi 1362041_pir__S56673
NCBI Description
                  ribosomal protein S23.e, cytosolic (clone RJ3) - garden
                  strawberry >gi_643074 (U19940) putative 40S ribosomal
                  protein s12 [Fragaria x ananassa]
                   419137
Seq. No.
                  uC-osroM202041f12b1
Seq. ID
                  BLASTX
Method
                   g4371296
NCBI GI
                   430
BLAST score
                   2.0e-42
E value
                   150
Match length
% identity
                   55
                  (AC006260) putative receptor protein kinase [Arabidopsis
NCBI Description
                   thaliana]
                   419138
Seq. No.
                   uC-osroM202041g03b1
Seq. ID
                   BLASTX
Method
NCBI GI
                   q3928088
                   184
BLAST score
                   1.0e-13
E value
Match length
                   60
                   52
% identity
NCBI Description (AC005770) putative peroxidase [Arabidopsis thaliana]
Seq. No.
                   419139
                   uC-osroM202041q04b1
Seq. ID
                   BLASTX
Method
NCBI GI
                   g100694
BLAST score
                   541
E value
                   2.0e-55
```

Seq. ID Method

NCBI GI

107 Match length 100 % identity peroxidase (EC 1.11.1.7) precursor - rice NCBI Description >gi 20286 emb CAA46916 (X66125) peroxidase [Oryza sativa] >gi 445620 prf 1909367A peroxidase [Oryza sativa] 419140 Seq. No. uC-osroM202041g05b1 Seq. ID BLASTX Method NCBI GI g1168537 387 BLAST score 2.0e-37 E value 100 Match length 79 % identity ASPARTIC PROTEINASE PRECURSOR >gi 82458 pir__JS0732 NCBI Description aspartic proteinase (EC 3.4.23.-) - rice >gi 218143 dbj_BAA02242_ (D12777) aspartic proteinase [Oryza sativa] 419141 Seq. No. Seq. ID uC-osroM202041g06b1 Method BLASTN NCBI GI g1504051 40 BLAST score 4.0e-13 E value 48 Match length 96 % identity Zea mays mRNA for Calcium-dependent protein kinase, NCBI Description complete cds Seq. No. 419142 uC-osroM202041g11b1 Seq. ID Method BLASTX g3786011 NCBI GI BLAST score 194 E value 1.0e-14 Match length 48 % identity 77 NCBI Description (AC005499) putative elongation factor [Arabidopsis thaliana] 419143 Seq. No. uC-osroM202041g12b1 Seq. ID Method BLASTX NCBI GI q5903045 BLAST score 252 E value 2.0e-21 Match length 99 % identity 53 (AC008016) Similar to gb AF108945 signal peptidase 18 kDa NCBI Description subunit from Homo sapiens. ESTs gb H76629, gb H76949 and gb H76216 come from this gene. [Arabidopsis thaliana] 419144 Seq. No.

54958

uC-osroM202041h01b1

BLASTX

g1706325



BLAST score 666
E value 4.0e-70
Match length 133
% identity 98
NCBI Description PYRUVATI
pyruvate

PYRUVATE DECARBOXYLASE ISOZYME 1 (PDC) >gi_476286 (U07339)

pyruvate decarboxylase 1 [Oryza sativa] >gi_1098559

(U26660) pyruvate decarboxylase [Oryza sativa]

Seq. No. 419145

Seq. ID uC-osroM202041h02b1

Method BLASTX
NCBI GI 94678225
BLAST score 531
E value 3.0e-54
Match length 128
% identity 78

NCBI Description (AC007135) unknown protein [Arabidopsis thaliana]

Seq. No. 419146

Seq. ID uC-osroM202041h04b1

Method BLASTX
NCBI GI g1184776
BLAST score 632
E value 5.0e-66
Match length 148
% identity 82

NCBI Description (U45857) cytosolic glyceroldehyde-3-phosphate dehydrogenase

GAPC4 [Zea mays]

Seq. No. 419147

Seq. ID uC-osroM202041h06b1

Method BLASTX
NCBI GI g5672692
BLAST score 586
E value 1.0e-60
Match length 124
% identity 82

NCBI Description (AB028448) nuclease I [Hordeum vulgare]

Seq. No. 419148

Seq. ID uC-osroM202041h07b1

Method BLASTX
NCBI GI g3928088
BLAST score 185
E value 9.0e-14
Match length 55
% identity 58

NCBI Description (AC005770) putative peroxidase [Arabidopsis thaliana]

Seq. No. 419149

Seq. ID uC-osroM202041h08b1

Method BLASTX
NCBI GI g4510377
BLAST score 355
E value 1.0e-33
Match length 126
% identity 58

54959

```
NCBI Description (AC007017) putative RNA helicase A [Arabidopsis thaliana]
                  419150
Seq. No.
                  uC-osroM202041h09b1
Seq. ID
Method
                  BLASTX
                  g2160174
NCBI GI
BLAST score
                  508
E value
                  2.0e-51
Match length
                  138
                  67
% identity
                  (AC000132) Identical to A. thaliana PUR2 (gb X74766). ESTs
NCBI Description
                  gb ATTS3927, gb N96446 come from this gene. [Arabidopsis
                  thaliana]
                  419151
Seq. No.
Seq. ID
                  uC-osroM202041h10b1
Method
                  BLASTX
NCBI GI
                  q3264596
BLAST score
                  526
                  1.0e-53
E value
Match length
                  138
% identity
                  76
                  (AF057183) putative tonoplast aquaporin [Zea mays]
NCBI Description
                  419152
Seq. No.
                  uC-osroM202041h12b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1632822
BLAST score
                  810
                  6.0e-87
E value
                  156
Match length
                  99
% identity
                  (Y08962) transmembrane protein [Oryza sativa] >gi 1667594
NCBI Description
                  (U77297) transmembrane protein [Oryza sativa]
                  419153
Seq. No.
Seq. ID
                  uC-osrocyp002a01b1
Method
                  BLASTX
NCBI GI
                  q4567246
BLAST score
                  371
E value
                  2.0e-35
Match length
                  131
                  59
% identity
NCBI Description (AC007070) unknown protein [Arabidopsis thaliana]
Seq. No.
                  419154
Seq. ID
                  uC-osrocyp002a02a1
Method
                  BLASTX
NCBI GI
                  g5729802
BLAST score
                  257
E value
                  3.0e-22
Match length
                  52
% identity
                  87
NCBI Description
                  similar to S. pombe dim1+ >gi 2565275 (AF023611) Dim1p
                  homolog [Homo sapiens]
Seq. No.
                  419155
```

54960

```
uC-osrocyp002a02b1
Seq. ID
                  BLASTX
Method
NCBI GI
                  g5729802
BLAST score
                  489
                  3.0e-49
E value
                  142
Match length
% identity
                  64
                  similar to S. pombe dim1+ >gi_2565275 (AF023611) Dim1p
NCBI Description
                  homolog [Homo sapiens]
                  419156
Seq. No.
                  uC-osrocyp002a03b1
Seq. ID
Method
                  BLASTX
                  g129591
NCBI GI
BLAST score
                  231
                  4.0e-19
E value
Match length
                  90
                  52
% identity
                  PHENYLALANINE AMMONIA-LYASE >gi_295824_emb_CAA34226_
NCBI Description
                  (X16099) phenylalanine ammonia-Tyase [Oryza sativa]
                  419157
Seq. No.
                  uC-osrocyp002a05b1
Seq. ID
Method
                  BLASTX
                  g1839188
NCBI GI
BLAST score
                  298
                   4.0e-27
E value
Match length
                  92
% identity
                  59
NCBI Description (U86081) root hair defective 3 [Arabidopsis thaliana]
                   419158
Seq. No.
                   uC-osrocyp002a08a1
Seq. ID
Method
                  BLASTX
                   g2529668
NCBI GI
                   416
BLAST score
                   7.0e-41
E value
                   122
Match length
% identity
                   59
NCBI Description (AC002535) putative photolyase/blue-light receptor
                   [Arabidopsis thaliana] >gi_3319288 (AF053366)
                   photolyase/blue light photoreceptor PHR2 [Arabidopsis
                   thaliana]
                   419159
Seq. No.
                   uC-osrocyp002a09b1
Seq. ID
                   BLASTX
Method
                   q4033424
NCBI GI
                   636
BLAST score
                   2.0e-66
E value
                   146
Match length
                   85
% identity
                   SOLUBLE INORGANIC PYROPHOSPHATASE (PYROPHOSPHATE
NCBI Description
                   PHOSPHO-HYDROLASE) (PPASE) >gi 2668746 (AF034947) inorganic
                   pyrophosphatase [Zea mays]
```

54961

419160

Seq. No.

```
uC-osrocyp002a12a1
Seq. ID
Method
                 BLASTX
                 q2696804
NCBI GI
                 292
BLAST score
                 2.0e-26
E value
Match length
                 53
                 100
% identity
                 (AB009665) water channel protein [Oryza sativa]
NCBI Description
                 419161
Seq. No.
                 uC-osrocyp002b01b1
Seq. ID
Method
                 BLASTX
NCBI GI
                 g1084461
                 475
BLAST score
E value
                 1.0e-47
Match length
                 133
                 71
% identity
NCBI Description RCc3 protein - rice >gi 786132 (L27208) RCc3 [Oryza sativa]
Seq. No.
                  419162
                 uC-osrocyp002b03a1
Seq. ID
Method
                 BLASTN
NCBI GI
                  g3617841
BLAST score
                  68
                  9.0e-30
E value
Match length
                  147
                  95
% identity
NCBI Description Oryza sativa clone F14605 calmodulin (CaM1) mRNA, complete
                  419163
Seq. No.
                  uC-osrocyp002b03b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g115511
                  674
BLAST score
                  6.0e-71
E value
Match length
                  132
% identity
                  63
                 CALMODULIN >gi_231682_sp_P29612_CALM_ORYSA CALMODULIN
NCBI Description
                  >gi_71682_pir__MCBH calmodulin - barley
                  >gi_100666_pir__S24952 calmodulin 1 (clone lambda DASH) -
                  >gi 170072 (L01431) calmodulin [Glycine max] >gi_310315
                  (L18913) calmodulin [Oryza sativa] >gi 506850 (L20691)
                  calmodulin [Vigna radiata] >gi_1478370_bbs_176852 (S81594)
                  auxin-regulated calmodulin, arCaM [Vigna radiata=mung bean,
                  Wilczek, seedling, Peptide, 149 aa] [Vigna radiata]
                  >gi 1742989 emb CAA70982 (Y09853) CaM protein [Cicer
                  arietinum] >gi_1754991 (U48242) calmodulin TaCaM1-1
                  [Triticum aestivum] >gi 1754993 (U48688) calmodulin
                  TaCaM1-2 [Triticum aestivum] >gi 1754995 (U48689)
                  calmodulin TaCaM1-3 [Triticum aestivum] >gi 1755003
                  (U48693) calmodulin TaCaM3-1 [Triticum aestīvum]
                  >gi 1755005 (U49103) calmodulin TaCaM3-2 [Triticum
                  aestivum] >gi 1755007 (U49104) calmodulin TaCaM3-3
```

[Triticum aestivum] >gi_1755009 (U49105) calmodulin

Seq. No.

Seq. ID Method

NCBI GI

E value Match length

BLAST score

% identity

Seq. No.

Seq. ID Method

NCBI GI

E value Match length

Seq. No.

Seq. ID

Method NCBI GI

E value

Seq. No.

Seq. ID Method

NCBI GI

E value

BLAST score

Match length % identity

BLAST score

Match length

% identity

BLAST score

% identity

```
TaCaM4-1 [Triticum aestivum] >gi_3617842 (AF042840)
                   calmodulin [Oryza sativa] >gi 226769_prf__1604476A
                   calmodulin [Hordeum vulgare var. distichum]
                   >gi_1583768_prf__2121384B calmodulin [Glycine max]
                   419164
                   uC-osrocyp002b04b1
                   BLASTN
                   g4519191
                   34
                   2.0e-09
                   86
                   85
                   Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
NCBI Description
                   K9P8, complete sequence
                   419165
                   uC-osrocyp002b06a1
                   BLASTX
                   q584893
                   269
                   1.0e-23
                   51
                   100
                   SERINE CARBOXYPEPTIDASE III PRECURSOR
NCBI Description
                   >gi_283002_pir__S22530 carboxypeptidase III (EC 3.4.16.-) -
                   rice >gi 218153 dbj BAA01757 (D10985) serine
                   carboxypeptidase III [Oryza sativa]
                   419166
                   uC-osrocyp002b06b1
                   BLASTX
                   g584893
                   547
                   1.0e-81
                   157
                   97
                   SERINE CARBOXYPEPTIDASE III PRECURSOR
NCBI Description
                   >gi_283002_pir___S22530 carboxypeptidase III (EC 3.4.16.-) -
rice >gi_218153_dbj_BAA01757_ (D10985) serine
                   carboxypeptidase III [Oryza sativa]
                   419167
                   uC-osrocyp002b12b1
                   BLASTX
                   g3738312
                   476
                   1.0e-47
                   143
                   (AC005309) hypothetical protein [Arabidopsis thaliana]
NCBI Description
```

419168 Seq. No.

uC-osrocyp002c02b1 Seq. ID

Method BLASTX g5080792 NCBI GI 297 BLAST score

E value 1.0e-26 Match length 119 % identity 51

NCBI Description (AC007576) Unknown protein [Arabidopsis thaliana]

Seq. No. 419169

Seq. ID uC-osrocyp002c03b1

Method BLASTX
NCBI GI g3941480
BLAST score 150
E value 2.0e-09
Match length 38
% identity 74

NCBI Description (AF062894) putative transcription factor [Arabidopsis

thaliana]

Seq. No. 419170

Seq. ID uC-osrocyp002c04a1

Method BLASTN
NCBI GI g22651
BLAST score 68
E value 9.0e-30
Match length 116
% identity 90

NCBI Description H.vulgare mRNA for GRP94 homologue

Seq. No. 419171

Seq. ID uC-osrocyp002c04b1

Method BLASTX
NCBI GI g544242
BLAST score 372
E value 5.0e-45
Match length 149
% identity 69

NCBI Description ENDOPLASMIN HOMOLOG PRECURSOR (GRP94 HOMOLOG)

>gi_485498_pir__S33533 heat shock protein 90 homolog

precursor - barley >gi_22652_emb_CAA48143_ (X67960) GRP94

homologue [Hordeum vulgare]

Seq. No. 419172

Seq. ID uC-osrocyp002c05a1

Method BLASTX
NCBI GI 9480450
BLAST score 269
E value 1.0e-23
Match length 61
% identity 87

NCBI Description ketol-acid reductoisomerase (EC 1.1.1.86) - Arabidopsis

thaliana >gi 402552 emb CAA49506_ (X69880) ketol-acid

reductoisomerase [Arabidopsis thaliana]

Seq. No. 419173

Seq. ID uC-osrocyp002c05b1

Method BLASTX
NCBI GI g480450
BLAST score 581
E value 5.0e-60

Match length 134 % identity 86

NCBI Description ketol-acid reductoisomerase (EC 1.1.1.86) - Arabidopsis thaliana >gi 402552 emb_CAA49506_ (X69880) ketol-acid

reductoisomerase [Arabidopsis thaliana]

Seq. No. 419174

Seq. ID uC-osrocyp002c06b1

Method BLASTX
NCBI GI g3549654
BLAST score 361
E value 3.0e-34
Match length 158
% identity 51

NCBI Description (AL031394) metal-transporting P-type ATPase (fragment)

[Arabidopsis thaliana]

Seq. No. 419175

Seq. ID uC-osrocyp002c08b1

Method BLASTX
NCBI GI g283008
BLAST score 897
E value 5.0e-97
Match length 177
% identity 97

NCBI Description sucrose synthase (EC 2.4.1.13) - rice

>gi 20366 emb CAA46017 (X64770) sucrose synthase [Oryza

sativa]

Seq. No. 419176

Seq. ID uC-osrocyp002c11b1

Method BLASTX
NCBI GI g2662343
BLAST score 685
E value 3.0e-72
Match length 134
% identity 99

NCBI Description (D63581) EF-1 alpha [Oryza sativa]

Seq. No. 419177

Seq. ID uC-osrocyp002c12b1

Method BLASTX
NCBI GI g3881836
BLAST score 148
E value 2.0e-09
Match length 80
% identity 41

NCBI Description (Z78019) Similarity to Yeast LPG22P protein (TR:G1151240);

cDNA EST EMBL:T00686 comes from this gene; cDNA EST EMBL:C12415 comes from this gene; cDNA EST EMBL:C12728 comes from this gene; cDNA EST EMBL:C10626 comes from this

Seq. No. 419178

Seq. ID uC-osrocyp002d01b1

Method BLASTX NCBI GI g4680207 BLAST score 323

9.0e-30 E value Match length 159 39 % identity (AF114171) disease resistance protein RPM1 homolog [Sorghum NCBI Description bicolor] 419179 Seq. No. uC-osrocyp002d02b1 Seq. ID BLASTX Method g1169736 NCBI GI 514 BLAST score 8.0e-54E value 163 Match length 66 % identity FKBP-RAPAMYCIN ASSOCIATED PROTEIN (FRAP) (RAPAMYCIN TARGET NCBI Description PROTEIN) >gi_1083778_pir__A54837 rapamycin/FKBP12 target 1 - rat >qi 511229 (U11681) rapamycin and FKBP12 target-1 protein [Rattus norvegicus] >gi 561858 (L37085) rapamycin target [Rattus norvegicus] 419180 Seq. No. uC-osrocyp002d03a1 Seq. ID Method BLASTN g6013290 NCBI GI 270 BLAST score 1.0e-150 E value 345 Match length % identity 41 Oryza sativa polyubiquitin (RUBQ2) gene, complete cds NCBI Description 419181 Seq. No. uC-osrocyp002d03b1 Seq. ID Method BLASTX g82734 NCBI GI 677 BLAST score 2.0e-71 E value 136 Match length 30 % identity ubiquitin precursor - maize (fragment) NCBI Description >gi_226763_prf__1604470A poly-ubiquitin [Zea mays] 419182 Seq. No. uC-osrocyp002d04a1 Seq. ID BLASTN Method NCBI GI g20280 BLAST score 128 1.0e-65 E value Match length 220 90 % identity NCBI Description Rice gene for phenylalanine ammonia-lyase (EC 4.3.1.5) 419183 Seq. No. Seq. ID uC-osrocyp002d04b1 BLASTX Method g129591 NCBI GI BLAST score 651 1.0e-74 E value

% identity

90

```
Match length
                  153
                  98
% identity
                  PHENYLALANINE AMMONIA-LYASE >gi 295824 emb CAA34226_
NCBI Description
                  (X16099) phenylalanine ammonia-lyase [Oryza sativa]
Seq. No.
                  419184
                  uC-osrocyp002d06a1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2982455
                  191
BLAST score
E value
                  2.0e-14
                  40
Match length
                  82
% identity
                  (AL022223) putative uracil phosphoribosyl transferase
NCBI Description
                  [Arabidopsis thaliana]
Seq. No.
                  419185
                  uC-osrocyp002d06b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3953458
BLAST score
                  428
                  4.0e-42
E value
                  156
Match length
% identity
                  60
                  (AC002328) F20N2.3 [Arabidopsis thaliana]
NCBI Description
                  419186
Seq. No.
                  uC-osrocyp002d07a1
Seq. ID
Method
                  BLASTN
                  g2331130
NCBI GI
BLAST score
                  254
E value
                  1.0e-141
                  278
Match length
                  98
% identity
NCBI Description Oryza sativa glycine-rich protein (OSGRP1) mRNA, complete
                  cds
Seq. No.
                   419187
                  uC-osrocyp002d07b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2293480
BLAST score
                   445
E value
                   3.0e-44
Match length
                  88
                   98
% identity
NCBI Description (AF011331) glycine-rich protein [Oryza sativa]
Seq. No.
                  419188
Seq. ID
                  uC-osrocyp002d08a1
Method
                  BLASTX
NCBI GI
                  q6015065
BLAST score
                  174
E value
                   2.0e-12
Match length
                   40
```

54967

(Z97178) elongation factor 2 [Beta vulgaris]

NCBI Description ELONGATION FACTOR 2 (EF-2) >gi 2369714 emb CAB09900

Seq. No.

419194

```
Seq. No.
                   419189
Seq. ID
                   uC-osrocyp002d08b1
Method
                   BLASTX
NCBI GI
                   g6015065
BLAST score
                   495
                   6.0e-50
E value
Match length
                   103
% identity
                   91
                   ELONGATION FACTOR 2 (EF-2) >gi_2369714_emb_CAB09900_
NCBI Description
                   (Z97178) elongation factor 2 [Beta vulgaris]
                   419190
Seq. No.
                   uC-osrocyp002d09b1
Seq. ID
Method
                   BLASTN
NCBI GI
                   q3618311
BLAST score
                   424
E value
                   0.0e + 00
Match length
                   471
                   98
% identity
                   Oryza sativa mRNA for zinc finger protein, complete cds,
NCBI Description
                   clone:R1479
Seq. No.
                   419191
                   uC-osrocyp002d11a1
Seq. ID
Method
                   BLASTN
NCBI GI
                   g2443401
BLAST score
                   267
E value
                   1.0e-148
Match length
                   343
                   94
% identity
NCBI Description Oryza sativa mRNA for orthophosphate dikinase, complete cds
Seq. No.
                   419192
                   uC-osrocyp002d11b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2443402
                   420
BLAST score
E value
                   2.0e-66
                   143
Match length
                   95
% identity
                   (D87745) orthophosphate dikinase [Oryza sativa]
NCBI Description
                   >gi 2443405 dbj BAA22420 (D87952) orthophosphate dikinase
                   [Oryza sativa]
Seq. No.
                   419193
                   uC-osrocyp002e03b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   q5679841
                   523
BLAST score
                   3.0e-53
E value
Match length
                   181
% identity
                   58
                   (AJ243961) contains eukaryotic protein kinase domain
NCBI Description
                   PF 00069 [Oryza sativa]
```

```
Seq. ID
                  uC-osrocyp002e04a1
                  BLASTN
Method
NCBI GI
                  g5257255
                  70
BLAST score
E value
                  6.0e-31
Match length
                  216
% identity
                  84
NCBI Description Oryza sativa genomic DNA, chromosome 8, clone:P0026F07
Seq. No.
                  419195
                  uC-osrocyp002e08b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1076746
BLAST score
                  469
E value
                  1.0e-76
Match length
                  168
% identity
                  89
NCBI Description
                  heat shock protein 70 - rice (fragment)
                  >qi 763160 emb CAA47948 (X67711) heat shock protein 70
                   [Oryza sativa]
                  419196
Seq. No.
Seq. ID
                  uC-osrocyp002e09b1
Method
                  BLASTX
NCBI GI
                  g1514643
BLAST score
                  717
                  6.0e-76
E value
Match length
                  176
% identity
                  80
                  (Z70524) PDR5-like ABC transporter [Spirodela polyrrhiza]
NCBI Description
                  419197
Seq. No.
Seq. ID
                  uC-osrocyp002e12b1
Method
                  BLASTX
NCBI GI
                  g480450
BLAST score
                  525
                  2.0e-53
E value
Match length
                  111
                  91
% identity
                  ketol-acid reductoisomerase (EC 1.1.1.86) - Arabidopsis
NCBI Description
                  thaliana >gi_402552_emb_CAA49506_ (X69880) ketol-acid
                  reductoisomerase [Arabidopsis thaliana]
                  419198
Seq. No.
                  uC-osrocyp002f01b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1498384
BLAST score
                  396
E value
                  1.0e-38
Match length
                  107
                  75
% identity
NCBI Description
                  (U60508) actin [Zea mays]
Seq. No.
                  419199
                  uC-osrocyp002f02a1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3264605
```

Match length

% identity

180

64

```
BLAST score
                  209
                  1.0e-16
E value
Match length
                  41
% identity
                  100
NCBI Description
                  (AF061508) ribosomal protein L25 [Zea mays]
Seq. No.
                  419200
                  uC-osrocyp002f03a1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g20280
BLAST score
                  336
E value
                  0.0e+00
Match length
                  352
% identity
                  99
NCBI Description
                 Rice gene for phenylalanine ammonia-lyase (EC 4.3.1.5)
Seq. No.
                  419201
Seq. ID
                  uC-osrocyp002f03b1
Method
                  BLASTX
NCBI GI
                  q129591
BLAST score
                  258
E value
                  8.0e-33
Match length
                  84
                  99
% identity
                  PHENYLALANINE AMMONIA-LYASE >qi 295824 emb CAA34226
NCBI Description
                   (X16099) phenylalanine ammonia-lyase [Oryza sativa]
Seq. No.
                   419202
Seq. ID
                  uC-osrocyp002f05b1
Method
                  BLASTX
NCBI GI
                  q3193287
BLAST score
                  262
E value
                  6.0e-48
                  155
Match length
                  59
% identity
                  (AF069298) Arabidopsis predicted protein of unknown
NCBI Description
                  function T10P11.19 (GB:AC002330) [Arabidopsis thaliana]
                  419203
Seq. No.
                  uC-osrocyp002f07a1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4512699
BLAST score
                  223
                  3.0e-18
E value
Match length
                  53
% identity
                  81
NCBI Description
                  (AC006569) putative NADH-ubiquinone oxireductase
                   [Arabidopsis thaliana]
Seq. No.
                   419204
                  uC-osrocyp002f07b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4512699
BLAST score
                  442
                  4.0e-52
E value
```

Method

BLASTX

```
NCBI Description
                  (AC006569) putative NADH-ubiquinone oxireductase
                   [Arabidopsis thaliana]
Seq. No.
                  419205
                  uC-osrocyp002f08a1
Seq. ID
                  BLASTX
Method
                  q4006829
NCBI GI
BLAST score
                  213
                  4.0e-17
E value
                  108
Match length
% identity
                   51
                  (AC005970) putative protein kinase [Arabidopsis thaliana]
NCBI Description
                   419206
Seq. No.
Seq. ID
                  uC-osrocyp002f08b1
                  BLASTX
Method
NCBI GI
                  q3980378
BLAST score
                   271
E value
                   1.0e-23
                   98
Match length
                   62
% identity
                  (AC004561) putative RNA binding protein [Arabidopsis
NCBI Description
                   thaliana]
                   419207
Seq. No.
                   uC-osrocyp002f11a1
Seq. ID
                   BLASTN
Method
NCBI GI
                   g1519250
BLAST score
                   240
                   1.0e-132
E value
                   375
Match length
                   94
% identity
NCBI Description Oryza sativa GF14-c protein mRNA, complete cds
                   419208
Seq. No.
                   uC-osrocyp002f11b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g1519251
BLAST score
                   343
                   2.0e-66
E value
                   139
Match length
                   99
% identity
NCBI Description (U65957) GF14-c protein [Oryza sativa]
                   419209
Seq. No.
                   uC-osrocyp002g02a1
Seq. ID
                   BLASTN
Method
NCBI GI
                   g415316
                   349
BLAST score
E value
                   0.0e + 00
                   361
Match length
% identity
NCBI Description Rice mRNA for acidic ribosomal protein PO, complete cds
Seq. No.
                   419210
                   uC-osrocyp002g02b1
Seq. ID
```

```
g730580
NCBI GI
BLAST score
                  285
                  4.0e-32
E value
Match length
                  84
                  95
% identity
NCBI Description 60S ACIDIC RIBOSOMAL PROTEIN PO >gi 455401 dbj BAA04668
                  (D21130) acidic ribosomal protein PO [Oryza sativa]
                  419211
Seq. No.
                  uC-osrocyp002g04a1
Seq. ID
                  BLASTN
Method
NCBI GI
                  q5051932
                  180
BLAST score
                  1.0e-96
E value
Match length
                  254
% identity
                  98
NCBI Description Oryza sativa MADS-box protein FDRMADS8 mRNA, complete cds
                  419212
Seq. No.
                  uC-osrocyp002g04b1
Seq. ID
Method
                  BLASTN
                  g5051932
NCBI GI
BLAST score
                  189
                  1.0e-102
E value
                  193
Match length
                  99
% identity
NCBI Description Oryza sativa MADS-box protein FDRMADS8 mRNA, complete cds
                  419213
Seq. No.
                  uC-osrocyp002g05a1
Seq. ID
                  BLASTX
Method
                  g3868758
NCBI GI
                  254
BLAST score
                   6.0e-22
E value
                  56
Match length
                  86
% identity
NCBI Description (D89802) elongation factor 1B gamma [Oryza sativa]
                   419214
Seq. No.
                  uC-osrocyp002g05b1
Seq. ID
Method
                  BLASTX
NCBI GI
                   g3868758
BLAST score
                   309
                   3.0e-28
E value
                  144
Match length
% identity
                   71
NCBI Description (D89802) elongation factor 1B gamma [Oryza sativa]
                   419215
Seq. No.
                   uC-osrocyp002g06b1
Seq. ID
                   BLASTX
Method
NCBI GI
                   g4538979
BLAST score
                   218
                   2.0e-17
E value
                   111
Match length
% identity
                   44
NCBI Description (AL049487) putative protein [Arabidopsis thaliana]
```

Seq. ID Method

```
Seq. No.
                  419216
Seq. ID
                  uC-osrocyp002g08b1
Method
                  BLASTX
NCBI GI
                  q1076708
BLAST score
                  698
                  7.0e-74
E value
Match length
                  140
                  25
% identity
                  seed tetraubiquitin - common sunflower
NCBI Description
                  >gi_303901_dbj_BAA03764_ (D16248) ubiquitin [Glycine max]
                  >gi_456714_dbj_BAA05670_ (D28123) Ubiquitin [Glycine max]
                  >gi 556688 emb CAA84440 (Z34988) seed tetraubiquitin
                  [Helianthus annuus] >gi 994785 dbj BAA05085
                                                                (D26092)
                  Ubiquitin [Glycine max] >gi 4263514 gb_AAD15340_ (AC004044)
                  putative polyubiquitin [Arabidopsis thaliana]
                  >qi 1096513 prf 2111434A tetraubiquitin [Helianthus
                  annuus]
Seq. No.
                  419217
Seq. ID
                  uC-osrocyp002g09b1
                  BLASTX
Method
NCBI GI
                  g547712
BLAST score
                  283
                  4.0e-25
E value
                  94
Match length
                  65
% identity
NCBI Description
                  EUKARYOTIC INITIATION FACTOR 4A (EIF-4A)
                  >qi 542153 pir S38358 translation initiation factor eIF-4A
                  - rice >gi 303844 dbj BAA02152 (D12627) eukaryotic
                  initiation factor 4A [Oryza sativa]
                  419218
Seq. No.
                  uC-osrocyp002g10a1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4874288
                  185
BLAST score
                  8.0e-14
E value
                  56
Match length
% identity
                 (AC007212) putative peroxidase [Arabidopsis thaliana]
NCBI Description
                  419219
Seq. No.
                  uC-osrocyp002g10b1
Seq. ID
Method
                  BLASTX
                  g1402918
NCBI GI
                  587
BLAST score
                  9.0e-61
E value
                  148
Match length
                  77
% identity
                  (X98320) peroxidase [Arabidopsis thaliana]
NCBI Description
                  >gi_1429215_emb_CAA67310_ (X98774) peroxidase ATP6a
                   [Arabidopsis thaliana]
                   419220
Seq. No.
```

54973

uC-osrocyp002g12a1

BLASTN

Seq. ID

Method

NCBI GI

```
NCBI GI
                  g3885887
BLAST score
                   71
                  1.0e-31
E value
                  159
Match length
                  86
% identity
NCBI Description
                  Oryza sativa high mobility group protein (HMG) mRNA,
                  complete cds
Seq. No.
                   419221
                  uC-osrocyp002g12b1
Seq. ID
                  BLASTX
Method
NCBI GI
                  q3885888
                  294
BLAST score
                  2.0e-26
E value
Match length
                  116
% identity
                  58
NCBI Description
                  (AF093632) high mobility group protein [Oryza sativa]
Seq. No.
                   419222
                  uC-osrocyp002h01b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2497903
                   220
BLAST score
                  8.0e-18
E value
                  59
Match length
                   68
% identity
                  METALLOTHIONEIN-LIKE PROTEIN TYPE 2
NCBI Description
                  >gi_1752831_dbj_BAA14038.1_ (D89931) metallothionein-like
                  protein [Oryza sativa] >gi 1815628 (U43530)
                  metallothionein-like type 2 [Oryza sativa]
                   419223
Seq. No.
                  uC-osrocyp002h02a1
Seq. ID
Method
                  BLASTX
NCBI GI
                   g211855
BLAST score
                   142
E value
                   8.0e-09
                   51
Match length
                   63
% identity
NCBI Description (J00869) histone H3 [Gallus gallus]
Seq. No.
                   419224
Seq. ID
                   uC-osrocyp002h02b1
Method
                   BLASTX
NCBI GI
                   g122070
BLAST score
                   353
E value
                   1.0e-33
Match length
                   73
% identity
                   97
                  HISTONE H3 >gi_82483_pir__A25564 histone H3 - rice
NCBI Description
                   >gi 169793 (M15664) histone 3 [Oryza sativa] >gi 940018
                   (U2\overline{5}664) histone H3 [Oryza sativa]
                   419225
Seq. No.
```

54974

uC-osrocyp002h03b1

BLASTX

g5031281

BLAST score 188
E value 2.0e-14
Match length 40
% identity 80

NCBI Description (AF139499) unknown [Prunus armeniaca]

Seq. No. 419226

Seq. ID uC-osrocyp002h04b1

Method BLASTX
NCBI GI g5823572
BLAST score 299
E value 5.0e-40
Match length 133
% identity 63

NCBI Description (AL049730) putative protein [Arabidopsis thaliana]

Seq. No. 419227

Seq. ID uC-osrocyp002h05a1

Method BLASTX
NCBI GI g3193292
BLAST score 283
E value 3.0e-25
Match length 72
% identity 72

NCBI Description (AF069298) similar to ATPases associated with various

cellular activites (Pfam: AAA.hmm, score: 230.91)

[Arabidopsis thaliana]

Seq. No. 419228

Seq. ID uC-osrocyp002h05b1

Method BLASTX
NCBI GI g3193293
BLAST score 278
E value 5.0e-26
Match length 153
% identity 50

NCBI Description (AF069298) contains a short region of similarity to another

Arabidopsis hypothetical protein F19K23.8 (GB:AC000375)

[Arabidopsis thaliana]

Seq. No. 419229

Seq. ID uC-osrocyp002h06b1

Method BLASTX
NCBI GI g5139541
BLAST score 268
E value 2.0e-23
Match length 80
% identity 57

NCBI Description (AJ243308) nodulin26-like major intrinsic protein [Pisum

sativum]

Seq. No. 419230

Seq. ID uC-osrocyp002h08a1

Method BLASTX
NCBI GI g4678208
BLAST score 239
E value 7.0e-27

Match length 126 % identity 54

NCBI Description (AC007134) putative sugar transporter [Arabidopsis

thaliana]

Seq. No. 419231

Seq. ID uC-osrocyp002h08b1

Method BLASTX
NCBI GI g1778093
BLAST score 197
E value 5.0e-29
Match length 96
% identity 72

NCBI Description (U64902) putative sugar transporter; member of major

facilitative superfamily; integral membrane protein [Beta

vulgaris]

Seq. No. 419232

Seq. ID uC-osrocyp002h11b1

Method BLASTX
NCBI GI g3023816
BLAST score 776
E value 7.0e-83
Match length 157
% identity 95

NCBI Description GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC

>gi 968996 (U31676) glyceraldehyde-3-phosphate

dehydrogenase [Oryza sativa]

Seq. No. 419233

Seq. ID uC-osrocyp002h12a1

Method BLASTN
NCBI GI g5051932
BLAST score 200
E value 1.0e-108
Match length 254
% identity 100

NCBI Description Oryza sativa MADS-box protein FDRMADS8 mRNA, complete cds

Seq. No. 419234

Seq. ID uC-osrocyp003a01a1

Method BLASTX
NCBI GI g6041808
BLAST score 283
E value 3.0e-25
Match length 100
% identity 53

NCBI Description (AC009755) unknown protein [Arabidopsis thaliana]

Seq. No. 419235

Seq. ID uC-osrocyp003a06a1

Method BLASTN
NCBI GI g20280
BLAST score 227
E value 1.0e-124
Match length 251
% identity 98

```
NCBI Description Rice gene for phenylalanine ammonia-lyase (EC 4.3.1.5)
                  419236
Seq. No.
Seq. ID
                  uC-osrocyp003a08a1
Method
                  BLASTX
                  q730456
NCBI GI
BLAST score
                  295
E value
                  1.0e-26
                  58
Match length
                  100
% identity
                 40S RIBOSOMAL PROTEIN S19
NCBI Description
Seq. No.
                  419237
                  uC-osrocyp003a09a1
Seq. ID
Method
                  BLASTX
                  q829283
NCBI GI
BLAST score
                  183
                  2.0e-13
E value
Match length
                  40
% identity
                  90
                 (Z15018) heat shock protein hsp82 [Oryza sativa]
NCBI Description
                  419238
Seq. No.
Seq. ID
                  uC-osrocyp003a12a1
Method
                  BLASTX
                  q129591
NCBI GI
                  194
BLAST score
                  1.0e-14
E value
Match length
                  37
% identity
                  95
                 PHENYLALANINE AMMONIA-LYASE >gi 295824 emb CAA34226
NCBI Description
                   (X16099) phenylalanine ammonia-lyase [Oryza sativa]
Seq. No.
                  419239
                  uC-osrocyp003b01a1
Seq. ID
Method
                  BLASTN
                  q6006355
NCBI GI
BLAST score
                  221
E value
                  1.0e-121
Match length
                  434
                  100
% identity
NCBI Description Oryza sativa genomic DNA, chromosome 6, clone:P0493C11
                   419240
Seq. No.
                  uC-osrocyp003b02a1
Seq. ID
Method
                  BLASTX
                  g2130072
NCBI GI
                  752
BLAST score
                   4.0e-80
E value
Match length
                  161
                   91
% identity
                  ferredoxin--nitrite reductase (EC 1.7.7.1) - rice
NCBI Description
                   >gi_809514_dbj_BAA09122_ (D50556) ferredoxin-nitrite
                   reductase [Oryza sativa]
                   419241
Seq. No.
                   uC-osrocyp003b06a1
Seq. ID
```

```
Method
                  BLASTN
NCBI GI
                  g2331130
BLAST score
                  216
                  1.0e-118
E value
Match length
                  216
                  100
% identity
                  Oryza sativa glycine-rich protein (OSGRP1) mRNA, complete
NCBI Description
                  cds
                  419242
Seq. No.
Seq. ID
                  uC-osrocyp003b09a1
                  BLASTN
Method
NCBI GI
                  q6006606
BLAST score
                  305
                  1.0e-171
E value
Match length
                  329
% identity
                  98
NCBI Description Oryza sativa mRNA for MADS-box protein
                  419243
Seq. No.
Seq. ID
                  uC-osrocyp003b10a1
                  BLASTX
Method
NCBI GI
                  g4926866
BLAST score
                  369
                   3.0e - 35
E value
Match length
                  116
                  59
% identity
                  (AC007509) putative amp-binding protein [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                   419244
                  uC-osrocyp003b11a1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3023713
BLAST score
                  351
                   4.0e-33
E value
                  71
Match length
                   97
% identity
NCBI Description
                  ENOLASE (2-PHOSPHOGLYCERATE DEHYDRATASE)
                   (2-PHOSPHO-D-GLYCERATE HYDRO-LYASE) (OSE1) >gi 780372
                   (U09450) enolase [Oryza sativa]
                   419245
Seq. No.
                   uC-osrocyp003b12a1
Seq. ID
Method
                  BLASTX
NCBI GI
                   g485518
                   259
BLAST score
                   2.0e-22
E value
                   65
Match length
                   78
% identity
                  ubiquitin / ribosomal protein CEP52 - rice
NCBI Description
                   >gi_303857_dbj_BAA02154_ (D12629) ubiquitin/ribosomal
                  polyprotein [Oryza sativa]
```

419246

BLASTX

uC-osrocyp003c08a1

Seq. No.

Seq. ID Method

```
NCBI GI
                  g2865394
BLAST score
                  183
E value
                  2.0e-13
                  92
Match length
                   43
% identity
                  (AF036949) basic leucine zipper protein [Zea mays]
NCBI Description
Seq. No.
                  419247
                  uC-osrocyp003c09a1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1706260
BLAST score
                  306
                  8.0e-28
E value
                  58
Match length
% identity
                  93
                  CYSTEINE PROTEINASE 1 PRECURSOR >gi 2118131_pir_ S59597
NCBI Description
                  cysteine proteinase 1 precursor - maize
                  >qi 643597 dbj BAA08244 (D45402) cysteine proteinase [Zea
                  mays]
                   419248
Seq. No.
                  uC-osrocyp003c11a1
Seq. ID
Method
                  BLASTX
NCBI GI
                   g3461821
BLAST score
                   483
                   2.0e-48
E value
Match length
                   163
                   61
% identity
                  (AC004138) putative nucleoside triphosphatase [Arabidopsis
NCBI Description
                   thaliana]
                   419249
Seq. No.
                  uC-osrocyp003c12a1
Seq. ID
Method
                  BLASTN
                   g5257255
NCBI GI
                   214
BLAST score
                   1.0e-117
E value
Match length
                   392
                   89
% identity
NCBI Description Oryza sativa genomic DNA, chromosome 8, clone:P0026F07
                   419250
Seq. No.
                   uC-osrocyp003d05a1
Seq. ID
Method
                  BLASTX
                   g4733973
NCBI GI
                   148
BLAST score
                   3.0e-09
E value
Match length
                   59
                   44
% identity
NCBI Description (AC007264) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   419251
                   uC-osrocyp003d09a1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g4531444
                   161
BLAST score
E value
                   7.0e-11
```

Match length

397

```
Match length
                  71
                  55
% identity
                  (AC006224) putative protein kinase [Arabidopsis thaliana]
NCBI Description
                  419252
Seq. No.
                  uC-osrocyp003d10a1
Seq. ID
Method
                  BLASTX
                  g5430753
NCBI GI
BLAST score
                  166
                  2.0e-11
E value
                  122
Match length
% identity
                   34
                  (AC007504) Unknown Protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   419253
                  uC-osrocyp003e03a1
Seq. ID
Method
                  BLASTX
NCBI GI
                   g121332
                   707
BLAST score
                   7.0e-75
E value
                   137
Match length
                   98
% identity
                  GLUTAMINE SYNTHETASE ROOT ISOZYME (GLUTAMATE--AMMONIA
NCBI Description
                   LIGASE) (CLONE LAMBDA-GS8) >gi 68590_pir__AJRZQB
                   glutamate--ammonia ligase (EC 6.3.1.2) beta, cytosolic -
                   rice >gi_20358_emb_CAA32460_ (X14244) cytosolic glutamine
                   syntethase (AA 1-357) [Oryza sativa]
                   419254
Seq. No.
                   uC-osrocyp003e05a1
Seq. ID
                   BLASTX
Method
                   g1076746
NCBI GI
                   483
BLAST score
                   1.0e-48
E value
                   125
Match length
                   80
% identity
                   heat shock protein 70 - rice (fragment)
NCBI Description
                   >gi_763160_emb_CAA47948_ (X67711) heat shock protein 70
                   [Oryza sativa]
                   419255
Seq. No.
                   uC-osrocyp003e10a1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g5031281
BLAST score
                   211
                   1.0e-16
E value
Match length
                   46
% identity
                   78
NCBI Description (AF139499) unknown [Prunus armeniaca]
                   419256
Seq. No.
Seq. ID
                   uC-osrocyp003e11a1
Method
                   BLASTN
NCBI GI
                   g5731736
BLAST score
                   397
                   0.0e+00
E value
```

```
% identity
                  100
NCBI Description Oryza sativa OsNHX1 mRNA, complete cds
Seq. No.
                  419257
Seq. ID
                  uC-osrocyp003f03a1
Method
                  BLASTX
NCBI GI
                  g4406804
BLAST score
                  352
                  1.0e-42
E value
Match length
                  98
                  81
% identity
                 (AC006304) proline iminopeptidase [Arabidopsis thaliana]
NCBI Description
                  419258
Seq. No.
                  uC-osrocyp003f05a1
Seq. ID
                  BLASTX
Method
NCBI GI
                  q5541697
BLAST score
                  167
E value
                  2.0e-11
Match length
                  43
                  77
% identity
                 (AL096860) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  419259
                  uC-osrocyp003f12a1
Seq. ID
                  BLASTX
Method
NCBI GI
                  g1170937
BLAST score
                  360
                  4.0e-34
E value
Match length
                  66
% identity
                  100
                  S-ADENOSYLMETHIONINE SYNTHETASE 1 (METHIONINE
NCBI Description
                  ADENOSYLTRANSFERASE 1) (ADOMET SYNTHETASE 1)
                  >qi 450549 emb CAA81481 (Z26867) S-adenosyl methionine
                  synthetase [Oryza sativa]
                  419260
Seq. No.
                  uC-osrocyp003g01a1
Seq. ID
Method
                  BLASTX
                  g1717950
NCBI GI
BLAST score
                  361
                  3.0e-34
E value
                  63
Match length
                  100
% identity
                  UBIQUINOL-CYTOCHROME C REDUCTASE IRON-SULFUR SUBUNIT 2
NCBI Description
                  PRECURSOR (RIESKE IRON-SULFUR PROTEIN 2) (RISP2) >gi 530052
                   (L16810) Rieske iron-sulfur protein [Nicotiana tabacum]
Seq. No.
                  419261
                  uC-osrocyp003g05a1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3548810
                  146
BLAST score
E value
                  3.0e-09
                  117
Match length
                  30
% identity
                  (AC005313) putative chloroplast nucleoid DNA binding
NCBI Description
```

```
protein [Arabidopsis thaliana]
Seq. No.
                  419262
                  uC-osrocyp003g06a1
Seq. ID
Method
                  BLASTX
                  g4689478
NCBI GI
BLAST score
                  182
                  3.0e-13
E value
Match length
                  48
                  58
% identity
                  (AC007213) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                  419263
Seq. No.
                  uC-osrocyp003g09a1
Seq. ID
Method
                  BLASTX
                  g4006890
NCBI GI
                  154
BLAST score
E value
                  3.0e-10
                  34
Match length
                  82
% identity
                  (Z99708) ubiquitin--protein ligase-like protein
NCBI Description
                   [Arabidopsis thaliana]
                  419264
Seq. No.
                  uC-osrocyp003h01a1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g451193
BLAST score
                  231
E value
                  1.0e-20
                  97
Match length
                   59
% identity
                  (L28008) wali7 [Triticum aestivum]
NCBI Description
                  >gi_1090845_prf__2019486B wali7 gene [Triticum aestivum]
                   419265
Seq. No.
                   uC-osrocyp003h02a1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2662343
BLAST score
                   146
                   3.0e-09
E value
                   36
Match length
                   81
% identity
NCBI Description (D63581) EF-1 alpha [Oryza sativa]
                   419266
Seq. No.
                   uC-osrocyp003h07a1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3242789
BLAST score
                   696
                   2.0e-73
E value
Match length
                   158
% identity
NCBI Description
                   (AF055357) respiratory burst oxidase protein D [Arabidopsis
                   thaliana]
```

Seq. No. 419267

Seq. ID uC-osrocyp003h10a1

% identity

76

```
Method
                  BLASTX
NCBI GI
                  g2342735
                   233
BLAST score
                   3.0e-19
E value
                  57
Match length
                  82
% identity
                  (AC002341) unknown protein [Arabidopsis thaliana]
NCBI Description
                   419268
Seq. No.
                  uC-osrocyp003h11a1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g5729704
BLAST score
                   211
E value
                  1.0e-16
                  73
Match length
% identity
                   49
                  (AC007927) unknown protein, 5' partial [Arabidopsis
NCBI Description
                  thaliana]
                   419269
Seq. No.
                  uC-osrocyp003h12a1
Seq. ID
                  BLASTN
Method
NCBI GI
                  g287834
                  53
BLAST score
                   8.0e-21
E value
Match length
                  65
                   95
% identity
NCBI Description Z.mays yptm2 cDNA
                   419270
Seq. No.
                   uC-osrocyp004a03a1
Seq. ID
Method
                  BLASTX
NCBI GI
                   g1653196
                   585
BLAST score
                   2.0e-60
E value
                  117
Match length
% identity
                   100
NCBI Description (D90911) hypothetical protein [Synechocystis sp.]
                   419271
Seq. No.
                   uC-osrocyp004a03b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g1653196
                   370
BLAST score
E value
                   2.0e-35
                   91
Match length
% identity
                   91
NCBI Description (D90911) hypothetical protein [Synechocystis sp.]
                   419272
Seq. No.
Seq. ID
                  uC-osrocyp004a04b1
Method
                  BLASTX
NCBI GI
                   q2984709
BLAST score
                   284
E value
                   2.0e-25
                   76
Match length
```

Seq. ID

```
NCBI Description
                 (AF053468) DnaJ-related protein ZMDJ1 [Zea mays]
Seq. No.
                  419273
                  uC-osrocyp004a05a1
Seq. ID
Method
                  BLASTN
NCBI GI
                  q1001396
BLAST score
                  73
E value
                  1.0e-32
Match length
                  157
                  87
% identity
                  Synechocystis sp. PCC6803 complete genome, 18/27,
NCBI Description
                  2267260-2392728
                  419274
Seq. No.
Seq. ID
                  uC-osrocyp004a05b1
                  BLASTX
Method
NCBI GI
                  q1001405
BLAST score
                  492
E value
                  1.0e-49
Match length
                  132
                  77
% identity
                  (D63999) riboflavin synthase alpha chain [Synechocystis
NCBI Description
                  sp.]
Seq. No.
                   419275
Seq. ID
                  uC-osrocyp004a07a1
Method
                  BLASTX
NCBI GI
                  g1653288
BLAST score
                  649
E value
                  5.0e-68
Match length
                  150
% identity
                  90
                 (D90912) hypothetical protein [Synechocystis sp.]
NCBI Description
                  419276
Seq. No.
                  uC-osrocyp004a08b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1652545
BLAST score
                   636
                  2.0e-66
E value
                  122
Match length
                  100
% identity
                 (D90906) hypothetical protein [Synechocystis sp.]
NCBI Description
                   419277
Seq. No.
                  uC-osrocyp004a09a1
Seq. ID
Method
                  BLASTX
NCBI GI
                   g2499191
                  986
BLAST score
E value
                  1.0e-107
                  192
Match length
                  98
% identity
                  SULFITE REDUCTASE (FERREDOXIN) >gi 1651943 dbj BAA16869
NCBI Description
                   (D90901) ferredoxin-sulfite reductase [Synechocystis sp.]
                   419278
Seq. No.
```

54984

uC-osrocyp004a10a1

E value

Match length

3.0e-40

85

```
BLASTX
Method
                  q3915395
NCBI GI
                  918
BLAST score
                  2.0e-99
E value
Match length
                  172
% identity
                  99
NCBI Description HYPOTHETICAL 21.0 KD PROTEIN SLR0612
Seq. No.
                  419279
                  uC-osrocyp004a10b1
Seq. ID
Method
                  BLASTX
                  g1651652
NCBI GI
BLAST score
                  892
                  2.0e-96
E value
                  175
Match length
                  95
% identity
NCBI Description (D90899) hypothetical protein [Synechocystis sp.]
Seq. No.
                  419280
                  uC-osrocyp004a11a1
Seq. ID
Method
                  BLASTN
NCBI GI
                  q1651768
BLAST score
                  481
E value
                  0.0e + 00
                  509
Match length
                  99
% identity
NCBI Description Synechocystis sp. PCC6803 complete genome, 2/27,
                  133860-271599
Seq. No.
                  419281
Seq. ID
                  uC-osrocyp004a11b1
Method
                  BLASTX
NCBI GI
                  q1651876
BLAST score
                  685
                  3.0e-72
E value
                  139
Match length
                  96
% identity
NCBI Description (D90900) hypothetical protein [Synechocystis sp.]
Seq. No.
                  419282
                  uC-osrocyp004b02a1
Seq. ID
                  BLASTN
Method
NCBI GI
                  g1001612
BLAST score
                  444
                  0.0e + 00
E value
Match length
                  537
                  95
% identity
NCBI Description Synechocystis sp. PCC6803 complete genome, 21/27,
                  2644795-2755702
                   419283
Seq. No.
                  uC-osrocyp004b03a1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2500610
BLAST score
                  413
```

% identity DNA-DIRECTED RNA POLYMERASE BETA CHAIN (TRANSCRIPTASE BETA NCBI Description CHAIN) (RNA POLYMERASE BETA SUBUNIT) >qi 1652443 dbj BAA17365 (D90905) RNA polymerase beta subunit [Synechocystis sp.] 419284 Seq. No. uC-osrocyp004b03b1 Seq. ID BLASTX Method NCBI GI g2501548 BLAST score 343 3.0e-32 E value Match length 70 97 % identity HYPOTHETICAL 29.3 KD PROTEIN SLL1786 NCBI Description >qi 1652444 dbj BAA17366 (D90905) hypothetical protein [Synechocystis sp.] Seq. No. 419285 uC-osrocyp004b04a1 Seq. ID BLASTN Method g1652618 NCBI GI 89 BLAST score E value 3.0e-42317 Match length 82 % identity Synechocystis sp. PCC6803 complete genome, 9/27, NCBI Description 1056467-1188885 Seq. No. 419286 Seq. ID uC-osrocyp004b04b1 Method BLASTN NCBI GI q1652618 BLAST score 148 2.0e-77 E value Match length 368 85 % identity NCBI Description Synechocystis sp. PCC6803 complete genome, 9/27, 1056467-1188885 419287 Seq. No. uC-osrocyp004b05a1 Seq. ID BLASTX Method NCBI GI g2496803 369 BLAST score 4.0e-35 E value 74 Match length 99 % identity HYPOTHETICAL 39.0 KD PROTEIN SLR1821 NCBI Description

>gi_1652842_dbj_BAA17761_ (D90908) hypothetical protein

[Synechocystis sp.]

Seq. No. 419288

Seq. ID uC-osrocyp004b05b1

Method BLASTN NCBI GI g1652725 BLAST score 437

```
E value
                  0.0e + 00
Match length
                  478
% identity
                   97
                  Synechocystis sp. PCC6803 complete genome, 10/27,
NCBI Description
                  1188886-1311234
Seq. No.
                   419289
                  uC-osrocyp004b06a1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2622565
BLAST score
                  145
E value
                   6.0e-09
Match length
                  94
                   33
% identity
                  (AE000906) unknown [Methanobacterium thermoautotrophicum]
NCBI Description
                   419290
Seq. No.
Seq. ID
                  uC-osrocyp004b07a1
Method
                  BLASTX
NCBI GI
                   g1652108
BLAST score
                   557
                   3.0e-57
E value
Match length
                  187
% identity
                   66
                  (D90902) hypothetical protein [Synechocystis sp.]
NCBI Description
                   419291
Seq. No.
Seq. ID
                  uC-osrocyp004b07b1
Method
                  BLASTN
NCBI GI
                   q1652027
                   447
BLAST score
                   0.0e+00
E value
                   486
Match length
                   98
% identity
                  Synechocystis sp. PCC6803 complete genome, 4/27,
NCBI Description
                   402290-524345
Seq. No.
                   419292
                   uC-osrocyp004b08a1
Seq. ID
Method
                   BLASTX
                   g1673315
NCBI GI
BLAST score
                   187
                   6.0e-14
E value
Match length
                   36
                   97
% identity
NCBI Description (D64003) hypothetical protein [Synechocystis sp.]
Seq. No.
                   419293
Seq. ID
                   uC-osrocyp004b08b1
Method
                   BLASTX
NCBI GI
                   q1006580
BLAST score
                   266
E value
                   8.0e-46
Match length
                   128
% identity
```

NCBI Description (D64005) hypothetical protein [Synechocystis sp.]

NCBI GI

```
Seq. No.
                   419294
Seq. ID
                   uC-osrocyp004b09a1
Method
                   BLASTN
NCBI GI
                   q1001291
BLAST score
                   333
                   0.0e + 00
E value
Match length
                   485
% identity
                   93
NCBI Description
                   Synechocystis sp. PCC6803 complete genome, 25/27,
                   3138604-3270709
Seq. No.
                   419295
Seq. ID
                   uC-osrocyp004b09b1
Method
                   BLASTN
NCBI GI
                   g1001291
BLAST score
                   398
E value
                   0.0e+00
Match length
                   474
% identity
                   96
                  Synechocystis sp. PCC6803 complete genome, 25/27,
NCBI Description
                   3138604-3270709
Seq. No.
                   419296
                   uC-osrocyp004b10b1
Seq. ID
Method
                   BLASTN
NCBI GI
                   g1652725
BLAST score
                   230
E value
                   1.0e-126
Match length
                   242
                   99
% identity
                  Synechocystis sp. PCC6803 complete genome, 10/27,
NCBI Description
                   1188886-1311234
                   419297
Seq. No.
                   uC-osrocyp004b12b1
Seq. ID
Method
                  BLASTX
NCBI GI
                   g1653435
BLAST score
                   282
E value
                   5.0e-25
                  57
Match length
% identity
                   100
NCBI Description (D90913) hypothetical protein [Synechocystis sp.]
Seq. No.
                   419298
                   uC-osrocyp004c01a1
Seq. ID
Method
                  BLASTX
NCBI GI
                   g1673315
BLAST score
                   377
E value
                   5.0e-36
Match length
                  75
% identity
                   97
NCBI Description
                  (D64003) hypothetical protein [Synechocystis sp.]
Seq. No.
                   419299
Seq. ID
                  uC-osrocyp004c02a1
Method
                   BLASTN
```

54988

g1653228

BLAST score 575 E value 0.0e + 00Match length 591 % identity 99 NCBI Description Synechocystis sp. PCC6803 complete genome, 14/27, 1719644-1848241 Seq. No. 419300 Seq. ID uC-osrocyp004c04a1 Method BLASTN NCBI GI q1001396 BLAST score 485 E value 0.0e+00500 Match length % identity 99 NCBI Description Synechocystis sp. PCC6803 complete genome, 18/27, 2267260-2392728 Seq. No. 419301 Seq. ID uC-osrocyp004c04b1 Method BLASTN NCBI GI g1001396 BLAST score 466 E value 0.0e + 00Match length 500 % identity 99 NCBI Description Synechocystis sp. PCC6803 complete genome, 18/27, 2267260-2392728 419302 Seq. No. uC-osrocyp004c07a1 Seq. ID Method BLASTX NCBI GI g5262760 BLAST score 283 3.0e-25 E value Match length 61 90 % identity NCBI Description (AL080283) Beta-COP-like protein [Arabidopsis thaliana] 419303 Seq. No. uC-osrocyp004c07b1 Seq. ID Method BLASTX NCBI GI q5262759 BLAST score 453 E value 4.0e-45 Match length 111 78 % identity NCBI Description (AL080283) putative protein [Arabidopsis thaliana] Seq. No. 419304 uC-osrocyp004c08b1 Seq. ID Method BLASTX

Method BLASTX
NCBI GI g3915173
BLAST score 454
E value 2.0e-45
Match length 88
% identity 97

```
TRNA PSEUDOURIDINE SYNTHASE A (PSEUDOURIDYLATE SYNTHASE I)
NCBI Description
                  (PSEUDOURIDINE SYNTHASE I) (URACIL HYDROLYASE)
                  >gi 1652401 dbj BAA17323_ (D90905) pseudouridine synthase 1
                  [Synechocystis sp.]
                  419305
Seq. No.
                  uC-osrocyp004c09a1
Seq. ID
                  BLASTX
Method
NCBI GI
                  g431176
                  346
BLAST score
                  2.0e-32
E value
Match length
                  118
                  58
% identity
                  (D21815) serine proteinase [Lilium longiflorum]
NCBI Description
                  419306
Seq. No.
                  uC-osrocyp004c09b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q431176
BLAST score
                  273
                  5.0e-24
E value
Match length
                  94
                  56
% identity
                  (D21815) serine proteinase [Lilium longiflorum]
NCBI Description
                  419307
Seq. No.
                  uC-osrocyp004c10a1
Seq. ID
Method
                  BLASTX
                  g3258569
NCBI GI
                  225
BLAST score
                  2.0e-18
E value
Match length
                  44
                  91
% identity
                  (U89959) Similar to yeast general negative regulator of
NCBI Description
                  transcription subunit 1 [Arabidopsis thaliana]
                  419308
Seq. No.
Seq. ID
                  uC-osrocyp004c11a1
Method
                  BLASTX
NCBI GI
                  g1652631
                   555
BLAST score
E value
                   6.0e-57
                  106
Match length
% identity
                  (D90907) glycogen phosphorylase [Synechocystis sp.]
NCBI Description
                   419309
Seq. No.
Seq. ID
                  uC-osrocyp004c12a1
Method
                  BLASTN
NCBI GI
                  q1651650
BLAST score
                   342
E value
                   0.0e + 00
Match length
                  350
% identity
NCBI Description Synechocystis sp. PCC6803 complete genome, 1/27, 1-133859
Seq. No.
                   419310
```

E value

7.0e-69

```
uC-osrocyp004d01a1
Seq. ID
Method
                  BLASTX
                  g1651666
NCBI GI
BLAST score
                  551
                  8.0e-57
E value
Match length
                  107
                  98
% identity
                  (D90899) ferric aerobactin receptor [Synechocystis sp.]
NCBI Description
                  419311
Seq. No.
                  uC-osrocyp004d02a1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1001461
BLAST score
                   414
E value
                  5.0e-41
Match length
                  81
                  18
% identity
                  (D63999) hypothetical protein [Synechocystis sp.]
NCBI Description
                  419312
Seq. No.
                  uC-osrocyp004d02b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1001461
                  284
BLAST score
                  6.0e-29
E value
                  80
Match length
                  90
% identity
NCBI Description
                 (D63999) hypothetical protein [Synechocystis sp.]
                  419313
Seq. No.
                  uC-osrocyp004d03b1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g1652618
BLAST score
                  203
                  1.0e-110
E value
Match length
                  275
% identity
                  95
NCBI Description
                  Synechocystis sp. PCC6803 complete genome, 9/27,
                  1056467-1188885
                   419314
Seq. No.
                  uC-osrocyp004d04a1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g1651768
BLAST score
                   513
                   0.0e + 00
E value
Match length
                   602
% identity
                   96
                  Synechocystis sp. PCC6803 complete genome, 2/27,
NCBI Description
                  133860-271599
                   419315
Seq. No.
Seq. ID
                  uC-osrocyp004d06a1
Method
                  BLASTN
NCBI GI
                  g1651650
BLAST score
                  133
```

Match length 153 % identity 97 Synechocystis sp. PCC6803 complete genome, 1/27, 1-133859 NCBI Description Seq. No. 419316 uC-osrocyp004d06b1 Seq. ID Method BLASTN g1651650 NCBI GI BLAST score 111 1.0e-55 E value Match length 139 % identity 95 NCBI Description Synechocystis sp. PCC6803 complete genome, 1/27, 1-133859 419317 Seq. No. Seq. ID uC-osrocyp004d08a1 Method BLASTX NCBI GI g1230542 BLAST score 898 3.0e-97 E value 174 Match length % identity 100 (L77077) ORFI [Synechocystis sp.] NCBI Description 419318 Seq. No. uC-osrocyp004d09a1 Seq. ID BLASTX Method NCBI GI q1001555 BLAST score 496 5.0e-50 E value Match length 116 91 % identity (D64000) ATP-dependent Clp protease regulatory subunit NCBI Description [Synechocystis sp.] 419319 Seq. No. uC-osrocyp004d09b1 Seq. ID BLASTX Method g1001555 NCBI GI BLAST score 762 3.0e-81 E value Match length 163 96 % identity NCBI Description (D64000) ATP-dependent Clp protease regulatory subunit [Synechocystis sp.] 419320 Seq. No. uC-osrocyp004d10a1 Seq. ID Method BLASTX g3024785 NCBI GI BLAST score 531 3.0e-54E value 113 Match length 91 % identity NCBI Description EXCINUCLEASE ABC SUBUNIT C >gi 1652700 dbj BAA17620

(D90907) excinuclease ABC subunit C [Synechocystis sp.]

```
Seq. No.
                   419321
                  uC-osrocyp004d10b1
Seq. ID
Method
                  BLASTN
                  g1652618
NCBI GI
                   375
BLAST score
                  0.0e+00
E value
Match length
                   432
                   97
% identity
                  Synechocystis sp. PCC6803 complete genome, 9/27,
NCBI Description
                  1056467-1188885
Seq. No.
                   419322
                  uC-osrocyp004d11a1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1176178
BLAST score
                  169
E value
                  1.0e-11
Match length
                  99
% identity
                  36
                 HYPOTHETICAL 18.5 KD PROTEIN IN SOHA-MTR INTERGENIC REGION
NCBI Description
                   (F167) >qi 606096 qb AAA57959.1 (U18997) ORF f167; end
                  overlaps end of o100 by 14 bases; start overlaps f174,
                   other starts possible [Escherichia coli] >gi 1789546
                   (AE000396) orf, hypothetical protein [Escherichia coli]
                   419323
Seq. No.
                  uC-osrocyp004e01a1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g2913890
                  303
BLAST score
                  1.0e-170
E value
Match length
                  323
                  98
% identity
NCBI Description Oryza sativa mRNA for LIP9, partial cds
Seq. No.
                   419324
                  uC-osrocyp004e02a1
Seq. ID
Method
                  BLASTX
                  g2313556
NCBI GI
BLAST score
                   301
E value
                   4.0e-27
                   182
Match length
% identity
                   36
                  (AE000560) conserved hypothetical protein [Helicobacter
NCBI Description
                  pylori 26695]
                   419325
Seq. No.
Seq. ID
                   uC-osrocyp004e02b1
Method
                  BLASTX
NCBI GI
                  g2313556
BLAST score
                   332
E value
                   9.0e-31
Match length
                  187
% identity
                   40
                  (AE000560) conserved hypothetical protein [Helicobacter
NCBI Description
```

pylori 26695]

```
Seq. No.
                   419326
                  uC-osrocyp004e03b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2500205
BLAST score
                  537
                   4.0e-55
E value
Match length
                  111
% identity
                   94
                  RIBOFLAVIN BIOSYNTHESIS PROTEIN RIBF [INCLUDES: RIBOFLAVIN
NCBI Description
                  KINASE (FLAVOKINASE); FMN ADENYLYLTRANSFERASE (FAD
                  PYROPHOSPHORYLASE) (FAD SYNTHETASE)]
                  >gi 1652777 dbj BAA17696 (D90908) hypothetical protein
                   [Synechocystis sp.]
Seq. No.
                   419327
Seq. ID
                  uC-osrocyp004e04b1
Method
                  BLASTX
NCBI GI
                  g3941480
BLAST score
                   343
E value
                   9.0e-47
Match length
                  110
% identity
                  82
NCBI Description
                  (AF062894) putative transcription factor [Arabidopsis
                  thaliana]
Seq. No.
                   419328
Seq. ID
                  uC-osrocyp004e05a1
Method
                  BLASTX
NCBI GI
                  g1651978
BLAST score
                   303
                   4.0e-28
E value
Match length
                  56
                   96
% identity
NCBI Description
                 (D90901) hypothetical protein [Synechocystis sp.]
Seq. No.
                   419329
                  uC-osrocyp004e05b1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g1651897
BLAST score
                  189
                  1.0e-102
E value
                  226
Match length
                  96
% identity
NCBI Description
                  Synechocystis sp. PCC6803 complete genome, 3/27,
                  271600-402289
Seq. No.
                   419330
Seq. ID
                  uC-osrocyp004e06a1
Method
                  BLASTX
NCBI GI
                  g1001150
BLAST score
                   703
E value
                   2.0e-74
Match length
                  144
% identity
                   97
NCBI Description
                  (D64001) general secretion pathway protein E [Synechocystis
                   sp.]
```

NCBI GI

BLAST score

g394735

```
Seq. No.
                   419331
Seq. ID
                  uC-osrocyp004e06b1
Method
                   BLASTX
NCBI GI
                   q1001150
BLAST score
                   881
E value
                   3.0e - 95
Match length
                  175
                   98
% identity
NCBI Description
                  (D64001) general secretion pathway protein E [Synechocystis
                  sp.]
Seq. No.
                   419332
Seq. ID
                  uC-osrocyp004e07a1
Method
                  BLASTX
NCBI GI
                  g1651911
BLAST score
                   332
E value
                  1.0e-31
Match length
                  67
                  100
% identity
NCBI Description
                 (D90901) hypothetical protein [Synechocystis sp.]
Seq. No.
                   419333
                  uC-osrocyp004e07b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1651911
BLAST score
                   341
E value
                   2.0e-32
                  69
Match length
                  100
% identity
NCBI Description
                  (D90901) hypothetical protein [Synechocystis sp.]
Seq. No.
                   419334
Seq. ID
                  uC-osrocyp004e08b1
Method
                  BLASTX
NCBI GI
                  g1321661
BLAST score
                   731
E value
                   1.0e-77
Match length
                  141
                   100
% identity
NCBI Description (D45423) ascorbate peroxidase [Oryza sativa]
Seq. No.
                   419335
Seq. ID
                  uC-osrocyp004e11a1
Method
                  BLASTX
NCBI GI
                  g479696
BLAST score
                   313
E value
                   4.0e-29
Match length
                  98
% identity
                  80
NCBI Description
                  oxidase lip19 - rice >gi_394736_emb_CAA40596_ (X57325)
                  basic/leucine zipper protein [Oryza sativa]
Seq. No.
                   419336
Seq. ID
                  uC-osrocyp004e11b1
Method
                  BLASTN
```

BLAST score

471

```
E value
                  0.0e+00
Match length
                  468
                  99
% identity
NCBI Description Rice lip19 mRNA for basic/leucine zipper protein
                  419337
Seq. No.
                  uC-osrocyp004e12a1
Seq. ID
                  BLASTN
Method
                  g1001396
NCBI GI
                  533
BLAST score
E value
                  0.0e+00
                  533
Match length
                  100
% identity
                  Synechocystis sp. PCC6803 complete genome, 18/27,
NCBI Description
                  2267260-2392728
                   419338
Seq. No.
                  uC-osrocyp004e12b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g118730
                  800
BLAST score
E value
                  1.0e-85
                  161
Match length
                   98
% identity
                  DNAK PROTEIN 2 (HEAT SHOCK PROTEIN 70) (HSP70)
NCBI Description
                  >gi 97632 pir C39025 70K heat shock protein dnaK -
                  Synechocystis sp. (PCC 6803) >gi_154468 (M57518) putative
                   [Synechocystis sp.] >gi_1001435_dbj_BAA10059_ (D63999) DnaK
                  protein [Synechocystis sp.]
                   419339
Seq. No.
Seq. ID
                  uC-osrocyp004f01a1
Method
                  BLASTX
NCBI GI
                  g3183135
BLAST score
                   758
                   7.0e-81
E value
Match length
                  147
% identity
                   95
                  PRIMOSOMAL PROTEIN N' (REPLICATION FACTOR Y)
NCBI Description
                   >gi_1653581_dbj_BAA18494_ (D90914) primosomal protein N
                   [Synechocystis sp.]
                   419340
Seq. No.
                   uC-osrocyp004f02a1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g1652137
BLAST score
                   432
E value
                   2.0e-42
Match length
                   78
% identity
                   100
                  (D90903) hypothetical protein [Synechocystis sp.]
NCBI Description
Seq. No.
                   419341
Seq. ID
                   uC-osrocyp004f02b1
Method
                   BLASTX
NCBI GI
                   q1652136
```

E value 5.0e-47Match length 92 97 % identity (D90903) hypothetical protein [Synechocystis sp.] NCBI Description 419342 Seq. No. Seq. ID uC-osrocyp004f03a1 Method BLASTX NCBI GI g3183135 BLAST score 490 3.0e-49E value Match length 100 96 % identity PRIMOSOMAL PROTEIN N' (REPLICATION FACTOR Y) NCBI Description >gi 1653581 dbj BAA18494 (D90914) primosomal protein N [Synechocystis sp.] Seq. No. 419343 uC-osrocyp004f03b1 Seq. ID Method BLASTX NCBI GI g3183135 BLAST score 593 E value 1.0e-61 Match length 118 % identity 98 PRIMOSOMAL PROTEIN N' (REPLICATION FACTOR Y) NCBI Description >gi_1653581_dbj_BAA18494 (D90914) primosomal protein N [Synechocystis sp.] Seq. No. 419344 Seq. ID uC-osrocyp004f05a1 Method BLASTX NCBI GI g1653506 BLAST score 581 E value 6.0e-60 122 Match length 92 % identity NCBI Description (D90914) hypothetical protein [Synechocystis sp.] 419345 Seq. No. uC-osrocyp004f06a1 Seq. ID Method BLASTN NCBI GI q1001396 BLAST score 275 E value 1.0e-153 423 Match length 91 % identity NCBI Description Synechocystis sp. PCC6803 complete genome, 18/27, 2267260-2392728 Seq. No. 419346 Seq. ID uC-osrocyp004f06b1 Method BLASTX NCBI GI q1001410 BLAST score 422 E value 2.0e-41 Match length 80

NCBI Description

```
% identity
NCBI Description (D63999) hypothetical protein [Synechocystis sp.]
Seq. No.
                   419347
Seq. ID
                   uC-osrocyp004f07b1
Method
                   BLASTX
NCBI GI
                   q433214
BLAST score
                   426
E value
                   5.0e-42
Match length
                   134
% identity
                   71
NCBI Description
                  (D13817) lactate dehydrogenase [Oryza sativa]
Seq. No.
                   419348
Seq. ID
                   uC-osrocyp004f10a1
Method
                   BLASTN
NCBI GI
                   q1001484
                   255
BLAST score
E value
                   1.0e-141
Match length
                   255
                   100
% identity
NCBI Description
                  Synechocystis sp. PCC6803 complete genome, 19/27,
                   2392729-2538999
Seq. No.
                   419349
Seq. ID
                   uC-osrocyp004f10b1
Method
                   BLASTN
NCBI GI
                   q1001484
BLAST score
                   251
E value
                   1.0e-139
Match length
                   255
% identity
                   100
NCBI Description
                  Synechocystis sp. PCC6803 complete genome, 19/27,
                   2392729-2538999
Seq. No.
                   419350
Seq. ID
                   uC-osrocyp004f12a1
Method
                   BLASTN
NCBI GI
                   q1001612
BLAST score
                   291
E value
                   1.0e-163
Match length
                   295
% identity
                   100
NCBI Description
                  Synechocystis sp. PCC6803 complete genome, 21/27,
                   2644795-2755702
Seq. No.
                   419351
Seq. ID
                   uC-osrocyp004f12b1
Method
                  BLASTN
NCBI GI
                   q1001612
BLAST score
                   227
E value
                   1.0e-124
Match length
                   283
                   95
% identity
```

2644795-2755702

Synechocystis sp. PCC6803 complete genome, 21/27,

```
Seq. No.
                   419352
Seq. ID
                  uC-osrocyp004g01b1
Method
                  BLASTX
NCBI GI
                  q2499959
BLAST score
                   300
E value
                   2.0e-27
Match length
                  103
% identity
                   64
NCBI Description
                  PROBABLE NICOTINATE-NUCLEOTIDE PYROPHOSPHORYLASE
                   [CARBOXYLATING] (QUINOLINATE PHOSPHORIBOSYLTRANSFERASE
                   [DECARBOXYLATING]) (QAPRTASE) >gi_1653482_dbj_BAA18395_
                   (D90914) nicotinate-nucleotide pyrophosphorylase
                   [Synechocystis sp.]
                   419353
Seq. No.
Seq. ID
                  uC-osrocyp004g02a1
Method
                  BLASTX
                  g1006608
NCBI GI
BLAST score
                  391
E value
                  1.0e-60
Match length
                  121
                  99
% identity
NCBI Description
                  (D64005) pyridoxal phosphate biosynthetic protein PdxA
                   [Synechocystis sp.]
                  419354
Seq. No.
Seq. ID
                  uC-osrocyp004g02b1
Method
                  BLASTX
NCBI GI
                  g1652329
BLAST score
                  518
E value
                  9.0e-53
Match length
                  135
% identity
                  79
NCBI Description
                 (D90904) NADH dehydrogenase subunit 4 [Synechocystis sp.]
Seq. No.
                  419355
Seq. ID
                  uC-osrocyp004g04a1
Method
                  BLASTX
NCBI GI
                  q1653479
BLAST score
                  146
E value
                  4.0e-09
Match length
                  67
                  48
% identity
NCBI Description
                  (D90914) regulatory components of sensory transduction
                  system [Synechocystis sp.]
Seq. No.
                  419356
Seq. ID
                  uC-osrocyp004q04b1
Method
                  BLASTX
NCBI GI
                  q1653478
BLAST score
                  182
E value
                  1.0e-13
Match length
                  90
% identity
                  (D90914) eukariotic protein kinase [Synechocystis sp.]
NCBI Description
Seq. No.
                  419357
```



uC-osrocyp004g06a1 Seq. ID Method BLASTX NCBI GI q4115377 BLAST score 194 E value 9.0e-15 48 Match length 77 % identity (AC005967) unknown protein [Arabidopsis thaliana] NCBI Description 419358 Seq. No. uC-osrocyp004g06b1 Seq. ID Method BLASTX NCBI GI g4115377 BLAST score 671 1.0e-70 E value 175 Match length % identity 71 NCBI Description (AC005967) unknown protein [Arabidopsis thaliana] 419359 Seq. No. uC-osrocyp004g07a1 Seq. ID Method BLASTX q1001739 NCBI GI BLAST score 687 2.0e-72 E value 140 Match length 99 % identity NCBI Description (D64004) ABC transporter [Synechocystis sp.] Seq. No. 419360 Seq. ID uC-osrocyp004g08a1 Method BLASTX NCBI GI g3860272 BLAST score 145 E value 5.0e-09 47 Match length % identity 60 (AC005824) putative suppressor protein [Arabidopsis NCBI Description thaliana] >gi 4314399_gb_AAD15609_ (AC006232) putative skd1 protein [Arabidopsis thaliana] 419361 Seq. No. uC-osrocyp004g08b1 Seq. ID BLASTX Method NCBI GI q3860272 342 BLAST score 3.0e-32 E value 75 Match length % identity 89 (AC005824) putative suppressor protein [Arabidopsis NCBI Description thaliana] >gi_4314399_gb_AAD15609_ (AC006232) putative skd1 protein [Arabidopsis thaliana]

Seq. No. 419362

Seq. ID uC-osrocyp004g09a1

Method BLASTN NCBI GI g1653083

```
BLAST score
                    353
                    0.0e + 00
E value
Match length
                    544
                    97
% identity
NCBI Description
                    Synechocystis sp. PCC6803 complete genome, 13/27,
                    1576593-1719643
                    419363
Seq. No.
                    uC-osrocyp004g09b1
Seq. ID
Method
                    BLASTN
NCBI GI
                    g1653083
BLAST score
                    238
E value
                    1.0e-131
                    471
Match length
                    100
% identity
NCBI Description
                    Synechocystis sp. PCC6803 complete genome, 13/27,
                    1576593-1719643
                    419364
Seq. No.
                    uC-osrocyp004g10a1
Seq. ID
Method
                    BLASTN
NCBI GI
                    g1001701
BLAST score
                    261
E value
                    1.0e-145
Match length
                    269
                    99
% identity
NCBI Description
                    Synechocystis sp. PCC6803 complete genome, 23/27,
                    2868767-3002965
                    419365
Seq. No.
Seq. ID
                    uC-osrocyp004g10b1
Method
                    BLASTN
NCBI GI
                    q1001701
BLAST score
                    285
E value
                    1.0e-159
Match length
                    293
% identity
                    99
NCBI Description
                    Synechocystis sp. PCC6803 complete genome, 23/27,
                    2868767-3002965
Seq. No.
                    419366
Seq. ID
                    uC-osrocyp004g12a1
Method
                    BLASTX
NCBI GI
                    g1708202
BLAST score
                    338
E value
                    2.0e-31
Match length
                    145
% identity
                    48
NCBI Description
                   HIRA PROTEIN (TUP1 LIKE ENHANCER OF SPLIT PROTEIN 1)
                    >gi_2135189_pir__I37465 gene HIRA protein - human
>gi_2135348_pir__S58177 HIRA protein - human
                    >gi_927419_emb_CAA61979_ (X89887) HIRA [Homo sapiens]
>gi_1017419_emb_CAA57436_ (X81844) HIRA [Homo sapiens]
                    >gi_1589055_prf__2210253A HIRA protein [Mus musculus]
Seq. No.
                    419367
Seq. ID
                    uC-osrocyp004h01a1
```

% identity

92

```
BLASTX
Method
                   g1006607
NCBI GI
BLAST score
                   621
E value
                   1.0e-64
Match length
                   128
% identity
                   95
NCBI Description (D64005) Ycf35 [Synechocystis sp.]
                   419368
Seq. No.
                   uC-osrocyp004h02a1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g1652513
BLAST score
                   401
E value
                   4.0e-39
Match length
                   117
% identity
                   68
NCBI Description (D90906) NADH dehydrogenase subunit 4 [Synechocystis sp.]
Seq. No.
                   419369
Seq. ID
                   uC-osrocyp004h04b1
Method
                   BLASTN
NCBI GI
                   g1001701
BLAST score
                   178
E value
                   1.0e-95
Match length
                   193
% identity
                   98
NCBI Description
                   Synechocystis sp. PCC6803 complete genome, 23/27,
                   2868767-3002965
                   419370
Seq. No.
Seq. ID
                   uC-osrocyp004h05a1
Method
                   BLASTX
NCBI GI
                   q1653718
BLAST score
                   933
E value
                   1.0e-101
Match length
                   180
% identity
                   98
NCBI Description (D90916) hypothetical protein [Synechocystis sp.]
Seq. No.
                   419371
Seq. ID
                   uC-osrocyp004h05b1
Method
                   BLASTX
NCBI GI
                   g1653718
BLAST score
                   936
E value
                   1.0e-104
Match length
                   196
% identity
                   92
NCBI Description (D90916) hypothetical protein [Synechocystis sp.]
Seq. No.
                   419372
Seq. ID
                   uC-osrocyp004h07a1
Method
                   BLASTX
NCBI GI
                   g1170937
BLAST score
                   311
E value
                   2.0e-28
Match length
                   62
```



NCBI Description S-ADENOSYLMETHIONINE SYNTHETASE 1 (METHIONINE ADENOSYLTRANSFERASE 1) (ADOMET SYNTHETASE 1)

>gi 450549 emb CAA81481 (Z26867) S-adenosyl methionine

synthetase [Oryza sativa]

Seq. No. 419373

Seq. ID uC-osrocyp004h07b1

Method BLASTX
NCBI GI g1170937
BLAST score 606
E value 6.0e-70
Match length 135
% identity 99

NCBI Description S-ADENOSYLMETHIONINE SYNTHETASE 1 (METHIONINE

ADENOSYLTRANSFERASE 1) (ADOMET SYNTHETASE 1)

>gi_450549_emb_CAA81481_ (Z26867) S-adenosyl methionine

synthetase [Oryza sativa]

Seq. No. 419374

Seq. ID uC-osrocyp004h10a1

Method BLASTX
NCBI GI g5733886
BLAST score 341
E value 6.0e-32
Match length 84
% identity 81

NCBI Description (AC007932) F11A17.20 [Arabidopsis thaliana]

Seq. No. 419375

Seq. ID uC-osrocyp004h10b1

Method BLASTX
NCBI GI g5733886
BLAST score 423
E value 2.0e-41
Match length 116
% identity 72

NCBI Description (AC007932) F11A17.20 [Arabidopsis thaliana]

Seq. No. 419376

Seq. ID uC-osrocyp004h11a1

Method BLASTN
NCBI GI g1653083
BLAST score 542
E value 0.0e+00
Match length 581
% identity 98

NCBI Description Synechocystis sp. PCC6803 complete genome, 13/27,

1576593-1719643

Seq. No. 419377

Seq. ID uC-osrocyp004h11b1

Method BLASTX
NCBI GI g1653201
BLAST score 929
E value 1.0e-100
Match length 184
% identity 99

```
NCBI Description (D90911) hypothetical protein [Synechocystis sp.]
                   419378
Seq. No.
                  uC-osrocyp004h12b1
Seq. ID
Method
                  BLASTX
                  g2088647
NCBI GI
BLAST score
                  662
E value
                  2.0e-69
Match length
                  182
% identity
                  70
                   (AF002109) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                  >gi 3158394 (AF036340) LRR-containing F-box protein
                   [Arabidopsis thaliana]
                  419379
Seq. No.
Seq. ID
                  uC-osrocyp005a04a1
Method
                  BLASTN
                  g3885887
NCBI GI
BLAST score
                  363
E value
                  0.0e+00
Match length
                  367
                  100
% identity
NCBI Description Oryza sativa high mobility group protein (HMG) mRNA,
                  complete cds
                  419380
Seq. No.
Seq. ID
                  uC-osrocyp005a04b1
Method
                  BLASTN
NCBI GI
                  q3885887
BLAST score
                  54
E value
                  1.0e-21
Match length
                  66
                  95
% identity
NCBI Description
                  Oryza sativa high mobility group protein (HMG) mRNA,
                  complete cds
Seq. No.
                  419381
Seq. ID
                  uC-osrocyp005a07b1
Method
                  BLASTX
NCBI GI
                  q5731998
BLAST score
                  500
E value
                  1.0e-50
Match length
                  156
% identity
                  (AF139532) aldehyde 5-hydroxylase [Liquidambar styraciflua]
NCBI Description
Seq. No.
                  419382
Seq. ID
                  uC-osrocyp005a09b1
Method
                  BLASTX
NCBI GI
                  g121950
BLAST score
                  178
E value
                  7.0e-13
                  58
Match length
                  62
% identity
NCBI Description HISTONE H1 >gi_22321_emb_CAA40362_ (X57077) H1 histone [Zea
```

mays]

E value

Match length

4.0e-20

69

```
Seq. No.
                   419383
Seq. ID
                   uC-osrocyp005a10a1
Method
                  BLASTX
NCBI GI
                  q4454482
BLAST score
                   303
E value
                  1.0e-27
Match length
                  96
% identity
                   56
NCBI Description (AC006234) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   419384
                  uC-osrocyp005a12a1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2737973
BLAST score
                  204
E value
                  5.0e-23
Match length
                  65
% identity
NCBI Description (U83625) protein kinase ZmMEK1 [Zea mays]
Seq. No.
                  419385
Seq. ID
                  uC-osrocyp005a12b1
Method
                  BLASTN
NCBI GI
                  q2737972
BLAST score
                  58
                  8.0e-24
E value
Match length
                  138
% identity
                  86
NCBI Description Zea mays protein kinase ZmMEK1 mRNA, complete cds
Seq. No.
                  419386
Seq. ID
                  uC-osrocyp005b01a1
Method
                  BLASTX
NCBI GI
                  g6002461
BLAST score
                  309
E value
                  3.0e-28
Match length
                  61
% identity
NCBI Description (D84400) peroxidase [Oryza sativa]
Seq. No.
                  419387
Seq. ID
                  uC-osrocyp005b01b1
Method
                  BLASTX
NCBI GI
                  g1097875
BLAST score
                  731
E value
                  1.0e-77
Match length
                  141
% identity
                  97
NCBI Description peroxidase: ISOTYPE=RPA [Oryza sativa]
Seq. No.
                  419388
Seq. ID
                  uC-osrocyp005b02a1
Method
                  BLASTX
NCBI GI
                  g2842490
BLAST score
                  240
```

```
% identity
NCBI Description
                  (AL021749) heat-shock protein [Arabidopsis thaliana]
                   419389
Seq. No.
Seq. ID
                  uC-osrocyp005b02b1
Method
                  BLASTX
                  g2842490
NCBI GI
BLAST score
                   275
E value
                   3.0e-24
Match length
                   62
                   85
% identity
NCBI Description
                  (AL021749) heat-shock protein [Arabidopsis thaliana]
                   419390
Seq. No.
                  uC-osrocyp005b03a1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g6015059
BLAST score
                   268
                   2.0e-23
E value
Match length
                  52
% identity
                   100
                  ELONGATION FACTOR 1-ALPHA (EF-1-ALPHA) >gi 2996096
NCBI Description
                   (AF030517) translation elongation factor-1 alpha; EF-1
                   alpha [Oryza sativa]
                   419391
Seq. No.
Seq. ID
                  uC-osrocyp005b03b1
Method
                  BLASTX
                  g2662343
NCBI GI
BLAST score
                   619
E value
                   2.0e-64
Match length
                   129
% identity
                   92
NCBI Description (D63581) EF-1 alpha [Oryza sativa]
Seq. No.
                   419392
Seq. ID
                   uC-osrocyp005b05b1
Method
                   BLASTX
NCBI GI
                   q2920587
BLAST score
                   509
E value
                   6.0e-53
Match length
                   162
                   63
% identity
NCBI Description
                   (AF038362) TBP-associated factor 172 [Homo sapiens]
                   >gi_2995136_emb_CAA04475_ (AJ001017) TAFII170 [Homo
                   sapiens]
Seq. No.
                   419393
Seq. ID
                   uC-osrocyp005b06a1
Method
                   BLASTN
NCBI GI
                   q2773153
BLAST score
                   372
E value
                   0.0e + 00
Match length
                   376
% identity
                   100
NCBI Description
                  Oryza sativa abscisic acid- and stress-inducible protein
                   (Asr1) mRNA, complete cds
```

Seq. ID

Seq. No.

419394

```
Seq. ID
                  uC-osrocyp005b06b1
Method
                  BLASTX
NCBI GI
                  g2773154
BLAST score
                  286
E value
                  1.0e-25
Match length
                  105
                  58
% identity
NCBI Description
                   (AF039573) abscisic acid- and stress-inducible protein
                   [Oryza sativa]
Seq. No.
                  419395
Seq. ID
                  uC-osrocyp005b07a1
Method
                  BLASTN
                  g3850620
NCBI GI
BLAST score
                  75
                  1.0e-34
E value
                  79
Match length
                  99
% identity
NCBI Description Arabidopsis thaliana mRNA for putative RNA binding protein
                  419396
Seq. No.
                  uC-osrocyp005b07b1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g3850620
BLAST score
                  77
                  7.0e-36
E value
                  77
Match length
                  100
% identity
NCBI Description Arabidopsis thaliana mRNA for putative RNA binding protein
                  419397
Seq. No.
Seq. ID
                  uC-osrocyp005b09a1
Method
                  BLASTX
NCBI GI
                  g3451075
BLAST score
                  577
                  1.0e-59
E value
Match length
                  146
% identity
                   69
NCBI Description
                  (AL031326) putative protein [Arabidopsis thaliana]
Seq. No.
                   419398
Seq. ID
                  uC-osrocyp005b10b1
Method
                  BLASTX
NCBI GI
                  g710626
BLAST score
                  188
E value
                   4.0e-14
Match length
                  45
% identity
NCBI Description
                   (D30719) ERD15 protein [Arabidopsis thaliana] >gi 3241941
                   (AC004625) dehydration-induced protein ERD15 [Arabidopsis
                   thaliana] >gi 3894181 (AC005662) ERD15 protein [Arabidopsis
                  thaliana]
Seq. No.
                   419399
```

55007

uC-osrocyp005b11b1



Method BLASTX
NCBI GI g2920587
BLAST score 419
E value 2.0e-41
Match length 134
% identity 64
NCBI Description (AF03836

NCBI Description (AF038362) TBP-associated factor 172 [Homo sapiens] >gi 2995136 emb CAA04475 (AJ001017) TAFII170 [Homo

sapiens]

Seq. No. 419400

Seq. ID uC-osrocyp005c01b1

Method BLASTX
NCBI GI g1617270
BLAST score 257
E value 4.0e-22
Match length 136
% identity 44

NCBI Description (X94624) acyl-CoA synthetase [Brassica napus]

Seq. No. 419401

Seq. ID uC-osrocyp005c02a1

Method BLASTN
NCBI GI g2331130
BLAST score 208
E value 1.0e-113
Match length 208
% identity 100

NCBI Description Oryza sativa glycine-rich protein (OSGRP1) mRNA, complete

cds

Seq. No. 419402

Seq. ID uC-osrocyp005c02b1

Method BLASTX
NCBI GI g2293480
BLAST score 449
E value 1.0e-44
Match length 89
% identity 98

NCBI Description (AF011331) glycine-rich protein [Oryza sativa]

Seq. No. 419403

Seq. ID uC-osrocyp005c03b1

Method BLASTX
NCBI GI g3080420
BLAST score 340
E value 6.0e-32
Match length 120
% identity 57

NCBI Description (AL022604) putative sugar transporter protein [Arabidopsis

thaliana]

Seq. No. 419404

Seq. ID uC-osrocyp005c04a1

Method BLASTX NCBI GI g4835234 BLAST score 180

```
E value
                   4.0e-13
                   46
Match length
                   67
% identity
NCBI Description
                   (AL049862) putative cold acclimation protein [Arabidopsis
                   thaliana]
Seq. No.
                   419405
Seq. ID
                  uC-osrocyp005c04b1
Method
                   BLASTX
NCBI GI
                   g1657855
BLAST score
                   298
E value
                   6.0e-27
Match length
                  113
% identity
                   55
NCBI Description
                  (U73216) cold acclimation protein WCOR413 [Triticum
                  aestivum]
                   419406
Seq. No.
Seq. ID
                  uC-osrocyp005c05a1
Method
                  BLASTX
NCBI GI
                  g6015059
BLAST score
                  268
E value
                   2.0e-23
Match length
                  52
% identity
                  100
NCBI Description
                  ELONGATION FACTOR 1-ALPHA (EF-1-ALPHA) >gi_2996096
                   (AF030517) translation elongation factor-1 alpha; EF-1
                  alpha [Oryza sativa]
                  419407
Seq. No.
Seq. ID
                  uC-osrocyp005c05b1
Method
                  BLASTX
```

NCBI GI g2662343
BLAST score 659
E value 3.0e-69
Match length 126
% identity 100

NCBI Description (D63581) EF-1 alpha [Oryza sativa]

Seq. No. 419408

Seq. ID uC-osrocyp005c06b1

Method BLASTX
NCBI GI 94220527
BLAST score 450
E value 3.0e-50
Match length 147
% identity 65

NCBI Description (AL035356) putative protein [Arabidopsis thaliana]

Seq. No. 419409

Seq. ID uC-osrocyp005c07b1

Method BLASTX
NCBI GI 94646206
BLAST score 150
E value 1.0e-09
Match length 34
% identity 79



NCBI Description (AC007230) Contains similarity to gb_D13630 KIAA0005 gene from Homo sapiens. ESTs gb_T45345, gb_T21086, gb_R90360, gb_T20468, gb_T45191 and gb_AI100459 come from this gene. [Arabidopsis thaliana]

Seq. No. 419410

Seq. ID uC-osrocyp005c08b1

Method BLASTX
NCBI GI g1703115
BLAST score 484
E value 8.0e-49
Match length 90
% identity 97

NCBI Description ACTIN 3 >gi_2129526_pir__S68112 actin 3 - Arabidopsis

thaliana >gi_1145695 (U39480) actin [Arabidopsis thaliana]

>gi_3236244 (AC004684) actin 3 protein [Arabidopsis

thaliana]

Seq. No. 419411

Seq. ID uC-osrocyp005c09a1

Method BLASTX
NCBI GI g2924772
BLAST score 242
E value 2.0e-20
Match length 56
% identity 75

NCBI Description (AC002334) unknown protein [Arabidopsis thaliana]

Seq. No. 419412

Seq. ID uC-osrocyp005c09b1

Method BLASTX
NCBI GI g2924772
BLAST score 351
E value 4.0e-33
Match length 78
% identity 85

NCBI Description (AC002334) unknown protein [Arabidopsis thaliana]

Seq. No. 419413

Seq. ID uC-osrocyp005c10a1

Method BLASTN
NCBI GI g2331130
BLAST score 216
E value 1.0e-118
Match length 216
% identity 100

NCBI Description Oryza sativa glycine-rich protein (OSGRP1) mRNA, complete

cds

Seq. No. 419414

Seq. ID uC-osrocyp005c10b1

Method BLASTX
NCBI GI g2293480
BLAST score 340
E value 6.0e-32
Match length 85
% identity 88

```
NCBI Description (AF011331) glycine-rich protein [Oryza sativa]
                   419415
Seq. No.
Seq. ID
                   uC-osrocyp005d03a1
Method
                   BLASTX
NCBI GI
                   g2276346
BLAST score
                   285
E value
                   2.0e-25
Match length
                   59
                   88
% identity
NCBI Description
                  (AJ000183) Glucose-6-phosphate dehydrogenase [Spinacia
                   oleracea]
                   419416
Seq. No.
Seq. ID
                   uC-osrocyp005d03b1
Method
                   BLASTX
NCBI GI
                   q5734502
BLAST score
                   578
E value
                   8.0e-60
Match length
                   126
% identity
                   86
NCBI Description
                  (AJ010712) glucose-6-phosphate 1-dehydrogenase [Solanum
                   tuberosum]
Seq. No.
                   419417
Seq. ID
                   uC-osrocyp005d05a1
Method
                   BLASTX
NCBI GI
                   q4730884
BLAST score
                   367
E value
                   5.0e - 35
Match length
                   70
% identity
                   100
NCBI Description
                   (AB007404) alanine aminotransferase [Oryza sativa]
                   >gi_4730886_dbj_BAA77261.1_ (AB007405) alanine
                   aminotransferase [Oryza sativa]
Seq. No.
                   419418
Seq. ID
                   uC-osrocyp005d05b1
Method
                   BLASTX
NCBI GI
                   g4730884
BLAST score
                   741
E value
                   3.0e-78
Match length
                   176
% identity
                   88
NCBI Description
                  (AB007404) alanine aminotransferase [Oryza sativa]
                   >gi_4730886_dbj_BAA77261.1_ (AB007405) alanine
                   aminotransferase [Oryza sativa]
Seq. No.
                   419419
Seq. ID
                   uC-osrocyp005d06a1
Method
                   BLASTN
NCBI GI
                   g5852170
BLAST score
                  83
E value
                  1.0e-38
                  153
Match length
% identity
                   88
```

55011

NCBI Description Oryza sativa indica(GLA4) genomic DNA, chromosome 4, BAC



clone:t17804

```
419420
Seq. No.
                  uC-osrocyp005d08a1
Seq. ID
Method
                  BLASTN
                  g2920319
NCBI GI
                  132
BLAST score
                  6.0e-68
E value
                  152
Match length
% identity
                  97
NCBI Description Oryza sativa mRNA for glutamyl-tRNA reductase, complete cds
                  419421
Seq. No.
                  uC-osrocyp005d08b1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g2920319
BLAST score
                  115
                  1.0e-57
E value
                  231
Match length
                  98
% identity
NCBI Description Oryza sativa mRNA for glutamyl-tRNA reductase, complete cds
                  419422
Seq. No.
                  uC-osrocyp005d09a1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g113240
BLAST score
                  256
                  4.0e-22
E value
Match length
                  52
                  94
% identity
NCBI Description ACTIN 2 >gi 71636 pir ATRZ2 actin 2 - rice
                  >gi 20329 emb CAA33873 (X15864) actin [Oryza sativa]
Seq. No.
                  419423
Seq. ID
                  uC-osrocyp005d09b1
Method
                  BLASTX
NCBI GI
                  g6103623
BLAST score
                  473
E value
                  6.0e-79
Match length
                  152
% identity
NCBI Description (AF172094) actin [Picea rubens]
                  419424
Seq. No.
                  uC-osrocyp005d10b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q5106764
BLAST score
                  429
E value
                  3.0e-42
Match length
                  149
% identity
                  62
                 (AF073329) eukaryotic translation initiation factor 3 large
NCBI Description
                  subunit [Zea mays]
```

Seq. No. 419425

Seq. ID uC-osrocyp005d11b1

Method BLASTX

BLAST score

E value

154

4.0e-10

```
g1747296
NCBI GI
BLAST score
                   765
                   1.0e-81
E value
Match length
                   163
                   93
% identity
                  (D45384) vacuolar H+-pyrophosphatase [Oryza sativa]
NCBI Description
                  >gi 3298476 dbj BAA31524 (AB012766) ovp2 [Oryza sativa]
                   419426
Seq. No.
Seq. ID
                  uC-osrocyp005d12b1
Method
                  BLASTX
NCBI GI
                  g2501189
BLAST score
                  304
                  8.0e-28
E value
                  104
Match length
                   69
% identity
NCBI Description
                  THIAMINE BIOSYNTHETIC ENZYME 1-1 PRECURSOR
                  >gi 2130146 pir S61419 thiamine biosynthetic enzyme thi1-1
                   - maize >gi 596078 (U17350) thiamine biosynthetic enzyme
                   [Zea mays]
Seq. No.
                   419427
Seq. ID
                  uC-osrocyp005e01b1
Method
                  BLASTX
NCBI GI
                  g5360595
BLAST score
                  200
E value
                  2.0e-15
Match length
                  65
                  52
% identity
NCBI Description (AB022330) nClpP5 [Arabidopsis thaliana]
Seq. No.
                  419428
Seq. ID
                  uC-osrocyp005e02b1
Method
                  BLASTX
NCBI GI
                  q4914402
BLAST score
                  386
E value
                  3.0e-37
Match length
                  148
% identity
                  51
NCBI Description (AL050352) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  419429
Seq. ID
                  uC-osrocyp005e05b1
Method
                  BLASTX
NCBI GI
                  g3420239
BLAST score
                  546
E value
                  1.0e-60
Match length
                  125
% identity
NCBI Description (AF059484) actin [Gossypium hirsutum]
Seq. No.
                  419430
Seq. ID
                  uC-osrocyp005e06b1
Method
                  BLASTX
NCBI GI
                  g416641
```

Match length 46 % identity NCBI Description Seq. No. Seq. ID

INDOLE-3-ACETIC ACID INDUCED PROTEIN ARG4

>gi 287568 dbj BAA03309 (D14413) ORF [Vigna radiata]

419431

uC-osrocyp005e07a1

Method BLASTN NCBI GI q3885887 BLAST score 415 E value 0.0e+00Match length 418 % identity 100

NCBI Description Oryza sativa high mobility group protein (HMG) mRNA,

complete cds

Seq. No. 419432

Seq. ID uC-osrocyp005e07b1

Method BLASTX NCBI GI g3885888 BLAST score 307 E value 6.0e-28 Match length 115 % identity 59

NCBI Description (AF093632) high mobility group protein [Oryza sativa]

Seq. No. 419433

Seq. ID uC-osrocyp005e08a1

Method BLASTX NCBI GI q129591 BLAST score 202 E value 1.0e-15 Match length 36 % identity 100

NCBI Description PHENYLALANINE AMMONIA-LYASE >gi_295824_emb CAA34226

(X16099) phenylalanine ammonia-lyase [Oryza sativa]

Seq. No. 419434

Seq. ID uC-osrocyp005e08b1

Method BLASTX NCBI GI g129591 BLAST score 432 E value 1.0e-42 Match length 112 76 % identity

NCBI Description PHENYLALANINE AMMONIA-LYASE >gi_295824 emb CAA34226

(X16099) phenylalanine ammonia-lyase [Oryza sativa]

Seq. No. 419435

Seq. ID uC-osrocyp005e09b1

Method BLASTX NCBI GI g4544419 BLAST score 268 E value 2.0e-23 Match length 88

% identity

NCBI Description (AC006955) unknown protein [Arabidopsis thaliana]

```
419436
Seq. No.
Seq. ID
                   uC-osrocyp005e10b1
Method
                   BLASTX
NCBI GI
                   g3184100
BLAST score
                   196
E value
                   7.0e-15
Match length
                   103
% identity
                   40
NCBI Description (AL023777) rna binding protein [Schizosaccharomyces pombe]
Seq. No.
                   419437
Seq. ID
                   uC-osrocyp005e12a1
Method
                   BLASTX
NCBI GI
                   q6056372
BLAST score
                   518
                   9.0e-53
E value
Match length
                   142
                   65
% identity
NCBI Description
                   (AC009894) Very similar to receptor-like serine/threonine
                   kinase [Arabidopsis thaliana]
Seq. No.
                   419438
Seq. ID
                   uC-osrocyp005e12b1
                   {\tt BLASTX}
Method
NCBI GI
                   g6056374
BLAST score
                   233
                   3.0e-19
E value
Match length
                   88
% identity
                   52
NCBI Description
                  (AC009894) Similar to serine/threonine kinases [Arabidopsis
                   thaliana]
Seq. No.
                   419439
Seq. ID
                   uC-osrocyp005f03b1
Method
                   BLASTX
NCBI GI
                   q2853041
BLAST score
                   150
E value
                   2.0e-09
Match length
                   134
% identity
                   31
NCBI Description
                  (X93564) 1-phosphatidylinositol-4,5-bisphosphate
                   phosphodiesterase [Solanum tuberosum]
Seq. No.
                   419440
Seq. ID
                   uC-osrocyp005f04b1
Method
                   BLASTX
NCBI GI
                   g3894191
BLAST score
                   160
E value
                   1.0e-10
Match length
                  119
                   30
% identity
NCBI Description (AC005662) unknown protein [Arabidopsis thaliana]
```

Seq. No. 419441

Seq. ID uC-osrocyp005f05a1

Method BLASTX

```
NCBI GI
                   q4586676
BLAST score
                   287
E value
                   8.0e-26
Match length
                   55
% identity
NCBI Description (AB025047) sterol 14-demethylase [Oryza sativa]
Seq. No.
                   419442
Seq. ID
                   uC-osrocyp005f05b1
Method
                   BLASTX
NCBI GI
                   q4586676
BLAST score
                   627
E value
                   2.0e-65
Match length
                   119
% identity
NCBI Description (AB025047) sterol 14-demethylase [Oryza sativa]
                   419443
Seq. No.
Seq. ID
                   uC-osrocyp005f06a1
Method
                   BLASTN
NCBI GI
                   q5051930
BLAST score
                   158
E value
                   2.0e-83
Match length
                  373
                   93
% identity
NCBI Description Oryza sativa MADS-box protein FDRMADS5 mRNA, partial cds
Seq. No.
                   419444
Seq. ID
                   uC-osrocyp005f06b1
Method
                   BLASTX
NCBI GI
                   q5295988
BLAST score
                   605
E value
                   7.0e-63
Match length
                  126
% identity
                   97
NCBI Description (AB003327) MADS box-like protein [Oryza sativa]
Seq. No.
                   419445
Seq. ID
                  uC-osrocyp005g01a1
Method
                  BLASTX
NCBI GI
                  g4337195
BLAST score
                  156
E value
                  3.0e-10
Match length
                  43
% identity
NCBI Description (AC006403) putative protein kinase [Arabidopsis thaliana]
Seq. No.
                  419446
Seq. ID
                  uC-osrocyp005g03a1
Method
                  BLASTN
```

NCBI GI q4105602 BLAST score 136 E value 2.0e-70 Match length 192 % identity 94

NCBI Description Oryza sativa metallothionein (MTe) gene, complete cds

419447 Seq. No. Seq. ID uC-osrocyp005g03b1 Method BLASTN NCBI GI q4097337 BLAST score 164 E value 5.0e-87 Match length 323 91 % identity NCBI Description Oryza sativa metallothionein-like protein mRNA, complete 419448 Seq. No. Seq. ID uC-osrocyp005g06b1 Method BLASTX NCBI GI g280523 BLAST score 279 E value 1.0e-24Match length 79 62 % identity NCBI Description hypothetical protein B0464.5 - Caenorhabditis elegans 419449 Seq. No. Seq. ID uC-osrocyp005g07a1 Method BLASTX NCBI GI g2576361 BLAST score 276 E value 2.0e-24Match length 65 % identity 69 NCBI Description (U39782) lysine and histidine specific transporter [Arabidopsis thaliana] 419450 Seq. No. Seq. ID uC-osrocyp005g07b1 Method BLASTX NCBI GI g2576361 BLAST score 427 E value 4.0e-42Match length 85 % identity NCBI Description (U39782) lysine and histidine specific transporter [Arabidopsis thaliana] Seq. No. 419451 Seq. ID uC-osrocyp005g08a1 Method BLASTX NCBI GI g2708745 BLAST score 161

E value 5.0e-11 Match length 121 % identity 30

NCBI Description (AC003952) putative calcium-dependent ser/thr protein

kinase [Arabidopsis thaliana]

Seq. No. 419452

Seq. ID uC-osrocyp005g09b1

Method BLASTX



```
NCBI GI
                   q4557495
BLAST score
                   161
E value
                   6.0e-11
Match length
                   104
% identity
                   38
NCBI Description
                   cleavage stimulation factor subunit 3
                   >gi_1082704_pir__S50852 cleavage stimulation factor 77K
                   chain - human >gi_632498 (U15782) cleavage stimulation
                   factor 77kDa subunit [Homo sapiens]
                   >gi_1092656_prf__2024339A cleavage stimulation factor [Homo
                   sapiens]
Seq. No.
                   419453
                   uC-osrocyp005g10b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   q1502430
BLAST score
                   415
                   1.0e-40
E value
                   112
Match length
                   71
% identity
NCBI Description
                   (U62331) phosphate transporter [Arabidopsis thaliana]
                   >gi 2564661 (AF022872) phosphate transporter [Arabidopsis
                   thaliana] >gi_3869206_dbj_BAA34398_ (AB016166) Phosphate Transporter 4 [Arabidopsis thaliana] >gi_3928081 (AC005770)
                   phosphate transporter, AtPT2 [Arabidopsis thaliana]
Seq. No.
                   419454
                   uC-osrocyp005g11b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g4538939
BLAST score
                   296
                   9.0e-27
E value
Match length
                   64
% identity
                   (AL049483) Col-O casein kinase I-like protein [Arabidopsis
NCBI Description
                   thaliana]
                   419455
Seq. No.
Seq. ID
                   uC-osrocyp005g12b1
Method
                   BLASTX
NCBI GI
                   q3264767
BLAST score
                   157
E value
                   2.0e-10
Match length
                   77
% identity
NCBI Description (AF071893) AP2 domain containing protein [Prunus armeniaca]
Seq. No.
                   419456
Seq. ID
                   uC-osrocyp005h01b1
Method
                   BLASTX
NCBI GI
                   q600769
BLAST score
                   349
E value
```

4.0e-33

NCBI Description (L29470) cyclophilin 2 [Oryza sativa]

76

86

Match length

% identity

NCBI GI

BLAST score

```
419457
Seq. No.
Seq. ID
                  uC-osrocyp005h02b1
Method
                  BLASTN
NCBI GI
                  g3293581
                  39
BLAST score
E value
                  4.0e-13
Match length
                  99
                  85
% identity
NCBI Description Arabidopsis thaliana BAC T24H24
                  419458
Seq. No.
Seq. ID
                  uC-osrocyp005h03a1
Method
                  BLASTX
                  g4455278
NCBI GI
BLAST score
                  166
E value
                  2.0e-11
Match length
                  78
% identity
                  45
NCBI Description (AL035527) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  419459
                  uC-osrocyp005h05b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1653718
BLAST score
                  204
E value
                  5.0e-16
Match length
                  119
% identity
NCBI Description (D90916) hypothetical protein [Synechocystis sp.]
Seq. No.
                  419460
                  uC-osrocyp005h07b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3377825
BLAST score
                  630
E value
                  6.0e-66
Match length
                  133
% identity
                  95
NCBI Description (AF075598) contains similarity to fibrillins [Arabidopsis
                  thaliana]
Seq. No.
                  419461
Seq. ID
                  uC-osrocyp005h10a1
Method
                  BLASTN
NCBI GI
                  g450548
BLAST score
                  135
E value
                  8.0e-70
Match length
                  211
% identity
                  92
NCBI Description O.sativa (pRSAM-1) gene for S-adenosyl methionine
                  synthetase
Seq. No.
                  419462
Seq. ID
                  uC-osrocyp005h10b1
Method
                  BLASTX
```

55019

g1170937

```
2.0e-47
E value
Match length
                  95
                  94
% identity
                  S-ADENOSYLMETHIONINE SYNTHETASE 1 (METHIONINE
NCBI Description
                  ADENOSYLTRANSFERASE 1) (ADOMET SYNTHETASE 1)
                  >gi_450549_emb_CAA81481_ (Z26867) S-adenosyl methionine
                  synthetase [Oryza sativa]
Seq. No.
                  419463
                  uC-osrocyp006a01b1
Seq. ID
Method
                  BLASTX
                  g1184774
NCBI GI
BLAST score
                  329
E value
                  1.0e-30
Match length
                  72
% identity
                  89
                 (U45856) cytosolic glyceroldehyde-3-phosphate dehydrogenase
NCBI Description
                  GAPC3 [Zea mays]
Seq. No.
                  419464
Seq. ID
                  uC-osrocyp006a02b1
Method
                  BLASTN
NCBI GI
                  g3819215
BLAST score
                  64
E value
                  3.0e-27
Match length
                  136
% identity
                  87
NCBI Description Hordeum vulgare partial mRNA; clone cMWG0706
Seq. No.
                  419465
Seq. ID
                  uC-osrocyp006a04b1
Method
                  BLASTX
NCBI GI
                  q2894607
BLAST score
                  157
E value
                  1.0e-11
Match length
                  64
% identity
NCBI Description (AL021889) NAM (no apical meristem)-like protein
                  [Arabidopsis thaliana]
```

Seq. No. 419466

Seq. ID uC-osrocyp006a05b1

Method BLASTX NCBI GI g4678205 BLAST score 577 E value 1.0e-59 Match length 160 % identity 63

NCBI Description (AC007134) hypothetical protein [Arabidopsis thaliana]

419467 Seq. No.

Seq. ID uC-osrocyp006a09b1

Method BLASTX NCBI GI g1518540 BLAST score 587 E value 9.0e-61 Match length 147



% identity 77

NCBI Description (U53418) UDP-glucose dehydrogenase [Glycine max]

Seq. No. 419468

Seq. ID uC-osrocyp006a10b1

Method BLASTX
NCBI GI g4519507
BLAST score 340
E value 7.0e-32
Match length 101
% identity 63

NCBI Description (D88434) protein abundantly expressed during apple fruit

...

development [Malus domestica]

Seq. No. 419469

Seq. ID uC-osrocyp006a11b1

Method BLASTX
NCBI GI g2961358
BLAST score 731
E value 1.0e-77
Match length 172
% identity 79

NCBI Description (AL022140) serine/threonine protein kinase like protein

[Arabidopsis thaliana]

Seq. No. 419470

Seq. ID uC-osrocyp006a12b1

Method BLASTX
NCBI GI g4587584
BLAST score 292
E value 1.0e-43
Match length 127
% identity 76

NCBI Description (AC007232) unknown protein [Arabidopsis thaliana]

Seq. No. 419471

Seq. ID uC-osrocyp006b01b1

Method BLASTX
NCBI GI g1808684
BLAST score 370
E value 9.0e-53
Match length 127
% identity 57

NCBI Description (Y10782) hypothetical protein [Sporobolus stapfianus]

Seq. No. 419472

Seq. ID uC-osrocyp006b02b1

Method BLASTX
NCBI GI g21699
BLAST score 354
E value 2.0e-33
Match length 140
% identity 51

NCBI Description (X66013) cathepsin B [Triticum aestivum]

Seq. No. 419473

Seq. ID uC-osrocyp006b03a1

Seq. ID

Method



```
Method
                     BLASTN
  NCBI GI
                     g169820
  BLAST score
                     39
- E value
                     2.0e-12
                     100
  Match length
  % identity
                     83
  NCBI Description
                    Oryza sativa triosephosphate isomerase (Rictpi) mRNA,
                     complete cds
                     419474
  Seq. No.
  Seq. ID
                     uC-osrocyp006b03b1
  Method
                     BLASTX
  NCBI GI
                     g553107
  BLAST score
                     515
  E value
                     5.0e-66
  Match length
                     138
  % identity
                     90
  NCBI Description (L04967) triosephosphate isomerase [Oryza sativa]
                     419475
  Seq. No.
  Seq. ID
                     uC-osrocyp006b04b1
  Method
                     BLASTX
  NCBI GI
                     g4056488
  BLAST score
                     202
                     2.0e-32
  E value
  Match length
                     99
  % identity
                     69
  NCBI Description (AC005896) unknown protein [Arabidopsis thaliana]
                     419476
  Seq. No.
  Seq. ID
                     uC-osrocyp006b06b1
  Method
                     BLASTX
  NCBI GI
                     g1076746
  BLAST score
                     698
  E value
                     8.0e-74
  Match length
                     144
  % identity
                     97
                    heat shock protein 70 - rice (fragment)
  NCBI Description
                     >gi_763160_emb_CAA47948_ (X67711) heat shock protein 70
                     [Oryza sativa]
  Seq. No.
                     419477
  Seq. ID
                     uC-osrocyp006b07a1
  Method
                     BLASTX
  NCBI GI
                     q584706
  BLAST score
                     210
  E value
                     9.0e-17
  Match length
                     45
  % identity
                     96
  NCBI Description
                    ASPARTATE AMINOTRANSFERASE, CYTOPLASMIC (TRANSAMINASE A)
                     >gi_2130066_pir__JC5124 aspartate transaminase (EC
                     2.6.1.1), cytoplasmic - rice >gi_287298_dbj_BAA03504_
                     (D14673) aspartate aminotransferase [Oryza sativa]
  Seq. No.
                     419478
```

55022

uC-osrocyp006b07b1

BLASTX



NCBI GI g584706
BLAST score 556
E value 8.0e-58
Match length 123
% identity 98
NCBI Description ASPARTA

NCBI Description ASPARTATE AMINOTRANSFERASE, CYTOPLASMIC (TRANSAMINASE A) >gi_2130066_pir__JC5124 aspartate transaminase (EC 2.6.1.1), cytoplasmic - rice >gi_287298_dbj_BAA03504_

(D14673) aspartate aminotransferase [Oryza sativa]

Seq. No. 419479

Seq. ID uC-osrocyp006b08b1

Method BLASTX
NCBI GI g21699
BLAST score 214
E value 2.0e-32
Match length 106
% identity 67

NCBI Description (X66013) cathepsin B [Triticum aestivum]

Seq. No. 419480

Seq. ID uC-osrocyp006b10a1

Method BLASTX
NCBI GI g2501578
BLAST score 312
E value 1.0e-28
Match length 70
% identity 89

NCBI Description ETHYLENE-INDUCIBLE PROTEIN HEVER >gi_2129913_pir__S60047

ethylene-responsive protein 1 - Para rubber tree

>gi_1209317 (M88254) ethylene-inducible protein [Hevea

brasiliensis]

Seq. No. 419481

Seq. ID uC-osrocyp006b10b1

Method BLASTX
NCBI GI g2501578
BLAST score 763
E value 2.0e-81
Match length 167
% identity 88

NCBI Description ETHYLENE-INDUCIBLE PROTEIN HEVER >gi_2129913_pir__S60047

ethylene-responsive protein 1 - Para rubber tree

>gi 1209317 (M88254) ethylene-inducible protein [Hevea

brasiliensis]

Seq. No. 419482

Seq. ID uC-osrocyp006b11a1

Method BLASTX
NCBI GI g2191135
BLAST score 194
E value 1.0e-14
Match length 108
% identity 39

NCBI Description (AF007269) A IG002N01.14 gene product [Arabidopsis

thaliana]

```
Seq. No.
                  419483
Seq. ID
                  uC-osrocyp006b12b1
Method
                  BLASTX
NCBI GI
                  g3540201
BLAST score
                  296
                  1.0e-26
E value
                  131
Match length
% identity
NCBI Description (AC004260) Putative nuclear protein [Arabidopsis thaliana]
                  419484
Seq. No.
                  uC-osrocyp006c03b1
Seq. ID
Method
                  BLASTX
                  g633110
NCBI GI
                  529
BLAST score
                  4.0e-66
E value
Match length
                  158
% identity
                  81
NCBI Description (D31843) plasma membrane H+-ATPase [Oryza sativa]
                  419485
Seq. No.
                  uC-osrocyp006c04a1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g5257255
                  224
BLAST score
                  1.0e-123
E value
                  446
Match length
% identity
NCBI Description Oryza sativa genomic DNA, chromosome 8, clone:P0026F07
Seq. No.
                   419486
Seq. ID
                  uC-osrocyp006c05a1
Method
                  BLASTX
NCBI GI
                  q4262142
BLAST score
                  235
E value
                  2.0e-19
Match length
                  105
% identity
NCBI Description
                  (AC005275) putative alcohol dehydrogenase [Arabidopsis
                  thaliana]
                   419487
Seq. No.
                   uC-osrocyp006c07a1
Seq. ID
Method
                  BLASTX
NCBI GI
                   g3132310
                  204
BLAST score
                   5.0e-16
E value
Match length
                   46
% identity
                   89
NCBI Description (AB012228) phosphoenolpyruvate carboxylase [Zea mays]
                   419488
Seq. No.
                   uC-osrocyp006c07b1
Seq. ID
                   BLASTX
Method
NCBI GI
                   q115587
BLAST score
                   424
```

55024

1.0e-45

E value

Match length 100 % identity 93 PHOSPHOENOLPYRUVATE CARBOXYLASE 1 (PEPCASE) (CP21) NCBI Description >gi_418801_pir__S31159 phosphoenolpyruvate carboxylase (EC 4.1.1.31) CP21 - sorghum >gi 21630 emb CAA39197 (X55664) phosphoenolpyruvate carboxylase [Sorghum bicolor] >gi 22615 emb CAA46267 (X65137) phosphoenolpyruvate carboxylase [Sorghum bicolor] 419489 Seq. No. uC-osrocyp006c11a1 Seq. ID Method BLASTX NCBI GI q3582335 BLAST score 305 1.0e-27 E value 73 Match length % identity 78 NCBI Description (AC005496) unknown protein [Arabidopsis thaliana] Seq. No. 419490 uC-osrocyp006c12a1 Sea. ID Method BLASTX g2624417 NCBI GI BLAST score 174 2.0e-12 E value 39 Match length % identity 87 NCBI Description (AJ002959) Ubiquitin carrier protein [Zea mays] Seq. No. 419491 Seq. ID uC-osrocyp006c12b1 Method BLASTX NCBI GI q136647 BLAST score 353 E value 3.0e-33Match length 73 % identity 92 NCBI Description UBIQUITIN-CONJUGATING ENZYME E2-20 KD (UBIQUITIN-PROTEIN LIGASE) (UBIQUITIN CARRIER PROTEIN) >gi 100813 pir A41547 ubiquitin-conjugating enzyme E2 - wheat Seq. No. 419492 uC-osrocyp006d01a1 Seq. ID Method BLASTX NCBI GI q1184112 BLAST score 430 E value 5.0e-47

Match length 118 % identity 78

NCBI Description (U46138) Zn-induced protein [Oryza sativa]

Seq. No. 419493

uC-osrocyp006d05a1 Seq. ID

Method BLASTX g1076746 NCBI GI BLAST score 395 E value 3.0e-38

106 Match length % identity 77 NCBI Description heat shock protein 70 - rice (fragment) >gi_763160_emb_CAA47948_ (X67711) heat shock protein 70 [Oryza sativa] 419494 Seq. No. Seq. ID uC-osrocyp006d05b1 Method BLASTX NCBI GI g1076746 BLAST score 441 E value 2.0e-67 Match length 165 % identity 87 NCBI Description heat shock protein 70 - rice (fragment) >gi_763160_emb_CAA47948_ (X67711) heat shock protein 70 [Oryza sativa] Seq. No. 419495 Seq. ID uC-osrocyp006d06a1 Method BLASTX NCBI GI g6015059 BLAST score 310 E value 2.0e-28 Match length 70 86 % identity NCBI Description ELONGATION FACTOR 1-ALPHA (EF-1-ALPHA) >gi 2996096 (AF030517) translation elongation factor-1 alpha; EF-1 alpha [Oryza sativa] Seq. No. 419496 Seq. ID uC-osrocyp006d07b1 Method BLASTX NCBI GI g1563719 BLAST score 180 E value 4.0e-28 Match length 110 % identity NCBI Description (Y08320) cyclophylin [Digitalis lanata] Seq. No. 419497 Seq. ID uC-osrocyp006d08b1 Method BLASTX NCBI GI q5080764 BLAST score 247 E value 2.0e-21 Match length 91 % identity 59 NCBI Description (AC007203) Hypothetical protein [Arabidopsis thaliana]

419498 Seq. No.

uC-osrocyp006d12a1 Seq. ID

BLASTX Method NCBI GI g6015059 BLAST score 319 E value 2.0e-29 Match length 62



```
% identity
                   100
NCBI Description
                  ELONGATION FACTOR 1-ALPHA (EF-1-ALPHA) >qi 2996096
                   (AF030517) translation elongation factor-1 alpha; EF-1
                  alpha [Oryza sativa]
Seq. No.
                   419499
Seq. ID
                  uC-osrocyp006d12b1
Method
                  BLASTX
NCBI GI
                  q2662343
BLAST score
                  554
E value
                  5.0e-57
Match length
                  117
% identity
                  98
NCBI Description (D63581) EF-1 alpha [Oryza sativa]
                  419500
Seq. No.
Seq. ID
                  uC-osrocyp006e02a1
Method
                  BLASTX
NCBI GI
                  q3789942
BLAST score
                  455
E value
                  3.0e-45
Match length
                  93
% identity
                  21
NCBI Description
                  (AF093505) polyubiquitin [Saccharum hybrid cultivar
                  H32-8560]
Seq. No.
                  419501
Seq. ID
                  uC-osrocyp006e02b1
Method
                  BLASTX
NCBI GI
                  q2760347
BLAST score
                  684
E value
                  3.0e-72
Match length
                  137
% identity
                  18
NCBI Description (U84968) ubiquitin [Arabidopsis thaliana]
                  419502
Seq. No.
                  uC-osrocyp006e04a1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q464981
BLAST score
                  441
E value
                  1.0e-43
Match length
                  84
% identity
                  98
NCBI Description UBIQUITIN-CONJUGATING ENZYME E2-17 KD (UBIQUITIN-PROTEIN
                  LIGASE) (UBIQUITIN CARRIER PROTEIN) >qi 388207 (L23762)
                  ubiquitin carrier protein [Lycopersicon esculentum]
Seq. No.
                  419503
                  uC-osrocyp006e04b1
Seq. ID
Method
                  BLASTX
```

NCBI GI g2668744 BLAST score 476 E value 5.0e-56 Match length 122 % identity

NCBI Description (AF034946) ubiquitin conjugating enzyme [Zea mays]

```
Seq. No.
                  419504
Seq. ID
                  uC-osrocyp006e06b1
Method
                  BLASTX
NCBI GI
                  g5103807
BLAST score
                  318
                  3.0e-29
E value
Match length
                  102
                  57
% identity
NCBI Description
                  (AC007591) Contains similarity to gb AF014403 type-2
                  phosphatidic acid phosphatase alpha-2 (PAP2 a2) from Homo
                  sapiens. ESTs gb T88254 and gb AA394650 come from this
                  gene. [Arabidopsis thaliana]
Seq. No.
                  419505
Seq. ID
                  uC-osrocyp006e08a1
Method
                  BLASTX
NCBI GI
                  q5902733
BLAST score
                  426
                  6.0e-42
E value
Match length
                  93
                  90
% identity
NCBI Description
                 ACTIN >gi 3127133 gb AAC16054.1 (AF061019) actin
                  [Coleochaete scutata]
                  419506
Seq. No.
                  uC-osrocyp006e08b1
Seq. ID
                  BLASTX
Method
NCBI GI
                  g231503
BLAST score
                  178
                  6.0e-20
E value
Match length
                  98
% identity
                  63
                  ACTIN 97 >qi 100417 pir S20098 actin - potato
NCBI Description
                  >gi 21544 emb CAA39280 (X55751) actin [Solanum tuberosum]
                  419507
Seq. No.
                  uC-osrocyp006e09b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4887131
BLAST score
                  281
                  7.0e-25
E value
                  139
Match length
                  49
% identity
                 (AF134732) 60S ribosomal protein L1 [Prunus armeniaca]
NCBI Description
                  419508
Seq. No.
                  uC-osrocyp006f01b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3860323
BLAST score
                  349
                  8.0e-33
E value
                  77
Match length
                  83
% identity
                  (AJ012688) hypothetical protein [Cicer arietinum]
NCBI Description
```

419509

Seq. No.

Method

NCBI GI

E value

BLAST score

BLASTX

213 7.0e-17

g2191135

```
uC-osrocyp006f06a1
    Seq. ID
   Method
                      BLASTX
    NCBI GI
                      q1841468
    BLAST score
                      203
    E value
                      9.0e-16
                      61
   Match length
    % identity
                      59
   NCBI Description (Y10990) Tyrosyl-tRNA synthetase [Nicotiana tabacum]
                      419510
    Seq. No.
                      uC-osrocyp006f06b1
    Seq. ID
   Method
                      BLASTX
   NCBI GI
                      g1841468
    BLAST score
                      338
                      5.0e-37
   E value
                      105
   Match length
    % identity
                      69
   NCBI Description (Y10990) Tyrosyl-tRNA synthetase [Nicotiana tabacum]
   Seq. No.
                      419511
   Seq. ID
                      uC-osrocyp006f08b1
   Method
                      BLASTX
   NCBI GI
                      q5882749
   BLAST score
                      146
                      2.0e-09
   E value
   Match length
                      98
    % identity
                      41
   NCBI Description (AC008263) Contains 2 PF_00612 IQ calmodulin-binding motif
                      domains. [Arabidopsis thaliana]
   Seq. No.
                      419512
   Seq. ID
                      uC-osrocyp006f09b1
   Method
                      BLASTX
   NCBI GI
                      g100664
   BLAST score
                      177
   E value
                      1.0e-23
   Match length
                      79
                      81
    % identity
   NCBI Description beta-glucanase - rice
   Seq. No.
                      419513
    Seq. ID
                      uC-osrocyp006f11a1
   Method
                      BLASTX
   NCBI GI
                      q2191135
   BLAST score
                      169
   E value
                      8.0e-12
   Match length
                      95
    % identity
                      43
   NCBI Description
                      (AF007269) A IG002N01.14 gene product [Arabidopsis
                      thaliana]
Seq. No.
                      419514
   Seq. ID
                      uC-osrocyp006f11b1
```

```
81
Match length
% identity
                  (AF007269) A IG002N01.14 gene product [Arabidopsis
NCBI Description
                  thaliana]
                  419515
Seq. No.
Seq. ID
                  uC-osrocyp006f12b1
                  BLASTX
Method
                  a3953458
NCBI GI
                  255
BLAST score
                  8.0e-22
E value
                  70
Match length
                  74
% identity
NCBI Description (AC002328) F20N2.3 [Arabidopsis thaliana]
                  419516
Seq. No.
Seq. ID
                  uC-osrocyp006g02a1
Method
                  BLASTX
NCBI GI
                  q2642159
                  382
BLAST score
                  7.0e-37
E value
                  78
Match length
                  91
% identity
NCBI Description
                  (AC003000) putative mannose-1-phosphate guanyltransferase
                   [Arabidopsis thaliana] >gi 3598958 (AF076484) GDP-mannose
                  pyrophosphorylase [Arabidopsis thaliana] >gi_4151925
                   (AF108660) CYT1 protein [Arabidopsis thaliana]
                   419517
Seq. No.
Seq. ID
                  uC-osrocyp006g05a1
                  BLASTX
Method
NCBI GI
                  q4512699
BLAST score
                  250
E value
                   3.0e-21
Match length
                   61
% identity
                  79
                  (AC006569) putative NADH-ubiquinone oxireductase
NCBI Description
                   [Arabidopsis thaliana]
                   419518
Seq. No.
Seq. ID
                  uC-osrocyp006g05b1
Method
                  BLASTX
                  q4512699
NCBI GI
                  281
BLAST score
                   5.0e-25
E value
                  71
Match length
                  82
% identity
```

NCBI Description (AC006569) putative NADH-ubiquinone oxireductase [Arabidopsis thaliana]

Seq. No. 419519 uC-osrocyp006g06a1 Seq. ID Method BLASTX

NCBI GI g82734 BLAST score 270 1.0e-23 E value Match length 54

we care to be

```
% identity
NCBI Description
                  ubiquitin precursor - maize (fragment)
                  >gi_226763_prf__1604470A poly-ubiquitin [Zea mays]
Seq. No.
                  419520
Seq. ID
                  uC-osrocyp006g06b1
```

Method BLASTX NCBI GI g1332579 BLAST score 639 6.0e-67 E value 140 Match length

% identity

NCBI Description (X98063) polyubiquitin [Pinus sylvestris]

419521 Seq. No.

uC-osrocyp006g08a1 Seq. ID

Method BLASTX NCBI GI g399204 BLAST score 164 E value 3.0e-11 57 Match length % identity 53

NCBI Description CORTICAL CELL DELINEATING PROTEIN PRECURSOR (ROOT-SPECIFIC

PROTEIN ZRP3) >gi_283052_pir__S28009 root-specific protein zrp3 - maize >gi 22252 emb CAA78088 (Z12103) unknown [Zea

mays]

Seq. No. 419522

Seq. ID uC-osrocyp006g08b1

Method BLASTX NCBI GI g1084461 BLAST score 260 2.0e-22 E value Match length 83 59 % identity

NCBI Description RCc3 protein - rice >gi 786132 (L27208) RCc3 [Oryza sativa]

Seq. No. 419523

Seq. ID uC-osrocyp006g09a1

Method BLASTX NCBI GI q1729971 BLAST score 362 E value 2.0e-34 Match length 66 100 % identity

NCBI Description TONOPLAST INTRINSIC PROTEIN, GAMMA (GAMMA TIP)

(AQUAPORIN-TIP) >gi_1076745_pir__S52004 gamma-Tip protein -

rice >gi_473997 dbj BAA05017 (D25534) gamma-Tip [Oryza

sativa]

Seq. No. 419524

Seq. ID uC-osrocyp006g09b1

Method BLASTX NCBI GI g1729971 BLAST score 235 E value 6.0e-32Match length 77



```
% identity
NCBI Description
                  TONOPLAST INTRINSIC PROTEIN, GAMMA (GAMMA TIP)
                   (AQUAPORIN-TIP) >gi_1076745 pir S52004 gamma-Tip protein -
                  rice >gi_473997_dbj_BAA05017_ (D25534) gamma-Tip [Oryza
                  sativa]
                419525
Seq. No.
Seq. ID
                  uC-osrocyp006g11a1
Method
                  BLASTX
                  g3914535
NCBI GI
BLAST score
                  177
                  1.0e-12
E value
Match length
                  51
% identity
                  67
NCBI Description 60S RIBOSOMAL PROTEIN L13A >gi 2791948 emb CAA11283
                  (AJ223363) ribosomal protein L13a [Lupinus luteus]
                  419526
Seq. No.
Seq. ID
                  uC-osrocyp006g12b1
                  BLASTX
Method
NCBI GI
                  q1084461
BLAST score
                  227
E value
                  8.0e-19
Match length
                  89
                  55
% identity
NCBI Description RCc3 protein - rice >gi_786132 (L27208) RCc3 [Oryza sativa]
Seq. No.
                  419527
Seq. ID
                  uC-osrocyp006h03a1
Method
                  BLASTX
NCBI GI
                  g129591
BLAST score
                  206
E value
                  3.0e-16
Match length
                  39
                  95
% identity
NCBI Description PHENYLALANINE AMMONIA-LYASE >qi 295824 emb CAA34226
                  (X16099) phenylalanine ammonia-lyase [Oryza sativa]
Seq. No.
                  419528
Seq. ID
                  uC-osrocyp006h07b1
Method
                  BLASTX
NCBI GI
                  q4558556
BLAST score
                  271
E value
                  7.0e-24
Match length
                  111
                  52
% identity
NCBI Description
                 (AC007138) predicted protein of unknown function
                  [Arabidopsis thaliana]
                  419529
Seq. No.
```

Seq. ID uC-osrocyp006h08a1

Method BLASTX
NCBI GI g3128167
BLAST score 186
E value 7.0e-14
Match length 77
% identity 52

Method

BLASTN

```
NCBI Description
                  (AC004521) hypothetical protein [Arabidopsis thaliana]
                   >gi_3212874 (AC004005) hypothetical protein [Arabidopsis
                   thaliana1
Seq. No.
                   419530
Seq. ID
                   uC-osrocyp006h09a1
Method
                   BLASTX
                   q1076820
NCBI GI
BLAST score
                   262
E value
                   9.0e-23
Match length
                   56
% identity
NCBI Description phosphoglycerate mutase (EC 5.4.2.1) - maize
Seq. No.
                   419531
Seq. ID
                  uC-osrocyp006h09b1
Method
                  BLASTX
NCBI GI
                  q400803
BLAST score
                   496
E value
                   3.0e-50
Match length
                   116
% identity
NCBI Description 2,3-BISPHOSPHOGLYCERATE-INDEPENDENT PHOSPHOGLYCERATE MUTASE
                   (PHOSPHOGLYCEROMUTASE) (BPG-INDEPENDENT PGAM) (PGAM-I)
                   >gi_283033 pir A42807 phosphoglycerate mutase (EC
                   5.4.2.1), \overline{2}, 3-\overline{b} isphosphoglycerate-independent - maize
                   >gi 168588 (M80912) 2,3-bisphosphoglycerate-independent
                  phosphoglycerate mutase [Zea mays]
Seq. No.
                  419532
Seq. ID
                  uC-osrocyp006h10a1
Method
                  BLASTX
NCBI GI
                  q1076820
BLAST score
                  240
E value
                  4.0e-20
Match length
                  56
% identity
                  82
NCBI Description phosphoglycerate mutase (EC 5.4.2.1) - maize
                  419533
Seq. No.
Seq. ID
                  uC-osrocyp006h10b1
Method
                  BLASTX
NCBI GI
                  q400803
BLAST score
                  264
E value
                  4.0e-23
Match length
                  68
% identity
                  75
NCBI Description 2,3-BISPHOSPHOGLYCERATE-INDEPENDENT PHOSPHOGLYCERATE MUTASE
                  (PHOSPHOGLYCEROMUTASE) (BPG-INDEPENDENT PGAM) (PGAM-I)
                  >gi 283033 pir A42807 phosphoglycerate mutase (EC
                  5.4.2.1), 2, 3-bisphosphoglycerate-independent - maize
                  >gi 168588 (M80912) 2,3-bisphosphoglycerate-independent
                  phosphoglycerate mutase [Zea mays]
Seq. No.
                  419534
Seq. ID
                  uC-osrocyp006h11a1
```

BLAST score

Match length

% identity

E value

268

70

70

2.0e-23



```
NCBI GI
                   g20280
BLAST score
                   62
E value
                   1.0e-26
Match length
                   110
% identity
                   92
NCBI Description Rice gene for phenylalanine ammonia-lyase (EC 4.3.1.5)
Seq. No.
                   419535
Seq. ID
                   uC-osrocyp006h11b1
Method
                  BLASTX
NCBI GI
                   q129591
BLAST score
                   771
E value
                   2.0e-82
Match length
                  159
                   97
% identity
NCBI Description PHENYLALANINE AMMONIA-LYASE >gi 295824 emb CAA34226
                   (X16099) phenylalanine ammonia-lyase [Oryza sativa]
Seq. No.
                   419536
Seq. ID
                  uC-osrocyp007a02b1
Method
                  BLASTX
NCBI GI
                  g3080439
BLAST score
                  296
E value
                  1.0e-26
Match length
                  99
                  57
% identity
NCBI Description (AL022605) putative protein [Arabidopsis thaliana]
Seq. No.
                  419537
Seq. ID
                  uC-osrocyp007a03b1
Method
                  BLASTX
NCBI GI
                  g2459421
BLAST score
                  152
E value
                  9.0e-10
Match length
                  89
% identity
                  39
NCBI Description
                  (AC002332) putative calcium-binding EF-hand protein
                   [Arabidopsis thaliana]
Seq. No.
                  419538
Seq. ID
                  uC-osrocyp007a04b1
Method
                  BLASTX
NCBI GI
                  g2829863
BLAST score
                  201
E value
                  1.0e-15
Match length
                  74
                  54
% identity
NCBI Description (AC002396) Putative peroxidase [Arabidopsis thaliana]
Seq. No.
                  419539
Seq. ID
                  uC-osrocyp007a05b1
Method
                  BLASTX
NCBI GI
                  g3152605
```

Seq. ID

Method

NCBI Description (AC004482) hypothetical protein [Arabidopsis thaliana] 419540 Seq. No. Seq. ID uC-osrocyp007a06b1 Method BLASTX NCBI GI g3023751 BLAST score 363 1.0e-34 E value 94 Match length 74 % identity 70 KD PEPTIDYLPROLYL ISOMERASE (PEPTIDYLPROLYL CIS-TRANS NCBI Description ISOMERASE) (CYCLOPHILIN) (PPIASE) >gi 1076772 pir S55383 peptidylprolyl isomerase (EC 5.2.1.8) - wheat >gi 854626 emb CAA60505 (X86903) peptidylprolyl isomerase [Triticum aestivum] 419541 Seq. No. Seq. ID uC-osrocyp007a07b1 Method BLASTX NCBI GI g4220481 291 BLAST score 6.0e-26 E value 119 Match length 50 % identity NCBI Description (AC006069) unknown protein [Arabidopsis thaliana] Seq. No. 419542 Seq. ID uC-osrocyp007a08a1 Method BLASTX NCBI GI g3023751 BLAST score 415 1.0e-40 E value 95 Match length 86 % identity 70 KD PEPTIDYLPROLYL ISOMERASE (PEPTIDYLPROLYL CIS-TRANS NCBI Description ISOMERASE) (CYCLOPHILIN) (PPIASE) >gi 1076772 pir S55383 peptidylprolyl isomerase (EC 5.2.1.8) - wheat >gi 854626 emb CAA60505 (X86903) peptidylprolyl isomerase [Triticum aestivum] 419543 Seq. No. Seq. ID uC-osrocyp007a08b1 Method BLASTX NCBI GI q3023751 BLAST score 479 E value 4.0e-48 132 Match length % identity 41 70 KD PEPTIDYLPROLYL ISOMERASE (PEPTIDYLPROLYL CIS-TRANS NCBI Description ISOMERASE) (CYCLOPHILIN) (PPIASE) >gi_1076772_pir__S55383 peptidylprolyl isomerase (EC 5.2.1.8) - wheat >gi_854626_emb_CAA60505_ (X86903) peptidylprolyl isomerase [Triticum aestivum] Seq. No. 419544

55035

uC-osrocyp007a09a1

BLASTX

```
g5702015
NCBI GI
                  269
BLAST score
                  2.0e-23
E value
                  76
Match length
                  70
% identity
                  (AJ012215) GAL83 protein [Solanum tuberosum]
NCBI Description
                  419545
Seq. No.
Seq. ID
                  uC-osrocyp007a11b1
Method
                  BLASTX
                  g2661422
NCBI GI
BLAST score
                  492
                  1.0e-49
E value
                  145
Match length
                  66
% identity
                  (AJ001342) Putative S-phase-specific ribosomal protein
NCBI Description
                   [Arabidopsis thaliana] >gi 3096936_emb_CAA18846.1
                   (AL023094) Putative S-phase-specific ribosomal protein
                   [Arabidopsis thaliana]
Seq. No.
                   419546
                  uC-osrocyp007a12a1
Seq. ID
                  BLASTN
Method
                  g20280
NCBI GI
BLAST score
                  327
                  0.0e+00
E value
                  355
Match length
                  98
% identity
NCBI Description Rice gene for phenylalanine ammonia-lyase (EC 4.3.1.5)
Seq. No.
                   419547
Seq. ID
                  uC-osrocyp007a12b1
Method
                  BLASTX
                  g129591
NCBI GI
BLAST score
                   412
                   2.0e-40
E value
                  100
Match length
% identity
NCBI Description PHENYLALANINE AMMONIA-LYASE >gi 295824 emb CAA34226
                   (X16099) phenylalanine ammonia-lyase [Oryza sativa]
Seq. No.
                   419548
Seq. ID
                   uC-osrocyp007b01b1
                   BLASTX
Method
NCBI GI
                   q5853313
BLAST score
                   452
E value
                   6.0e-45
Match length
                   148
% identity
```

NCBI Description (AF181687) metal ion transporter [Arabidopsis thaliana]

419549 Seq. No. Seq. ID uC-osrocyp007b02a1

Method BLASTX q4115377 NCBI GI BLAST score 188 2.0e-14 E value

Method

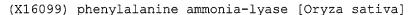
BLASTX

```
67
Match length
                  63
% identity
NCBI Description (AC005967) unknown protein [Arabidopsis thaliana]
                  419550
Seq. No.
Seq. ID
                  uC-osrocyp007b03b1
Method
                  BLASTX
NCBI GI
                  g1332579
BLAST score
                  264
                  9.0e-39
E value
                  89
Match length
                  10
% identity
NCBI Description (X98063) polyubiquitin [Pinus sylvestris]
Seq. No.
                  419551
Seq. ID
                  uC-osrocyp007b04a1
Method
                  BLASTN
                  g1132482
NCBI GI
BLAST score
                  373
E value
                  0.0e + 00
Match length
                  397
                  98
% identity
NCBI Description Rice mRNA for ADP-ribosylation factor, complete cds
Seq. No.
                  419552
Seq. ID
                  uC-osrocyp007b04b1
                  BLASTN
Method
NCBI GI
                  g1132482
BLAST score
                  166
E value
                  2.0e-88
Match length
                  226
                  94
% identity
NCBI Description Rice mRNA for ADP-ribosylation factor, complete cds
Seq. No.
                  419553
                  uC-osrocyp007b05b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g5302775
BLAST score
                  160
E value
                  2.0e-11
Match length
                  42
% identity
                  64
NCBI Description (Z97337) hypothetical protein [Arabidopsis thaliana]
                  419554
Seq. No.
                  uC-osrocyp007b09b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2961378
BLAST score
                  354
                  2.0e-33
E value
                  90
Match length
                  35
% identity
NCBI Description (AL022141) putative protein [Arabidopsis thaliana]
                  419555
Seq. No.
                  uC-osrocyp007b11b1
Seq. ID
```

```
NCBI GI
                  q1669655
                  170
BLAST score
                  3.0e-12
E value
                  47
Match length
% identity
                  66
NCBI Description (X95962) CER3 [Arabidopsis thaliana]
                  419556
Seq. No.
Seq. ID
                  uC-osrocyp007c01a1
Method
                  BLASTN
NCBI GI
                  g6041757
BLAST score
                  124
                  4.0e-63
E value
                  234
Match length
                  89
% identity
NCBI Description Genomic Sequence For Oryza sativa Clone 10P20, Lemont
                  Strain, Complete Sequence, complete sequence
                  419557
Seq. No.
Seq. ID
                  uC-osrocyp007c03b1
Method
                  BLASTX
NCBI GI
                  g4220482
                  190
BLAST score
                  3.0e-14
E value
                  83
Match length
                  49
% identity
NCBI Description (AC006069) hypothetical protein [Arabidopsis thaliana]
                  419558
Seq. No.
Seq. ID
                  uC-osrocyp007c04a1
Method
                  BLASTN
NCBI GI
                  q4126808
BLAST score
                  122
E value
                  5.0e-62
Match length
                  138
% identity
NCBI Description Oryza sativa mRNA for glyoxalase I, complete cds
                  419559
Seq. No.
Seq. ID
                  uC-osrocyp007c04b1
Method
                  BLASTX
NCBI GI
                  g4126809
BLAST score
                  683
                  4.0e-72
E value
Match length
                  127
% identity
                  55
NCBI Description (AB017042) glyoxalase I [Oryza sativa]
Seq. No.
                  419560
Seq. ID
                  uC-osrocyp007c07b1
Method
                  BLASTX
NCBI GI
                  g129591
BLAST score
                  418
                  4.0e-41
E value
Match length
                  101
% identity
                  81
NCBI Description PHENYLALANINE AMMONIA-LYASE >gi 295824 emb CAA34226
```

Seq. ID





```
Seq. No.
                  419561
Seq. ID
                  uC-osrocyp007c08b1
                  BLASTX
Method
NCBI GI
                  g3123270
BLAST score
                  705
E value
                  1.0e-74
                  135
Match length
                  100
% identity
NCBI Description 40S RIBOSOMAL PROTEIN S4 (SCAR PROTEIN SS620)
                  >gi 2463335 emb CAA75242 (Y15009) ribosomal protein S4
                  [Oryza sativa]
                  419562
Seq. No.
Seq. ID
                  uC-osrocyp007c09b1
                  BLASTX
Method
NCBI GI
                  g2463098
BLAST score
                  199
E value
                  3.0e-15
                  138
Match length
                  36
% identity
NCBI Description (Y13907) serine proteinase [Heterodera glycines]
                  419563
Seq. No.
Seq. ID
                  uC-osrocyp007c10b1
Method
                  BLASTX
NCBI GI
                  g4049341
BLAST score
                  350
E value
                  5.0e-33
Match length
                  106
% identity
                  63
NCBI Description (AL034567) putative protein [Arabidopsis thaliana]
Seq. No.
                  419564
                  uC-osrocyp007c11a1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4902476
BLAST score
                  167
E value
                  2.0e-11
Match length
                  58
% identity
                  57
NCBI Description (AJ238802) MAP kinase [Arabidopsis thaliana]
Seq. No.
                  419565
Seq. ID
                  uC-osrocyp007d01b1
Method
                  BLASTX
NCBI GI
                  g2645729
BLAST score
                  169
E value
                  1.0e-11
Match length
                  105
% identity
NCBI Description (AF033095) testis enhanced gene transcript protein [Homo
                  sapiens]
Seq. No.
                  419566
```

55039

uC-osrocyp007d02b1



BLASTX Method NCBI GI q3834321 BLAST score 694 2.0e-73 E value Match length 149 % identity 88 NCBI Description

(AC005679) Strong similarity to F13P17.9 gi 3337356 transport protein SEC61 alpha subunit homolog from Arabidopsis thaliana BAC gb AC004481. [Arabidopsis

thaliana]

Seq. No. 419567

Seq. ID uC-osrocyp007d04b1

Method BLASTX q4433618 NCBI GI BLAST score 223 E value 6.0e-18 121 Match length % identity 43

(AF107585) putative myosin heavy chain [Dendrobium grex NCBI Description

Madame Thong-IN]

419568 Seq. No.

Seq. ID uC-osrocyp007d06b1

Method BLASTX g2984709 NCBI GI BLAST score 460 7.0e-46E value Match length 88

% identity 98

NCBI Description (AF053468) DnaJ-related protein ZMDJ1 [Zea mays]

Seq. No. 419569

Seq. ID uC-osrocyp007d07b1

Method BLASTX NCBI GI g3157932 BLAST score 519 1.0e-52 E value Match length 143 % identity 73

(AC002131) Similar to hypothetical protein HYP1 gb_Z97338 NCBI Description

from A. thaliana. [Arabidopsis thaliana]

419570 Seq. No.

uC-osrocyp007d08b1 Seq. ID

Method BLASTX NCBI GI g3128218 152 BLAST score 1.0e-09 E value 51 Match length % identity 63

NCBI Description (AC004077) putative end13 protein [Arabidopsis thaliana]

419571 Seq. No.

uC-osrocyp007d09a1 Seq. ID

BLASTN Method NCBI GI g6016845

```
BLAST score
                  47
                  2.0e-17
E value
                  67
Match length
% identity
                  93
NCBI Description Oryza sativa genomic DNA, chromosome 1, clone:P0711E10
                  419572
Seq. No.
Seq. ID
                  uC-osrocyp007d09b1
Method
                  BLASTX
NCBI GI
                  q6016877
BLAST score
                  232
                  5.0e-19
E value
Match length
                  53
% identity
                  81
NCBI Description (AP000570) ESTs AU077642(E30706), AU077641(E30706)
                  correspond to a region of the predicted gene.; hypothetical
                  protein [Oryza sativa]
Seq. No.
                  419573
Seq. ID
                  uC-osrocyp007d11a1
Method
                  BLASTX
NCBI GI
                  g5002232
                  329
BLAST score
                  1.0e-30
E value
Match length
                  82
                  74-
% identity
NCBI Description (AF145234) NADPH:quinone oxidoreductase [Arabidopsis
                  thaliana]
Seq. No.
                  419574
Seq. ID
                  uC-osrocyp007d11b1
Method
                  BLASTX
NCBI GI
                  g5002232
BLAST score
                  459
                  1.0e-45
E value
Match length
                  133
% identity
                  65
NCBI Description (AF145234) NADPH:quinone oxidoreductase [Arabidopsis
                  thaliana]
                  419575
Seq. No.
Seq. ID
                  uC-osrocyp007d12a1
Method
                  BLASTN
NCBI GI
                  a20241
                  442
BLAST score
E value
                  0.0e + 00
                  461
Match length
                  99
% identity
NCBI Description O. sativa (rice) root-specific GOS9 gene
Seq. No.
                  419576
                  uC-osrocyp007d12b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q121528
BLAST score
                  443
E value
                  3.0e-44
Match length
                  92
```



% identity 95

NCBI Description GOS9 PROTEIN >gi_100683_pir__S19115 GOS9 protein - rice >gi_20242_emb_CAA36189_ (X51909) GOS9 [Oryza sativa]

Seq. No. 419577

Seq. ID uC-osrocyp007e01a1

Method BLASTN
NCBI GI 9474011
BLAST score 293
E value 1.0e-164
Match length 364
% identity 96

NCBI Description Rice mRNA, partial homologous to sucrose phosphate synthase

gene

Seq. No. 419578

Seq. ID uC-osrocyp007e01b1

Method BLASTX
NCBI GI g283008
BLAST score 585
E value 1.0e-60
Match length 132
% identity 87

NCBI Description sucrose synthase (EC 2.4.1.13) - rice

>gi_20366_emb_CAA46017_ (X64770) sucrose synthase [Oryza

sativa]

Seq. No. 419579

Seq. ID uC-osrocyp007e02b1

Method BLASTX
NCBI GI g3386565
BLAST score 561
E value 1.0e-57
Match length 133
% identity 79

NCBI Description (AF079588) 1-aminocyclopropane-1-carboxylate oxidase

[Sorghum bicolor]

Seq. No. 419580

Seq. ID uC-osrocyp007e03b1

Method BLASTX
NCBI GI 94008156
BLAST score 757
E value 1.0e-80
Match length 177
% identity 81

NCBI Description (AB008845) NADH dependent Glutamate Synthase [Oryza sativa]

Seq. No. 419581

Seq. ID uC-osrocyp007e06b1

Method BLASTX
NCBI GI g5453880
BLAST score 201
E value 2.0e-15
Match length 122
% identity 39

NCBI Description Putative human HLA class II associated protein I

Match length

NCBI Description

% identity

168 61

>gi_730318_sp_P39687_PHA1_HUMAN POTENT HEAT-STABLE PROTEIN PHOSPHATASE 2A INHIBITOR T1PP2A (HLA-DR ASSOCIATED PROTEIN I) (PHAPI) (ACIDIC NUCLEAR PHOSPHOPROTEIN PP32) (CEREBELLAR LEUCINE RICH ACIDIC NUCLEAR PROTEIN) >gi_631325_pir__S43309 probable HLA class II-associated protein PHAPI - human >gi_403007_emb_CAA52981_ (X75090) PHAPI (Putative HLA DR Associated Protein I) [Homo sapiens] >gi_1408224 (U60823) potent heat-stable protein phosphatase 2Ā inhibitor I1PP2A [Homo sapiens] >gi_1763273 (U73477) acidic nuclear phosphoprotein pp32 [Homo sapiens] >gi_2589221 (AF025684) cerebellar leucine rich acidic nuclear protein [Homo sapiens]

419582 Seq. No. Seq. ID uC-osrocyp007e08b1 Method BLASTX NCBI GI q2493318 BLAST score 222 E value 6.0e-18 Match length 99 46 % identity NCBI Description BLUE COPPER PROTEIN PRECURSOR >gi 562779 emb CAA80963 (Z25471) blue copper protein [Pisum sativum] >gi 1098264_prf__2115352A blue Cu protein [Pisum sativum] 419583 Seq. No. uC-osrocyp007e09a1 Seq. ID BLASTN Method NCBI GI q20332 BLAST score 61 E value 2.0e-25 Match length 69 % identity 97 NCBI Description O.sativa RAc7 gene for actin Seq. No. 419584 Seq. ID uC-osrocyp007e09b1 Method BLASTX NCBI GI q1669387 BLAST score 309 E value 3.0e-28 Match length 63 % identity 94 NCBI Description (U41998) actin 2 [Arabidopsis thaliana] 419585 Seq. No. uC-osrocyp007e10b1 Seq. ID Method BLASTX NCBI GI g4760370 BLAST score 525 2.0e-53 E value

(AF082565) ATP dependent copper transporter [Arabidopsis thaliana] >gi_4760380_gb_AAD29115.1_ (AF091112) ATP dependent copper transporter [Arabidopsis thaliana]



```
419586
Seq. No.
Seq. ID
                  uC-osrocyp007e11b1
Method
                  BLASTX
NCBI GI
                  g2791806
BLAST score
                  439
E value
                  2.0e-43
                  131
Match length
% identity
                  63
NCBI Description (AF041433) bet3 [Mus musculus]
                  419587
Seq. No.
Seq. ID
                  uC-osrocyp007e12a1
                  BLASTX
Method
NCBI GI
                  g1703380
                  297
BLAST score
                  9.0e-27
E value
                  57
Match length
                  98
% identity
NCBI Description ADP-RIBOSYLATION FACTOR >gi 1132483 dbj BAA04607 (D17760)
                  ADP-ribosylation factor [Oryza sativa]
                  419588
Seq. No.
                  uC-osrocyp007e12b1
Seq. ID
                  BLASTX
Method
NCBI GI
                  g1703380
BLAST score
                  686
                  3.0e-72
E value
                  139
Match length
                  98
% identity
NCBI Description ADP-RIBOSYLATION FACTOR >gi_1132483_dbj BAA04607 (D17760)
                  ADP-ribosylation factor [Oryza sativa]
                  419589
Seq. No.
                  uC-osrocyp007f02a1
Seq. ID
Method
                  BLASTN
                  q3298473
NCBI GI
BLAST score
                  331
                  0.0e + 00
E value
Match length
                  368
% identity
                  97
NCBI Description Oryza sativa gene for ovpl, complete cds
Seq. No.
                  419590
Seq. ID
                  uC-osrocyp007f02b1
Method
                  BLASTX
NCBI GI
                  q1747294
BLAST score
                  837
                  5.0e-90
E value
Match length
                  168
% identity
                  98
NCBI Description (D45383) vacuolar H+-pyrophosphatase [Oryza sativa]
Seq. No.
                  419591
                  uC-osrocyp007f03a1
Seq. ID
```

Method BLASTN NCBI GI q20280 BLAST score 370

```
E value
                   0.0e + 00
Match length
                   410
% identity
                   98
NCBI Description Rice gene for phenylalanine ammonia-lyase (EC 4.3.1.5)
Seq. No.
                   419592
Seq. ID
                   uC-osrocyp007f03b1
Method
                   BLASTX
NCBI GI
                   g82496
BLAST score
                   366
E value
                   6.0e-64
Match length
                   144
                   90
% identity
NCBI Description phenylalanine ammonia-lyase (EC 4.3.1.5) - rice
                   419593
Seq. No.
Seq. ID
                   uC-osrocyp007f04b1
Method
                   BLASTX
NCBI GI
                   g1076316
BLAST score
                   150
E value
                   1.0e-09
Match length
                   82
% identity
                   34
NCBI Description
                   drought-induced protein Di19 - Arabidopsis thaliana
                   >gi_469110_emb CAA55321 (X78584) Di19 [Arabidopsis
                   thaliana]
                   419594
Seq. No.
Seq. ID
                   uC-osrocyp007f05b1
Method
                   BLASTX
NCBI GI
                   g3212852
BLAST score
                   187
                   9.0e-14
E value
Match length
                   109
% identity
NCBI Description (AC004005) unknown protein [Arabidopsis thaliana]
Seq. No.
                   419595
Seq. ID
                   uC-osrocyp007f07b1
Method
                   BLASTX
NCBI GI
                   q3786009
BLAST score
                   552
E value
                   1.0e-56
Match length
                   150
% identity
                   74
NCBI Description (AC005499) unknown protein [Arabidopsis thaliana]
Seq. No.
                   419596
                   uC-osrocyp007f08b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g4972075
BLAST score
                   328
E value
                   2.0e-30
Match length
                   163
% identity
                   47
```

NCBI Description (AL078467) proton pump interactor [Arabidopsis thaliana]



```
419597
Seq. No.
Seq. ID
                   uC-osrocyp007f09b1
Method
                   BLASTX
NCBI GI
                   g1931647
BLAST score
                   380
E value
                   2.0e-36
                   122
Match length
                   60
% identity
NCBI Description
                  (U95973) endomembrane protein EMP70 precusor isolog
                   [Arabidopsis thaliana]
                   419598
Seq. No.
Seq. ID
                   uC-osrocyp007f12b1
Method
                  BLASTX
NCBI GI
                   g4006932
BLAST score
                   167
                   1.0e-11
E value
Match length
                   120
                   37
% identity
NCBI Description
                  (AJ011400) NADH: ubiquinone oxidoreductase b17.2 subunit
                   [Bos taurus]
                   419599
Seq. No.
Seq. ID
                   uC-osrocyp007g01b1
Method
                  BLASTN
NCBI GI
                   g6016845
BLAST score
                   179
                   5.0e-96
E value
Match length
                   227
% identity
                   95
NCBI Description Oryza sativa genomic DNA, chromosome 1, clone:P0711E10
Seq. No.
                   419600
Seq. ID
                   uC-osrocyp007g02b1
Method
                   BLASTX
NCBI GI
                   g2088650
BLAST score
                   438
E value
                   2.0e-43
Match length
                   149
% identity
NCBI Description
                  (AF002109) peroxisomal ATP/ADP carrier protein isolog
                   [Arabidopsis thaliana]
Seq. No.
                   419601
Seq. ID
                   uC-osrocyp007g05b1
Method
                   BLASTX
NCBI GI
                   g2493318
BLAST score
                   227
E value
                   1.0e-18
Match length
                   99
                   47
% identity
NCBI Description BLUE COPPER PROTEIN PRECURSOR >gi 562779 emb CAA80963
                   (Z25471) blue copper protein [Pisum sativum]
```

Seq. No. 419602

Seq. ID uC-osrocyp007g06a1

>gi 1098264 prf 2115352A blue Cu protein [Pisum sativum]

Method

NCBI GI

E value

BLAST score

BLASTX

303

q1370603

1.0e-27

```
Method
                  BLASTX
NCBI GI
                  g4530585
BLAST score
                  151
E value
                  7.0e-10
Match length
                  52
% identity
                  50
NCBI Description (AF130978) B12D protein [Ipomoea batatas]
Seq. No.
                  419603
Seq. ID
                  uC-osrocyp007g06b1
Method
                  BLASTX
                  g4530585
NCBI GI
BLAST score
                  258
E value
                  3.0e-22
Match length
                  83
                  53
% identity
NCBI Description (AF130978) B12D protein [Ipomoea batatas]
Seq. No.
                  419604
Seq. ID
                  uC-osrocyp007g07b1
Method
                  BLASTX
NCBI GI
                  q6063536
BLAST score
                  194
E value
                  8.0e-16
Match length
                  48
% identity
                  86
                  (AP000615) ESTs C22369(C12239), C22370(C12239),
NCBI Description
                  AU057852(S21844), AU057853(S21844) correspond to a region of
                  the predicted gene.; similar to calcium dependent protein
                  kinase. (AF048691) [Oryza sativa]
Seq. No.
                  419605
Seq. ID
                  uC-osrocyp007g08b1
Method
                  BLASTX
NCBI GI
                  g5123547
BLAST score
                  296
E value
                  8.0e-27
Match length
                  104
% identity
                  53
NCBI Description (AL079344) putative protein [Arabidopsis thaliana]
Seq. No.
                  419606
Seq. ID
                  uC-osrocyp007g09b1
Method
                  BLASTX
NCBI GI
                  q4220521
BLAST score
                  229
E value
                  5.0e-19
Match length
                  57
                  74
% identity
NCBI Description (AL035356) putative protein [Arabidopsis thaliana]
Seq. No.
                  419607
Seq. ID
                  uC-osrocyp007g10a1
```



Match length 67 % identity 91

NCBI Description (X98245) annexin p35 [Zea mays]

Seq. No. 419608

Seq. ID uC-osrocyp007g10b1

Method BLASTX
NCBI GI g1370603
BLAST score 609
E value 3.0e-63
Match length 165
% identity 72

NCBI Description (X98245) annexin p35 [Zea mays]

Seq. No. 419609

Seq. ID uC-osrocyp007g11a1

Method BLASTX
NCBI GI g3702323
BLAST score 215
E value 3.0e-17
Match length 54
% identity 76

NCBI Description (AC005397) unknown protein [Arabidopsis thaliana]

Seq. No. 419610

Seq. ID uC-osrocyp007h03b1

Method BLASTX
NCBI GI g3236253
BLAST score 625
E value 3.0e-65
Match length 146
% identity 77

NCBI Description (AC004684) receptor-like protein kinase [Arabidopsis

thaliana]

Seq. No. 419611

Seq. ID uC-osrocyp007h07b1

Method BLASTX
NCBI GI g2500036
BLAST score 460
E value 5.0e-46
Match length 115
% identity 76

NCBI Description DIHYDROOROTASE PRECURSOR (DHOASE) >gi 2121273 (AF000146)

dihydroorotase [Arabidopsis thaliana]

>gi 3292818 emb CAA19808.1 (AL031018) dihydroorotase

[Arabidopsis thaliana]

Seq. No. 419612

Seq. ID uC-osrocyp007h08a1

Method BLASTX
NCBI GI g3738338
BLAST score 217
E value 2.0e-17
Match length 98
% identity 45

NCBI Description (AC005170) putative polygalacturonase [Arabidopsis

NCBI Description



thaliana]

419613 Seq. No. Seq. ID uC-osrocyp007h09a1 BLASTX Method g2435522 NCBI GI 258 BLAST score E value 3.0e-2279 Match length 63 % identity (AF024504) contains similarity to other AMP-binding enzymes NCBI Description [Arabidopsis thaliana] Seq. No. 419614 Seq. ID uC-osrocyp007h10b1 Method BLASTX g2832677 NCBI GI BLAST score 248 4.0e-21 E value Match length 131 % identity 44 NCBI Description (AL021712) hypothetical protein [Arabidopsis thaliana] Seq. No. 419615 Seq. ID uC-osrocyp008a01a1 Method BLASTX g118011 NCBI GI BLAST score 339 1.0e-31 E value 64 Match length % identity 100 CYTOCHROME C >gi 625189 pir CCRZ cytochrome c - rice NCBI Description >qi 169786 (M63704) cytochrome c [Oryza sativa] >gi 218249 dbj BAA02159 (D12634) 'cytochrome C' [Oryza sativa] Seq. No. 419616 uC-osrocyp008a01b1 Seq. ID Method BLASTX NCBI GI g2842493 BLAST score 377 E value 4.0e-36 Match length 101 % identity NCBI Description (AL021749) predicted protein [Arabidopsis thaliana] Seq. No. 419617 Seq. ID uC-osrocyp008a02a1 Method BLASTX NCBI GI g451193 BLAST score 409 E value 7.0e-40Match length 112 % identity 72

>gi 1090845 prf 2019486B wali7 gene [Triticum aestivum]

(L28008) wali7 [Triticum aestivum]

BLAST score

E value

284

1.0e-159

```
Seq. No.
                   419618
Seq. ID
                  uC-osrocyp008a02b1
Method
                  BLASTX
NCBI GI
                  g6056399
BLAST score
                  214
                   5.0e-17
E value
Match length
                  135
% identity
                   41
NCBI Description
                  (AC009324) AP2 domain containing protein RAP2.12
                   [Arabidopsis thaliana]
                   419619
Seq. No.
Seq. ID
                  uC-osrocyp008a03a1
Method
                  BLASTX
NCBI GI
                  g4093169
BLAST score
                  235
E value
                  2.0e-19
Match length
                  61
                  69
% identity
NCBI Description (AF095933) p20-Arc [Dictyostelium discoideum]
Seq. No.
                  419620
Seq. ID
                  uC-osrocyp008a04a1
Method
                  BLASTX
NCBI GI
                  q3953479
BLAST score
                  168
E value
                  1.0e-11
                  67
Match length
                  54
% identity
NCBI Description (AC002328) F2202.24 [Arabidopsis thaliana]
Seq. No.
                  419621
                  uC-osrocyp008a04b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4559381
BLAST score
                  230
E value
                  4.0e-20
Match length
                  85
% identity
                  53
NCBI Description (AC006526) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  419622
Seq. ID
                  uC-osrocyp008a05a1
Method
                  BLASTX
NCBI GI
                  q1143445
BLAST score
                  442
E value
                  9.0e-44
Match length
                  114
% identity
NCBI Description (X88797) cinnamyl alcohol dehydrogenase [Eucalyptus gunnii]
Seq. No.
                  419623
Seq. ID
                  uC-osrocyp008a05b1
Method
                  BLASTN
NCBI GI
                  q5091597
```

```
314
Match length
                  97
% identity
NCBI Description Oryza sativa chromosome 1 BAC 10A19I, complete sequence
                  419624
Seq. No.
Seq. ID
                  uC-osrocyp008a06a1
                  BLASTN
Method
NCBI GI
                  g758354
BLAST score
                  49
                  2.0e-18
E value
                  85
Match length
                  89
% identity
NCBI Description Z.mays mRNA for plasma membrane H+ ATPase
Seq. No.
                  419625
Seq. ID
                  uC-osrocyp008a07b1
Method
                  BLASTX
NCBI GI
                  g4567246
BLAST score
                  243
E value
                  2.0e-20
                  130
Match length
% identity
                  44
NCBI Description (AC007070) unknown protein [Arabidopsis thaliana]
Seq. No.
                  419626
Seq. ID
                  uC-osrocyp008a08b1
Method
                  BLASTX
NCBI GI
                  g4574139
BLAST score
                  760
E value
                  5.0e-81
Match length
                  164
                  93
% identity
NCBI Description (AF073697) cysteine synthase [Oryza sativa]
Seq. No.
                  419627
                  uC-osrocyp008a09a1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4587589
BLAST score
                  416
E value
                  9.0e-41
Match length
                  98
% identity
NCBI Description (AC007232) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  419628
Seq. ID
                  uC-osrocyp008a11a1
Method
                  BLASTX
NCBI GI
                  g1076746
BLAST score
                  409
E value
                  7.0e-40
Match length
                  110
% identity
                  77
NCBI Description
                  heat shock protein 70 - rice (fragment)
                  >gi 763160 emb CAA47948 (X67711) heat shock protein 70
                  [Oryza sativa]
```

55051

419629

Seq. No.

```
uC-osrocyp008a11b1
Seq. ID
                  BLASTX
Method
                  g3450842
NCBI GI
BLAST score
                  150
                  6.0e-19
E value
                  96
Match length
                  54
% identity
                  (AF080436) mitogen activated protein kinase kinase [Oryza
NCBI Description
                  sativa]
                  419630
Seq. No.
                  uC-osrocyp008b02b1
Seq. ID
                  BLASTN
Method
NCBI GI
                  g1777454
BLAST score
                  190
                  1.0e-102
E value
                  254
Match length
                  94
% identity
NCBI Description Oryza sativa pyruvate decarboxylase 2 (pdc2) gene, complete
                  cds
                  419631
Seq. No.
                  uC-osrocyp008b03a1
Seq. ID
                  BLASTX
Method
NCBI GI
                  g5031275
BLAST score
                  269
                  2.0e-23
E value
                  64
Match length
                  75
% identity
NCBI Description (AF139496) unknown [Prunus armeniaca]
                  419632
Seq. No.
Seq. ID
                  uC-osrocyp008b04a1
                  BLASTN
Method
NCBI GI
                  g6016845
BLAST score
                  134
                  5.0e-69
E value
Match length
                  205
                  93
% identity
NCBI Description Oryza sativa genomic DNA, chromosome 1, clone:P0711E10
Seq. No.
                   419633
Seq. ID
                  uC-osrocyp008b04b1
Method
                  BLASTX
NCBI GI
                  g3122386
BLAST score
                  578
                  7.0e-60
E value
                  126
Match length
                  84
% identity
NCBI Description WD-40 REPEAT PROTEIN MSI1 >gi 2394227 (AF016845) WD-40
                   repeat protein [Lycopersicon esculentum]
                   419634
Seq. No.
                   uC-osrocyp008b05a1
Seq. ID
```

55052

BLASTX

566

g3242789

Method

NCBI GI

BLAST score

3.0e-58 E value 160 Match length % identity 66 NCBI Description thaliana]

(AF055357) respiratory burst oxidase protein D [Arabidopsis

419635 Seq. No.

uC-osrocyp008b07b1 Seq. ID

Method BLASTX q5091509 NCBI GI 907 BLAST score 3.0e-98 E value Match length 181 98 % identity

(AB023482) EST AU065533(C2174) corresponds to a region of NCBI Description

the predicted gene.; Similar to Homo sapiens splicing factor Prp8 mRNA, complete cds.(AF092565) [Oryza sativa]

419636 Seq. No.

uC-osrocyp008b08a1 Seq. ID

Method BLASTX g5103846 NCBI GI 191 BLAST score 3.0e-14E value Match length 66 % identity 56

NCBI Description (AC007591) F9L1.43 [Arabidopsis thaliana]

419637 Seq. No.

uC-osrocyp008b08b1 Seq. ID

BLASTX Method g4574139 NCBI GI 590 BLAST score 4.0e-61 E value 157 Match length 76 % identity

NCBI Description (AF073697) cysteine synthase [Oryza sativa]

419638 Seq. No.

Seq. ID uC-osrocyp008b09a1

Method BLASTX NCBI GI q2340166 BLAST score 174 E value 2.0e-12 57 Match length 56 % identity

(AF008124) glutathione S-conjugate transporting ATPase NCBI Description

[Arabidopsis thaliana] >gi_2459949 (AF008125) multidrug

resistance-associated protein homolog [Arabidopsis

thaliana]

419639 Seq. No.

Seq. ID uC-osrocyp008b10a1

Method BLASTX NCBI GI q2340166 BLAST score 198 E value 4.0e-15

Match length 63 % identity 57

NCBI Description (AF008124) glutathione S-conjugate transporting ATPase [Arabidopsis thaliana] >gi_2459949 (AF008125) multidrug

resistance-associated protein homolog [Arabidopsis

thaliana]

Seq. No. 419640

Seq. ID uC-osrocyp008b11a1

Method BLASTN
NCBI GI g2773153
BLAST score 508
E value 0.0e+00
Match length 516
% identity 100

NCBI Description Oryza sativa abscisic acid- and stress-inducible protein

(Asr1) mRNA, complete cds

Seq. No. 419641

Seq. ID uC-osrocyp008b12a1

Method BLASTX
NCBI GI g2252472
BLAST score 544
E value 1.0e-55
Match length 152
% identity 75

NCBI Description (297558) argininosuccinate lyase [Arabidopsis thaliana]

Seq. No. 419642

Seq. ID uC-osrocyp008c02a1

Method BLASTX
NCBI GI g3928543
BLAST score 354
E value 2.0e-33
Match length 158
% identity 45

NCBI Description (AB016819) UDP-glucose glucosyltransferase [Arabidopsis

thaliana]

Seq. No. 419643

Seq. ID uC-osrocyp008c02b1

Method BLASTX
NCBI GI g3023713
BLAST score 787
E value 3.0e-84
Match length 161
% identity 93

NCBI Description ENOLASE (2-PHOSPHOGLYCERATE DEHYDRATASE)

(2-PHOSPHO-D-GLYCERATE HYDRO-LYASE) (OSE1) >gi 780372

(U09450) enolase [Oryza sativa]

Seq. No. 419644

Seq. ID uC-osrocyp008c03a1

Method BLASTX
NCBI GI g2827002
BLAST score 740
E value 1.0e-78

```
154
Match length
% identity
NCBI Description
                  (AF005993) HSP70 [Triticum aestivum]
                   419645
Seq. No.
Seq. ID
                  uC-osrocyp008c03b1
Method
                  BLASTN
NCBI GI
                  q6016845
                   78
BLAST score
                   8.0e-36
E value
                  244
Match length
% identity
                   84
NCBI Description Oryza sativa genomic DNA, chromosome 1, clone:P0711E10
                   419646
Seq. No.
Seq. ID
                  uC-osrocyp008c05a1
Method
                  BLASTN
NCBI GI
                  g2331130
BLAST score
                   216
                  1.0e-118
E value
                   334
Match length
                   97
% identity
NCBI Description Oryza sativa glycine-rich protein (OSGRP1) mRNA, complete
                  cds
                   419647
Seq. No.
Seq. ID
                  uC-osrocyp008c06a1
Method
                  BLASTN
NCBI GI
                  g3885887
BLAST score
                   480
                   0.0e + 00
E value
                   488
Match length
                   100
% identity
NCBI Description Oryza sativa high mobility group protein (HMG) mRNA,
                  complete cds
Seq. No.
                   419648
Seq. ID
                  uC-osrocyp008c07b1
Method
                  BLASTX
NCBI GI
                  g2293480
BLAST score
                   435
E value
                   6.0e-43
Match length
                  86
% identity
                   98
NCBI Description (AF011331) glycine-rich protein [Oryza sativa]
                   419649
Seq. No.
                  uC-osrocyp008c08a1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1170937
```

Method BLASTX
NCBI GI g1170937
BLAST score 371
E value 2.0e-35
Match length 68
% identity 100

NCBI Description S-ADENOSYLMETHIONINE SYNTHETASE 1 (METHIONINE

ADENOSYLTRANSFERASE 1) (ADOMET SYNTHETASE 1)

>gi 450549 emb CAA81481 (Z26867) S-adenosyl methionine



synthetase [Oryza sativa]

Seq. No. 419650 Seq. ID uC-osrocyp008c09a1 Method BLASTX NCBI GI q2641619 BLAST score 280 E value 1.0e-24 Match length 68 79 % identity NCBI Description (AF032468) ubiquitin-conjugating enzyme protein E2 [Zea mays] Seq. No. 419651 Seq. ID uC-osrocyp008c10b1 BLASTX Method NCBI GI g1703380 BLAST score 347 E value 1.0e-57 Match length 119 97 % identity NCBI Description ADP-RIBOSYLATION FACTOR >gi 1132483 dbj BAA04607 (D17760) ADP-ribosylation factor [Oryza sativa] Seq. No. 419652 Seq. ID uC-osrocyp008c11a1 BLASTX Method NCBI GI q2895866 BLAST score 480 3.0e-48 E value Match length 116 % identity NCBI Description (AF045770) methylmalonate semi-aldehyde dehydrogenase [Oryza sativa] Seq. No. 419653 Seq. ID uC-osrocyp008c12a1 Method BLASTX NCBI GI g129591 BLAST score 326 4.0e-30 E value Match length 61 % identity 98 NCBI Description PHENYLALANINE AMMONIA-LYASE >qi 295824 emb CAA34226 (X16099) phenylalanine ammonia-lyase [Oryza sativa] Seq. No. 419654 uC-osrocyp008d01b1 Seq. ID Method BLASTX NCBI GI g3885888 BLAST score 299 E value 6.0e-27 107 Match length % identity NCBI Description (AF093632) high mobility group protein [Oryza sativa]

Seq. No. 419655

Seq. ID

Seq. ID uC-osrocyp008d02b1 Method BLASTX NCBI GI q1168537 BLAST score 489 E value 3.0e-49 Match length 156 61 % identity NCBI Description ASPARTIC PROTEINASE PRECURSOR >gi 82458 pir JS0732 aspartic proteinase (EC 3.4.23.-) - rice >gi_218143_dbj_BAA02242_ (D12777) aspartic proteinase [Oryza sativa] Seq. No. 419656 Seq. ID uC-osrocyp008d04b1 Method BLASTX NCBI GI g3420239 BLAST score 679 E value 2.0e-71 Match length 131 % identity NCBI Description (AF059484) actin [Gossypium hirsutum] Seq. No. 419657 Seq. ID uC-osrocyp008d05b1 Method BLASTX NCBI GI g1778149 BLAST score 249 E value 4.0e-21 Match length 53 % identity 96 (U66404) phosphate/phosphoenolpyruvate translocator NCBI Description precursor [Zea mays] Seq. No. 419658 Seq. ID uC-osrocyp008d06a1 Method BLASTX NCBI GI g4567232 BLAST score 195 E value 5.0e-15 Match length 52 75 % identity NCBI Description (AC007119) putative 40S ribosomal protein S25 [Arabidopsis thaliana] Seq. No. 419659 Seq. ID uC-osrocyp008d08a1 Method BLASTX NCBI GI g2895866 BLAST score 574 E value 3.0e-59 Match length 120 % identity 96 NCBI Description (AF045770) methylmalonate semi-aldehyde dehydrogenase [Oryza sativa] Seq. No. 419660

55057

uC-osrocyp008d10b1

Seq. No.

419665

```
Method
                  BLASTX
NCBI GI
                  g4056425
BLAST score
                  201
E value
                  9.0e-17
Match length
                  68
% identity
                  68
                  (AC005322) ESTs gb_H36249, gb_AA59732 and gb AA651219 come
NCBI Description
                  from this gene. [Arabidopsis thaliana]
Seq. No.
                  419661
Seq. ID
                  uC-osrocyp008d11b1
Method
                  BLASTX
NCBI GI
                  q3242717
BLAST score
                  317
E value
                  5.0e-29
                  81
Match length
                  75
% identity
NCBI Description (AC003040) putative APG protein [Arabidopsis thaliana]
Seq. No.
                  419662
Seq. ID
                  uC-osrocyp008d12a1
Method
                  BLASTX
NCBI GI
                  g129591
BLAST score
                  284
E value
                  3.0e-25
Match length
                  53
                  98
% identity
NCBI Description PHENYLALANINE AMMONIA-LYASE >gi 295824 emb CAA34226
                  (X16099) phenylalanine ammonia-lyase [Oryza sativa]
Seq. No.
                  419663
Seq. ID
                  uC-osrocyp008d12b1
Method
                  BLASTX
NCBI GI
                  q2760349
BLAST score
                  662
E value
                  1.0e-69
                  137
Match length
% identity
                  21
NCBI Description (U84969) ubiquitin [Arabidopsis thaliana]
Seq. No.
                  419664
Seq. ID
                  uC-osrocyp008e01a1
Method
                  BLASTX
NCBI GI
                  q481477
BLAST score
                  437
E value
                  3.0e-43
Match length
                  89
                  17
% identity
NCBI Description
                  ubiquitin precursor - rice >gi 416038 emb CAA53665
                  (X76064) polyubiquitin [Oryza sativa] >gi_1574944 (U37687)
                  polyubiquitin [Oryza sativa]
                  >gi_6013289_gb_AAF01315.1_AF184279_1 (AF184279)
                  polyubiquitin [Oryza sativa]
                  >gi_6013291_gb_AAF01316.1 AF184280 1 (AF184280)
                  polyubiquitin [Oryza sativa]
```

Seq. ID

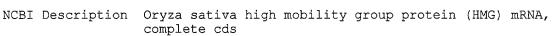
```
BLASTX
Method
NCBI GI
                  g82496
BLAST score
                   521
E value
                   5.0e-53
                  131
Match length
                  79
% identity
NCBI Description phenylalanine ammonia-lyase (EC 4.3.1.5) - rice
Seq. No.
                  419666
Seq. ID
                  uC-osrocyp008e02a1
Method
                  BLASTX
NCBI GI
                  g3242717
BLAST score
                  384
E value
                  6.0e-37
                  107
Match length
                  64
% identity
NCBI Description (AC003040) putative APG protein [Arabidopsis thaliana]
Seq. No.
                  419667
Seq. ID
                  uC-osrocyp008e02b1
Method
                  BLASTX
NCBI GI
                  g3395431
BLAST score
                  355
                  1.0e-33
E value
Match length
                  102
                  67
% identity
NCBI Description (AC004683) unknown protein [Arabidopsis thaliana]
                  419668
Seq. No.
Seq. ID
                  uC-osrocyp008e03a1
Method
                  BLASTX
NCBI GI
                  g3319370
BLAST score
                  215
E value
                  4.0e-17
                  50
Match length
% identity
                  78
NCBI Description (AF077409) contains similarity to C3HC4-type zinc fingers
                   (Pfam: zf-C3HC4.hmm, score: 32.94) [Arabidopsis thaliana]
                  419669
Seq. No.
Seq. ID
                  uC-osrocyp008e04b1
Method
                  BLASTX
NCBI GI
                  g100598
BLAST score
                   469
E value
                  3.0e - 56
Match length
                  141
% identity
                  ubiquitin / ribosomal protein S27a-1 - barley >gi_167073
NCBI Description
                   (M60175) ubiquitin [Hordeum vulgare]
Seq. No.
                  419670
Seq. ID
                  uC-osrocyp008e05b1
Method
                  BLASTX
NCBI GI
                  g2895866
BLAST score
                  463
E value
                  3.0e-46
```

uC-osrocyp008e01b1

Match length 123 % identity 77 NCBI Description (AF045770) methylmalonate semi-aldehyde dehydrogenase [Oryza sativa] Seq. No. 419671 Seq. ID uC-osrocyp008e07b1 Method BLASTX NCBI GI q4567232 BLAST score 298 8.0e-27 E value Match length 72 % identity 81 (AC007119) putative 40S ribosomal protein S25 [Arabidopsis NCBI Description thaliana] Seq. No. 419672 Seq. ID uC-osrocyp008e08b1 Method BLASTX NCBI GI q3258575 BLAST score 311 2.0e-28 E value 99 Match length % identity 61 (U89959) Hypothetical protein [Arabidopsis thaliana] NCBI Description 419673 Seq. No. uC-osrocyp008e09a1 Seq. ID Method BLASTN g20332 NCBI GI BLAST score 41 E value 2.0e-13 Match length 41 % identity 100 NCBI Description O.sativa RAc7 gene for actin 419674 Seq. No. uC-osrocyp008e11a1 Seq. ID Method BLASTX NCBI GI q1168537 BLAST score 296 9.0e-27 E value Match length 62 87 % identity ASPARTIC PROTEINASE PRECURSOR >gi 82458 pir JS0732 NCBI Description aspartic proteinase (EC 3.4.23.-) - rice >gi_218143_dbj_BAA02242_ (D12777) aspartic proteinase [Oryza sativa] 419675 Seq. No. uC-osrocyp008e12a1 Seq. ID

Method BLASTN
NCBI GI g3885887
BLAST score 462
E value 0.0e+00
Match length 462
% identity 100





Seq. No. 419676

Seq. ID uC-osrocyp008e12b1

Method BLASTX
NCBI GI g5802955
BLAST score 183
E value 6.0e-20
Match length 100
% identity 49

NCBI Description (AF178990) stress related protein [Vitis riparia]

Seq. No. 419677

Seq. ID uC-osrocyp008f01b1

Method BLASTX
NCBI GI g1172002
BLAST score 193
E value 3.0e-21
Match length 66
% identity 76

NCBI Description PHENYLALANINE AMMONIA-LYASE >gi_556424 (L36822)

phenylalanine ammonia lyase [Stylosanthes humilis]

Seq. No. 419678

Seq. ID uC-osrocyp008f02b1

Method BLASTN
NCBI GI g2895865
BLAST score 227
E value 1.0e-125
Match length 267
% identity 96

NCBI Description Oryza sativa methylmalonate semi-aldehyde dehydrogenase

(MMSDH1) mRNA, complete cds

Seq. No. 419679

Seq. ID uC-osrocyp008f03a1

Method BLASTX
NCBI GI g1703380
BLAST score 259
E value 3.0e-22
Match length 50
% identity 98

NCBI Description ADP-RIBOSYLATION FACTOR >gi 1132483 dbj BAA04607 (D17760)

ADP-ribosylation factor [Oryza sativa]

Seq. No. 419680

Seq. ID uC-osrocyp008f04b1

Method BLASTX
NCBI GI g2641619
BLAST score 595
E value 1.0e-61
Match length 122
% identity 88

NCBI Description (AF032468) ubiquitin-conjugating enzyme protein E2 [Zea

mays]

Seq. ID

Method

```
Seq. No.
                           419681
        Seq. ID
                           uC-osrocyp008f05b1
        Method
                           BLASTX
        NCBI GI
                           q1170937
        BLAST score
                           683
        E value
                           5.0e-72
        Match length
                           132
        % identity
                           98
        NCBI Description
                         S-ADENOSYLMETHIONINE SYNTHETASE 1 (METHIONINE
                          ADENOSYLTRANSFERASE 1) (ADOMET SYNTHETASE 1)
                           >gi_450549_emb CAA81481 (Z26867) S-adenosyl methionine
                           synthetase [Oryza sativa]
        Seq. No.
                           419682
        Seq. ID
                          uC-osrocyp008f06a1
        Method
                          BLASTN
        NCBI GI
                          q2331130
        BLAST score
                          205
        E value
                          1.0e-111
        Match length
                          245
        % identity
                          100
        NCBI Description Oryza sativa glycine-rich protein (OSGRP1) mRNA, complete
        Seq. No.
                          419683
        Seq. ID
                          uC-osrocyp008f07b1
        Method
                          BLASTX
        NCBI GI
                          q3885888
        BLAST score
                          270
        E value
                          1.0e-23
        Match length
                          104
        % identity
                          59
        NCBI Description (AF093632) high mobility group protein [Oryza sativa]
        Seq. No.
                          419684
        Seq. ID
                          uC-osrocyp008f08b1
        Method
                          BLASTX
        NCBI GI
                          g2293480
        BLAST score
                          410
        E value
                          5.0e-40
        Match length
                          89
        % identity
                          92
        NCBI Description (AF011331) glycine-rich protein [Oryza sativa]
        Seq. No.
                          419685
        Seq. ID
                          uC-osrocyp008f09a1
        Method
                          BLASTN
        NCBI GI
                          g1132482
        BLAST score
                          43
                          5.0e-15
        E value
Match length
                          183
       % identity
                          81
        NCBI Description Rice mRNA for ADP-ribosylation factor, complete cds
                          419686
        Seq. No.
```

55062

uC-osrocyp008f09b1

BLASTX

NCBI GI

BLAST score

```
NCBI GI
                   g3258575
BLAST score
                   509
E value
                   1.0e-51
Match length
                   136
% identity
                   71
NCBI Description (U89959) Hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   419687
Seq. ID
                   uC-osrocyp008f10a1
Method
                   BLASTN
                   g6016845
NCBI GI
BLAST score
                   41
E value
                   1.0e-13
Match length
                   77
% identity
                   88
NCBI Description Oryza sativa genomic DNA, chromosome 1, clone:P0711E10
Seq. No.
                   419688
Seq. ID
                   uC-osrocyp008f10b1
Method
                  BLASTX
NCBI GI
                   g2642648
BLAST score
                   801
E value
                   8.0e-86
Match length
                   177
% identity
                   89
NCBI Description
                  (AF033852) cytosolic heat shock 70 protein; HSC70-3
                   [Spinacia oleracea] >gi_2660768 (AF034616) cytosolic heat
                   shock 70 protein [Spinacia oleracea] >gi_2660770 (AF034617)
                   cytosolic heat shock 70 protein [Spinacia oleracea]
Seq. No.
                   419689
Seq. ID
                  uC-osrocyp008f11a1
Method
                  BLASTX
NCBI GI
                  q1169528
BLAST score
                   461
E value
                   6.0e-46
Match length
                  97
% identity
                   95
NCBI Description
                  ENOLASE 2 (2-PHOSPHOGLYCERATE DEHYDRATASE 2)
                   (2-PHOSPHO-D-GLYCERATE HYDRO-LYASE 2) >gi_602253 (U17973)
                  enolase [Zea mays]
Seq. No.
                  419690
Seq. ID
                  uC-osrocyp008f12b1
Method
                  BLASTX
NCBI GI
                  q3264767
BLAST score
                  216
E value
                  2.0e-17
Match length
                  55
% identity
                  71
NCBI Description (AF071893) AP2 domain containing protein [Prunus armeniaca]
Seq. No.
                  419691
Seq. ID
                  uC-osrocyp008g02b1
Method
                  BLASTN
```

55063

g2773153



E value 1.0e-82 Match length 184 % identity 96

NCBI Description Oryza sativa abscisic acid- and stress-inducible protein

(Asr1) mRNA, complete cds

Seq. No. 419692

Seq. ID uC-osrocyp008g03b1

Method BLASTX
NCBI GI g3132479
BLAST score 149
E value 4.0e-10
Match length 59
% identity 56

NCBI Description (AC003096) multidrug resistance-associated protein, AtMRP2

[Arabidopsis thaliana]

Seq. No. 419693

Seq. ID uC-osrocyp008g04b1

Method BLASTX
NCBI GI g2909781
BLAST score 716
E value 8.0e-76
Match length 179
% identity 77

NCBI Description (AF020288) MgATP-energized glutathione S-conjugate pump

[Arabidopsis thaliana]

Seq. No. 419694

Seq. ID uC-osrocyp008g05a1

Method BLASTX
NCBI GI g4574139
BLAST score 427
E value 5.0e-42
Match length 98
% identity 93

NCBI Description (AF073697) cysteine synthase [Oryza sativa]

Seq. No. 419695

Seq. ID uC-osrocyp008g06a1

Method BLASTX
NCBI GI g5091509
BLAST score 564
E value 3.0e-58
Match length 125
% identity 91

NCBI Description (AB023482) EST AU065533(C2174) corresponds to a region of

the predicted gene.; Similar to Homo sapiens splicing factor Prp8 mRNA, complete cds.(AF092565) [Oryza sativa]

Seq. No. 419696

Seq. ID uC-osrocyp008g08a1

Method BLASTX
NCBI GI g285741
BLAST score 200
E value 2.0e-15
Match length 81

Method

BLASTX

```
% identity
NCBI Description (D14550) EDGP precursor [Daúcus carota]
Seq. No.
                   419697
Seq. ID
                   uC-osrocyp008g09b1
Method
                   BLASTN
NCBI GI
                   q6016845
BLAST score
                   326
E value
                   0.0e + 00
Match length
                   442
                   93
% identity
NCBI Description Oryza sativa genomic DNA, chromosome 1, clone:P0711E10
Seq. No.
                   419698
Seq. ID
                  uC-osrocyp008g10b1
Method
                  BLASTX
NCBI GI
                  q5031275
BLAST score
                   556
                  4.0e-57
E value
Match length
                  143
                  73
% identity
NCBI Description (AF139496) unknown [Prunus armeniaca]
Seq. No.
                   419699
Seq. ID
                  uC-osrocyp008g11a1
Method
                  BLASTN
NCBI GI
                  q1009709
BLAST score
                  218
E valuė
                  1.0e-119
Match length
                   448
                  88
% identity
NCBI Description Oryza sativa pyruvate decarboxylase 2 (Pdc2) mRNA, complete
Seq. No.
                  419700
Seq. ID
                  uC-osrocyp008g12b1
Method
                  BLASTX
NCBI GÎ
                  g4972778
BLAST score
                  157
E value
                  3.0e-10
Match length
                  128
% identity
                  12
NCBI Description
                  (AF132196) unknown [Drosophila melanogaster]
Seq. No.
                  419701
Seq. ID
                  uC-osrocyp008h02b1
Method
                  BLASTN
NCBI GI
                  g736271
BLAST score
                  76
E value
                  6.0e-35
Match length
                  108
% identity
                  93
NCBI Description O.sativa hsp70 gene for heat shock protein
Seq. No.
                  419702
Seq. ID
                  uC-osrocyp008h04a1
```

```
NCBI GI
                   g5001830
BLAST score
                   324
E value
                   7.0e-30
Match length
                   61
% identity
                   98
                  (AF132743) 3-phosphoinositide-dependent protein kinase-1
NCBI Description
                   [Oryza sativa]
Seq. No.
                   419703
Seq. ID
                   uC-osrocyp008h04b1
Method
                   BLASTX
NCBI GI
                   g4587589
BLAST score
                   196
E value
                   6.0e-15
Match length
                   107
% identity
                   41
NCBI Description (AC007232) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   419704
Seq. ID
                  uC-osrocyp008h05a1
Method
                  BLASTX
NCBI GI
                  g4574139
BLAST score
                   408
E value
                   8.0e-40
Match length
                  98
% identity
                   88
NCBI Description (AF073697) cysteine synthase [Oryza sativa]
Seq. No.
                   419705
Seq. ID
                   uC-osrocyp008h06a1
Method
                   BLASTX
NCBI GI
                  g4567246
BLAST score
                   234
E value
                  2.0e-19
Match length
                   64
% identity
                   67
NCBI Description (AC007070) unknown protein [Arabidopsis thaliana]
Seq. No.
                   419706
Seq. ID
                   uC-osrocyp008h07b1
Method
                   BLASTX
NCBI GI
                   g1076809
BLAST score
                   708
E value
                   6.0e-75
Match length
                  153
% identity
                   88
                  H+-transporting ATPase (EC 3.6.1.35) - maize
NCBI Description
                   >gi_758355_emb_CAA59800 (X85805) H(+)-transporting ATPase
                   [Zea mays]
Seq. No.
                  419707
Seq. ID
                  uC-osrocyp008h08a1
Method
                  BLASTN
NCBI GI
                  g5091597
BLAST score
                  468
E value
                  0.0e + 00
Match length
                  468
```

```
% identity
  NCBI Description Oryza sativa chromosome 1 BAC 10A19I, complete sequence
  Seq. No.
                    419708
  Seq. ID
                   uC-osrocyp008h08b1
  Method
                   BLASTX
  NCBI GI
                   g5852203
  BLAST score
                   256
  E value
                   4.0e-22
  Match length
                   62
  % identity
                   79
  NCBI Description (AF033851) aldehyde reductase [Vigna radiata]
  Seq. No.
                   419709
  Seq. ID
                   uC-osrocyp008h10b1
 Method
                   BLASTX
 NCBI GI
                   g4093169
 BLAST score
                   409
 E value
                   8.0e-40
 Match length
                   111
  % identity
                   71
 NCBI Description (AF095933) p20-Arc [Dictyostelium discoideum]
 Seq. No.
                   419710
 Seq. ID
                   uC-osrocyp008h11b1
 Method
                   BLASTX
 NCBI GI
                   q451193
 BLAST score
                   364
 E value
                   1.0e-34
 Match length
                   98
 % identity
                   76
 NCBI Description (L28008) wali7 [Triticum aestivum]
                   >gi_1090845_prf 2019486B wali7 gene [Triticum aestivum]
 Seq. No.
                   419711
 Seq. ID
                   uC-osrocyp008h12b1
 Method
                   BLASTX
 NCBI GI
                   g118011
 BLAST score
                   531
 E value
                   3.0e-54
 Match length
                   99
 % identity
                   99
 NCBI Description
                   >gi 169786 (M63704) cytochrome c [Oryza sativa]
                   >gi_218249_dbj_BAA02159_ (D12634) 'cytochrome C' [Oryza
                   sativa]
 Seq. No.
                   419712
 Seq. ID
                   uC-osrocyp009a01a1
 Method
                   BLASTX
 NCBI GI
                   g2129550
BLAST score
                   194
 E value
                   1.0e-14
 Match length
                   48
 % identity
                   73
 NCBI Description calcium-dependent protein kinase (EC 2.7.1.-) CDPK6 -
                   Arabidopsis thaliana >gi_2129554_pir__S71901
```

calcium-dependent protein kinase 6 - Arabidopsis thaliana >gi_836940 (U20623) calcium-dependent protein kinase [Arabidopsis thaliana] >gi_836944 (U20625) calcium-dependent protein kinase [Arabidopsis thaliana] >gi_4454034_emb_CAA23031.1_ (AL035394) calcium-dependent protein kinase (CDPK6) [Arabidopsis thaliana]

Seq. No. 419713 Seq. ID uC-osrocyp009a02a1 Method BLASTX NCBI GI q464981 BLAST score 211 E value 2.0e-23 Match length 78 % identity 76

NCBI Description UBIQUITIN-CONJUGATING ENZYME E2-17 KD (UBIQUITIN-PROTEIN LIGASE) (UBIQUITIN CARRIER PROTEIN) >gi_388207 (L23762)

ubiquitin carrier protein [Lycopersicon esculentum]

Seq. No. 419714

Seq. ID uC-osrocyp009a02b1

Method BLASTX
NCBI GI g5263310
BLAST score 257
E value 5.0e-22
Match length 77
% identity 66

NCBI Description (AC007727) EST gb_N95925 comes from this gene. [Arabidopsis

thaliana]

Seq. No. 419715

Seq. ID uC-osrocyp009a03b1

Method BLASTX
NCBI GI g2959370
BLAST score 243
E value 2.0e-20
Match length 124
% identity 37

NCBI Description (AL022117) hypothetical protein [Schizosaccharomyces pombe]

Seq. No. 419716

Seq. ID uC-osrocyp009a04a1

Method BLASTX
NCBI GI g267056
BLAST score 419
E value 4.0e-41
Match length 83
% identity 96

NCBI Description SUCROSE SYNTHASE 1 (SUCROSE-UDP GLUCOSYLTRANSFERASE 1)

>gi_100710_pir__S25526 sucrose synthase (EC 2.4.1.13) rice >gi_20374_emb_CAA78747_ (Z15028) sucrose synthase

[Oryza sativa]

Seq. No. 419717

Seq. ID uC-osrocyp009a06b1

Method BLASTX NCBI GI g1665771

NCBI GI

E value

BLAST score

q571484

6.0e-37

384

```
BLAST score
                   154
E value
                   5.0e-10
Match length
                   126
% identity
                   33
NCBI Description
                   (D87440) Similar to Plasmodium falciparum glutamic
                   acid-rich protein precursor (A54514) [Homo sapiens]
Seq. No.
                   419718
Seq. ID
                   uC-osrocyp009a07a1
Method
                   BLASTX
NCBI GI
                   q3258575
BLAST score
                   284
E value
                   3.0e-25
Match length
                   76
% identity
                   72
NCBI Description (U89959) Hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   419719
Seq. ID
                   uC-osrocyp009a07b1
Method
                   BLASTX
NCBI GI
                   q82734
BLAST score
                   697
E value
                   1.0e-73
Match length
                   145
% identity
                   29
NCBI Description
                  ubiquitin precursor - maize (fragment)
                   >gi_226763_prf__1604470A poly-ubiquitin [Zea mays]
Seq. No.
                   419720
Seq. ID
                   uC-osrocyp009a08b1
Method
                   BLASTX
NCBI GI
                   g4666287
BLAST score
                   350
E value
                   3.0e-42
Match length
                   134
% identity
                   71
NCBI Description
                  (D85764) cytosolic monodehydroascorbate reductase [Oryza
                   sativa]
Seq. No.
                   419721
Seq. ID
                   uC-osrocyp009a10a1
Method
                  BLASTX
NCBI GI
                   g3176664
BLAST score
                   157
E value
                   3.0e-10
Match length
                  58
% identity
                   57
NCBI Description
                  (AC004393) Contains similarity to beta scruin gb_Z47541
                   from Limulus polyphemus. ESTs gb_T04493 and gb_\overline{A}A585955
                  come from this gene. [Arabidopsis thaliana]
Seq. No.
                  419722
Seq. ID
                  uC-osrocyp009a10b1
Method
                  BLASTX
```

Match length 106 % identity NCBI Description (U16727) peroxidase precursor [Medicago truncatula] Seq. No. 419723 Seq. ID uC-osrocyp009a12a1 Method BLASTX NCBI GI g3822223 BLAST score 300 E value 3.0e-27 Match length 95 % identity 53 NCBI Description (AF077955) branched-chain alpha keto-acid dehydrogenase E1 alpha subunit [Arabidopsis thaliana] Seq. No. 419724 Seq. ID uC-osrocyp009b01a1 Method BLASTX NCBI GI q4680193 BLAST score 347 E value 1.0e-32 Match length 102 % identity 69 NCBI Description (AF111710) putative farnesyl pyrophosphate synthase [Oryza sativa subsp. indica] Seq. No. 419725 Seq. ID uC-osrocyp009b02a1 Method BLASTX NCBI GI g1076746 BLAST score 242 E value 2.0e-20 Match length 68 % identity 71 NCBI Description heat shock protein 70 - rice (fragment) >gi_763160_emb_CAA47948_ (X67711) heat shock protein 70 [Oryza sativa] Seq. No. 419726 Seq. ID uC-osrocyp009b02b1 Method BLASTX NCBI GI g1084461 BLAST score 167 E value 1.0e-13 Match length 71 % identity 52 NCBI Description RCc3 protein - rice >gi_786132 (L27208) RCc3 [Oryza sativa] Seq. No. 419727 Seq. ID uC-osrocyp009b03b1 Method BLASTX

Method BLASTX
NCBI GI 94049341
BLAST score 464
E value 3.0e-46
Match length 137
% identity 67

NCBI Description (AL034567) putative protein [Arabidopsis thaliana]

Seq. No. 419728 Seq. ID uC-osrocyp009b05b1 Method BLASTX NCBI GI g2541876 BLAST score 173 E value 3.0e-12 Match length 116 % identity 40 NCBI Description (D26015) CND41, chloroplast nucleoid DNA binding protein [Nicotiana tabacum] Seq. No. 419729 Seq. ID uC-osrocyp009b07a1 Method BLASTX NCBI GI g1076746 BLAST score 301 E value 3.0e-27 Match length 88 % identity 73 NCBI Description heat shock protein 70 - rice (fragment) >gi_763160_emb CAA47948 (X67711) heat shock protein 70 [Oryza sativa] Seq. No. 419730 Seq. ID uC-osrocyp009b07b1 Method BLASTX NCBI GI g5596484 BLAST score 839 E value 3.0e-90 Match length 173 % identity NCBI Description (AL096882) beta-adaptin-like protein [Arabidopsis thaliana] Seq. No. 419731 Seq. ID uC-osrocyp009b08a1 Method BLASTN NCBI GI g3273242 BLAST score 372 E value 0.0e+00Match length 404 % identity 98 NCBI Description Oryza sativa mRNA for NLS receptor, complete cds Seq. No. 419732 Seq. ID uC-osrocyp009b08b1 Method BLASTX NCBI GI g4502043 BLAST score 341 E value 7.0e - 32Match length 166 % identity 44 NCBI Description aldehyde dehydrogenase 7 >gi 1169285 sp P43353 DHA7 HUMAN

[Homo sapiens]

ALDEHYDE DEHYDROGENASE 7 >gi_601780 (U10868) ALDH7 [Homo sapiens] >gi_1093619_prf__2104286A aldehyde dehydrogenase



```
Seq. No.
                   419733
Seq. ID
                   uC-osrocyp009b11a1
Method
                   BLASTX
NCBI GI
                   g417154
BLAST score
                   373
E value
                   3.0e-36
Match length
                   100
% identity
                   85
                   HEAT SHOCK PROTEIN 82 >gi_100685_pir__S25541 heat shock
NCBI Description
                   protein 82 - rice (strain Taichung Native One)
                   >gi_20256_emb_CAA77978_ (Z11920) heat shock protein 82
                   (HSP82) [Oryza sativa]
Seq. No.
                   419734
Seq. ID
                   uC-osrocyp009b11b1
Method
                   BLASTX
NCBI GI
                   q4678384
BLAST score
                   263
E value
                   7.0e-23
Match length
                   59
% identity
                   83
NCBI Description (AL049656) putative protein [Arabidopsis thaliana]
Seq. No.
                   419735
Seq. ID
                   uC-osrocyp009b12a1
Method
                   BLASTX
NCBI GI
                   q2271477
BLAST score
                   228
E value
                   1.0e-18
Match length
                   44
                   95
% identity
NCBI Description (AF009631) AP47/50p [Arabidopsis thaliana]
Seq. No.
                   419736
Seq. ID
                   uC-osrocyp009c02a1
Method
                   BLASTX
NCBI GI
                   g3695403
BLAST score
                   255
E value
                   7.0e-22
Match length
                   75
% identity
                   67
                  (AF096373) contains similarity to the pfkB family of
NCBI Description
                   carbohydrate kinases (Pfam: PF00294, E=1.6e-75)
                   [Arabidopsis thaliana] >gi 4538955 emb CAB39779.1
                   (AL049488) fructokinase-like protein [Arabidopsis thaliana]
Seq. No.
                   419737
Seq. ID
                  uC-osrocyp009c02b1
Method
                  BLASTX
NCBI GI
                  g4512699
BLAST score
                  592
```

E value 2.0e-61 Match length 169 % identity 66

(AC006569) putative NADH-ubiquinone oxireductase NCBI Description

[Arabidopsis thaliana]

E value

4.0e-37

```
Seq. No.
                   419738
Seq. ID
                   uC-osrocyp009c03a1
Method
                   BLASTX
NCBI GI
                   q3377509
BLAST score
                   384
E value
                   6.0e-37
Match length
                   145
% identity
                   48
NCBI Description (AF056027) auxin transport protein REH1 [Oryza sativa]
Seq. No.
                   419739
Seq. ID
                   uC-osrocyp009c03b1
Method
                  BLASTX
NCBI GI
                   g4056488
BLAST score
                   329
E value
                   2.0e-30
Match length
                   83
% identity
                   70
NCBI Description (AC005896) unknown protein [Arabidopsis thaliana]
                   419740
Seq. No.
                  uC-osrocyp009c04a1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4559380
BLAST score
                   185
E value
                   9.0e-14
Match length
                   66
% identity
                   56
NCBI Description
                  (AC006526) putative auxin-responsive GH3 protein
                   [Arabidopsis thaliana]
                   419741
Seq. No.
Seq. ID
                  uC-osrocyp009c04b1
Method
                  BLASTX
NCBI GI
                  g4581119
BLAST score
                  351
E value
                  4.0e-33
Match length
                  124
% identity
                  57
NCBI Description (AC005825) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  419742
Seq. ID
                  uC-osrocyp009c05b1
Method
                  BLASTX
NCBI GI
                  g5689377
BLAST score
                  177
E value
                  1.0e-12
Match length
                  78
% identity
                  45
NCBI Description (AB030653) epsilon-adaptin [Homo sapiens]
Seq. No.
                  419743
Seq. ID
                  uC-osrocyp009c06a1
Method
                  BLASTX
NCBI GI
                  g133867
BLAST score
                  385
```

```
Match length
                      74
    % identity
                      96
    NCBI Description
                      40S RIBOSOMAL PROTEIN S11 >gi_82722_pir__S16577 ribosomal
                      protein S11 - maize >gi_22470_emb_CAA39438_ (X55967)
                      ribosomal protein S11 [Zea mays]
                      419744
    Seq. No.
    Seq. ID
                      uC-osrocyp009c06b1
    Method
                      BLASTX
    NCBI GI
                      g2467088
    BLAST score
                      197
                      5.0e-15
    E value
    Match length
                      76
    % identity
                      49
    NCBI Description (AJ001911) putative Ckc2 [Arabidopsis thaliana]
                      419745
    Seq. No.
    Seq. ID
                      uC-osrocyp009c07a1
    Method
                      BLASTX
    NCBI GI
                      q4585976
    BLAST score
                      221
                      8.0e-18
    E value
                      62
    Match length
                      63
    % identity
    NCBI Description (AC005287) Unknown protein [Arabidopsis thaliana]
                      419746
    Seq. No.
    Seq. ID
                      uC-osrocyp009c07b1
    Method
                      BLASTX
    NCBI GI
                      q2191135
    BLAST score
                      257
                      5.0e-22
    E value
    Match length
                      154
                      33
    % identity
    NCBI Description (AF007269) A IG002N01.14 gene product [Arabidopsis
                      thaliana]
    Seq. No.
                      419747
    Seq. ID
                      uC-osrocyp009c08b1
    Method
                      BLASTX
    NCBI GI
                      g3169174
    BLAST score
                      317
    E value
                      4.0e-29
    Match length
                      121
    % identity
                      50
                     (AC004401) putative serine carboxypeptidase I [Arabidopsis
    NCBI Description
                      thaliana]
    Seq. No.
                      419748
    Seq. ID
                      uC-osrocyp009c09a1
    Method
                      BLASTX
NCBI GI
                      g466044
    BLAST score
                      211
    E value
                      1.0e-16
    Match length
                      75
                      49
    % identity
    NCBI Description HYPOTHETICAL ZINC FINGER PROTEIN ZK686.4 IN CHROMOSOME III
```

E value

Match length

% identity

4.0e-42

112

79

```
GenBank: M88869 and T01933; putative [Caenorhabditis
                   elegans]
Seq. No.
                   419749
Seq. ID
                   uC-osrocyp009c09b1
Method
                   BLASTX
NCBI GI
                   q4895248
BLAST score
                   396
E value
                   2.0e-38
Match length
                   86
% identity
                   88
                  (AC007659) putative mitochondrial elongation factor G
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                   419750
Seq. ID
                   uC-osrocyp009c10b1
Method
                   BLASTX
NCBI GI
                   q728881
BLAST score
                   157
                   2.0e-10
E value
                   70
Match length
% identity
                   47
NCBI Description
                  ADP-RIBOSYLATION FACTOR 2 >gi 1079047 pir A53859
                   ADP-ribosylation factor 2 - fruit fly (Drosophila
                  melanogaster) >gi_507232 (L25062) ADP ribosylation factor 2
                   [Drosophila melanogaster]
Seq. No.
                   419751
Seq. ID
                   uC-osrocyp009c11a1
Method
                   BLASTX
NCBI GI
                   q4335735
BLAST score
                   164
E value
                   3.0e-11
Match length
                  75
% identity
                   47
NCBI Description (AC006248) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   419752
Seq. ID
                  uC-osrocyp009d01b1
Method
                  BLASTN
NCBI GI
                   g218180
BLAST score
                   188
E value
                  1.0e-101
Match length
                  209
                   97
% identity
NCBI Description Rice mRNA for oryzain alpha (EC 3.4.22)
Seq. No.
                   419753
                  uC-osrocyp009d02a1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2293566
BLAST score
                  429
```

>gi_630780_pir__S44909 ZK686.4 protein - Caenorhabditis
elegans >gi_304346 (L17337) coded for by C. elegans cDNAs

% identity

NCBI Description

84

GAPC3 [Zea mays]



```
NCBI Description (AF012896) ADP-ribosylation factor 1 [Oryza sativa]
Seq. No.
                  419754
Seq. ID
                  uC-osrocyp009d03b1
Method
                  BLASTX
NCBI GI
                  q1076746
                  835
BLAST score
E value
                  8.0e-90
Match length
                  164
                  99
% identity
NCBI Description heat shock protein 70 - rice (fragment)
                  >gi_763160_emb_CAA47948_ (X67711) heat shock protein 70
                  [Oryza sativa]
                  419755
Seq. No.
Seq. ID
                  uC-osrocyp009d04b1
Method
                  BLASTX
NCBI GI
                  g82496
BLAST score
                  670
E value
                  2.0e-70
                  153
Match length
                  86
% identity
NCBI Description phenylalanine ammonia-lyase (EC 4.3.1.5) - rice
Seq. No.
                  419756
Seq. ID
                  uC-osrocyp009d05a1
Method
                  BLASTX
NCBI GI
                  g1170937
BLAST score
                  285
                  2.0e-25
E value
Match length
                  61
                  98
% identity
NCBI Description
                  S-ADENOSYLMETHIONINE SYNTHETASE 1 (METHIONINE
                  ADENOSYLTRANSFERASE 1) (ADOMET SYNTHETASE 1)
                  >gi_450549 emb CAA81481 (Z26867) S-adenosyl methionine
                  synthetase [Oryza sativa]
Seq. No.
                  419757
Seq. ID
                  uC-osrocyp009d05b1
Method
                  BLASTX
NCBI GI
                  g3702327
BLAST score
                  176
E value
                  1.0e-12
Match length
                  130
% identity
                  41
NCBI Description (AC005397) unknown protein [Arabidopsis thaliana]
                  419758
Seq. No.
                  uC-osrocyp009d06b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1184774
BLAST score
                  656
E value
                  8.0e-69
                  151
Match length
```

55076

(U45856) cytosolic glyceroldehyde-3-phosphate dehydrogenase

E value

Match length

% identity

1.0e-42

168

51

```
419759
Seq. No.
Seq. ID
                   uC-osrocyp009d07a1
Method
                   BLASTX
                   g549063
NCBI GI
BLAST score
                   362
E value
                   2.0e-34
Match length
                   68
% identity
                   100
                   TRANSLATIONALLY CONTROLLED TUMOR PROTEIN HOMOLOG (TCTP)
NCBI Description
                   >gi_1072464_pir__A38958 IgE-dependent histamine-releasing
factor homolog - rice >gi_303835_dbj_BAA02151_ (D12626)
                   21kd polypeptide [Oryza sativa]
                   419760
Seq. No.
Seq. ID
                   uC-osrocyp009d09b1
Method
                   BLASTX
NCBI GI
                   q82496
BLAST score
                   590
E value
                   4.0e-61
Match length
                   147
% identity
                   80
NCBI Description phenylalanine ammonia-lyase (EC 4.3.1.5) - rice
Seq. No.
                   419761
Seq. ID
                   uC-osrocyp009d10b1
Method
                   BLASTX
NCBI GI
                   g120666
BLAST score
                   295
E value
                   1.0e-55
Match length
                   152
% identity
                   71
                   GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC
NCBI Description
                   >gi_66012_pir__DESKG glyceraldehyde-3-phosphate
                   dehydrogenase (EC 1.2.1.12) - garden snapdragon
Seq. No.
                   419762
Seq. ID
                   uC-osrocyp009d11a1
Method
                   BLASTX
NCBI GI
                   g129591
BLAST score
                   199
E value
                   2.0e-15
Match length
                   39
% identity
                   90
NCBI Description
                  PHENYLALANINE AMMONIA-LYASE >qi 295824 emb CAA34226
                   (X16099) phenylalanine ammonia-lyase [Oryza sativa]
                   419763
Seq. No.
                   uC-osrocyp009d11b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2252834
BLAST score
                   432
```

55077

NCBI Description (AF013293) similar to light repressible receptor protein

kinase [Arabidopsis thaliana]

```
>gi_6049876_gb_AAF02791.1_AF195115_11 (AF195115) similar to
light repressible receptor protein kinase [Arabidopsis
thaliana]
```

Seq. ID uC-osrocyp009e02b1
Method BLASTX
NCBI GI g82496
BLAST score 598
E value 4.0e-62
Match length 144
% identity 81

Seq. No.

NCBI Description phenylalanine ammonia-lyase (EC 4.3.1.5) - rice

Seq. No. 419765

Seq. ID uC-osrocyp009e03a1

Method BLASTX
NCBI GI g3023816
BLAST score 302
E value 2.0e-27
Match length 62
% identity 94

NCBI Description GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC

>gi 968996 (U31676) glyceraldehyde-3-phosphate

dehydrogenase [Oryza sativa]

Seq. No. 419766

Seq. ID uC-osrocyp009e03b1

Method BLASTX
NCBI GI g3559805
BLAST score 725
E value 7.0e-77
Match length 180
% identity 72

NCBI Description (AJ006787) putative phytochelatin synthetase [Arabidopsis

thaliana]

Seq. No. 419767

Seq. ID uC-osrocyp009e04a1

Method BLASTX
NCBI GI g129591
BLAST score 269
E value 2.0e-23
Match length 49
% identity 100

NCBI Description PHENYLALANINE AMMONIA-LYASE >gi_295824_emb_CAA34226_ (X16099) phenylalanine ammonia-lyase [Oryza sativa]

Seq. No. 419768

Seq. ID uC-osrocyp009e04b1

Method BLASTX
NCBI GI g3559805
BLAST score 200
E value 2.0e-15
Match length 104
% identity 43

NCBI Description (AJ006787) putative phytochelatin synthetase [Arabidopsis

thaliana]

Seq. No. 419769 Seq. ID uC-osrocyp009e05b1 Method BLASTX NCBI GI g1136122 BLAST score 518 E value 8.0e-53 Match length 96 % identity 98 NCBI Description (X91807) alfa-tubulin [Oryza sativa] Seq. No. 419770 Seq. ID uC-osrocyp009e06b1 Method BLASTX NCBI GI g549063 BLAST score 425 E value 1.0e-41 Match length 142 % identity 51 TRANSLATIONALLY CONTROLLED TUMOR PROTEIN HOMOLOG (TCTP) NCBI Description >gi_1072464_pir__A38958 IgE-dependent histamine-releasing factor homolog - rice >gi_303835_dbj_BAA02151_ (D12626) 21kd polypeptide [Oryza sativa] Seq. No. 419771 Seq. ID uC-osrocyp009e07a1 Method BLASTX NCBI GI g120668 BLAST score 424 E value 1.0e-41 96 Match length 84 % identity NCBI Description GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC >gi_82399_pir__A24159 glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1.12), cytosolic - barley (fragment) >gi_167044 (M36650) glyceraldehyde-3-phosphate dehydrogenase [Hordeum vulgare] >gi 225347 prf 1301218A dehydrogenase, glyceraldehydephosphate [Hordeum vulgare var. distichum] Seq. No. 419772 Seq. ID uC-osrocyp009e08b1 Method BLASTX NCBI GI g1170937 BLAST score 514 E value 3.0e-52 Match length 113 89 % identity NCBI Description S-ADENOSYLMETHIONINE SYNTHETASE 1 (METHIONINE ADENOSYLTRANSFERASE 1) (ADOMET SYNTHETASE 1) >gi_450549_emb_CAA81481_ (Z26867) S-adenosyl methionine synthetase [Oryza sativa]

Seq. No. 419773

Seq. ID uC-osrocyp009e11a1

Method BLASTN

E value

1.0e-36

```
NCBI GI
                    g20332
BLAST score
                    34
E value
                    2.0e-09
Match length
                    62
% identity
                    89
NCBI Description O.sativa RAc7 gene for actin
Seq. No.
                    419774
Seq. ID
                    \verb"uC-osrocyp009e11b1"
Method
                    BLASTX
NCBI GI
                    g1351974
BLAST score
                    580
E value
                    7.0e-60
Match length
                    119
% identity
                    95
NCBI Description ADP-RIBOSYLATION FACTOR >gi_1076788_pir_ S49325
                    ADP-ribosylation factor - maize >gi_1076789_pir_ S53486
ADP-ribosylation factor - maize >gi_556686_emb_CAA56351_
                    (X80042) ADP-ribosylation factor [Zea mays]
Seq. No.
                    419775
Seq. ID
                    uC-osrocyp009e12a1
Method
                    BLASTN
NCBI GI
                    g218180
BLAST score
                    115
E value
                    6.0e-58
Match length
                    207
% identity
                    89
NCBI Description Rice mRNA for oryzain alpha (EC 3.4.22)
Seq. No.
                    419776
Seq. ID
                    uC-osrocyp009e12b1
Method
                    BLASTX
NCBI GI
                    g4539525
BLAST score
                    203
E value
                    1.0e-15
Match length
                    158
% identity
NCBI Description (AJ012370) NAALADase II protein [Homo sapiens]
Seq. No.
                    419777
Seq. ID
                   uC-osrocyp009f03a1
Method
                   BLASTN
NCBI GI
                    g5148935
BLAST score
                    258
E value
                   1.0e-143
Match length
                   334
% identity
                   94
NCBI Description Oryza sativa NADP-specific isocitrate dehydrogenase mRNA,
                   complete cds
Seq. No.
                   419778
Seq. ID
                   uC-osrocyp009f03b1
Method
                   BLASTX
NCBI GI
                   g4836901
BLAST score
                   382
```



```
88
        Match length
        % identity
                           81
        NCBI Description
                          (AC007369) Unknown protein [Arabidopsis thaliana]
                           419779
        Seq. No.
        Seq. ID
                           uC-osrocyp009f04a1
        Method
                           BLASTX
        NCBI GI
                           q4895248
        BLAST score
                           651
        E value
                           3.0e-68
        Match length
                           154
% laentity
NCBI Description
                           81
                          (AC007659) putative mitochondrial elongation factor G
                           [Arabidopsis thaliana]
                           419780
        Seq. No.
        Seq. ID
                           uC-osrocyp009f05a1
        Method
                           BLASTX
        NCBI GI
                           q584892
        BLAST score
                           345
        E value
                           2.0e-32
        Match length
                           100
                           55
        % identity
                          SERINE CARBOXYPEPTIDASE I PRECURSOR (CARBOXYPEPTIDASE C)
        NCBI Description
                           >gi_629805_pir__S43516 serine carboxypeptidase I - rice
                           >gi_409580_dbj_BAA04510_ (D17586) serine carboxypeptidase I
                           [Oryza sativa]
        Seq. No.
                           419781
                           uC-osrocyp009f05b1
        Seq. ID
        Method
                           BLASTX
        NCBI GI
                           g5302799
        BLAST score
                           273
        E value
                           7.0e-24
        Match length
                           151
        % identity
                           39
        NCBI Description (Z97341) gibberellin oxidase-like protein [Arabidopsis
                           thaliana]
        Seq. No.
                           419782
        Seq. ID
                           uC-osrocyp009f06b1
        Method
                           BLASTX
        NCBI GI
                           g4585976
        BLAST score
                           251
        E value
                           2.0e-21
                           97
        Match length
                           53
        % identity
        NCBI Description (AC005287) Unknown protein [Arabidopsis thaliana]
        Seq. No.
                           419783
        Seq. ID
                           uC-osrocyp009f07b1
```

Method BLASTX NCBI GI g133867 BLAST score 372 E value 1.0e-35 Match length 92 % identity 80

```
NCBI Description 40S RIBOSOMAL PROTEIN S11 >gi 82722 pir S16577 ribosomal
                  protein S11 - maize >gi 22470 emb_CAA39438_ (X55967)
                  ribosomal protein S11 [Zea mays]
                  419784
Seq. No.
Seq. ID
                  uC-osrocyp009f09b1
                  BLASTX
Method
NCBI GI
                  g4559380
                   529
BLAST score
                   6.0e-54
E value
                  170
Match length
                   57
% identity
                  (AC006526) putative auxin-responsive GH3 protein
NCBI Description
                   [Arabidopsis thaliana]
                   419785
Seq. No.
Seq. ID
                   uC-osrocyp009f10b1
Method
                   BLASTX
NCBI GI
                   q3785972
                   158
BLAST score
                   2.0e-10
E value
                   50
Match length
                   60
% identity
                  (AC005560) putative auxin transport protein [Arabidopsis
NCBI Description
                   thaliana] >gi_4262249_gb_AAD14542_ (AC006200) putative
                   auxin transport protein [Arabidopsis thaliana]
                   419786
Seq. No.
Seq. ID
                   uC-osrocyp009f11a1
Method
                   BLASTX
NCBI GI
                   q4512699
BLAST score
                   354
                   2.0e-33
E value
Match length
                   87
% identity
                   75
NCBI Description (AC006569) putative NADH-ubiquinone oxireductase
                   [Arabidopsis thaliana]
Seq. No.
                   419787
                   uC-osrocyp009f11b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g1052973
BLAST score
                   234
                   3.0e-32
E value
                   118
Match length
                   64
% identity
NCBI Description (U37838) fructokinase [Beta vulgaris]
                   419788
Seq. No.
                   uC-osrocyp009f12b1
Seq. ID
Method
                   BLASTN
                   g6015437
NCBI GI
                   37
BLAST score
E value
                   4.0e-11
                   46
Match length
                   65
% identity
NCBI Description Homo sapiens PEX1 mRNA, complete cds
```

```
Seq. No.
                  419789
Seq. ID
                  uC-osrocyp009g01b1
                  BLASTX
Method
NCBI GI
                  q283008
                  276
BLAST score
                   2.0e-24
E value
Match length
                  72
                  78
% identity
NCBI Description
                  sucrose synthase (EC 2.4.1.13) - rice
                  >gi 20366 emb CAA46017 (X64770) sucrose synthase [Oryza
                  satīva]
                   419790
Seq. No.
Seq. ID
                  uC-osrocyp009g02a1
                  BLASTX
Method
NCBI GI
                  q4678384
BLAST score
                   217
E value
                   2.0e-17
Match length
                   64
                   62
% identity
NCBI Description (AL049656) putative protein [Arabidopsis thaliana]
                   419791
Seq. No.
                  uC-osrocyp009g02b1
Seq. ID
                  BLASTX
Method
                  q417154
NCBI GI
BLAST score
                   230
E value
                   5.0e-27
Match length
                   92
                   67
% identity
NCBI Description HEAT SHOCK PROTEIN 82 >gi 100685 pir S25541 heat shock
                  protein 82 - rice (strain Taichung Native One)
                   >gi 20256 emb CAA77978 (Z11920) heat shock protein 82
                   (HSP82) [Oryza sativa]
                   419792
Seq. No.
                   uC-osrocyp009g05b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3273243
BLAST score
                   645
                   2.0e-67
E value
Match length
                   147
                   90
% identity
                  (AB004660) NLS receptor [Oryza sativa]
NCBI Description
                   >gi_3273245_dbj_BAA31166_ (AB004814) NLS receptor [Oryza
                   sativa]
Seq. No.
                   419793
                   uC-osrocyp009g06a1
Seq. ID
Method
                   BLASTX
NCBI GI
                  g5596484
BLAST score
                   332
E value
                   9.0e - 31
                   97
Match length
                   63
% identity
                  (AL096882) beta-adaptin-like protein [Arabidopsis thaliana]
NCBI Description
```

Seq. No.

Match length

% identity

36

72

419794

Seq. ID uC-osrocyp009g06b1 Method BLASTX NCBI GI q1076746 BLAST score 822 3.0e-88 E value Match length 160 100 % identity heat shock protein 70 - rice (fragment) NCBI Description >gi 763160 emb CAA47948 (X67711) heat shock protein 70 [Oryza sativa] 419795 Seq. No. Seq. ID uC-osrocyp009g08a1 Method BLASTX NCBI GI q2541876 BLAST score 218 E value 1.0e-17 122 Match length % identity 39 NCBI Description (D26015) CND41, chloroplast nucleoid DNA binding protein [Nicotiana tabacum] 419796 Seq. No. Seq. ID uC-osrocyp009g08b1 Method BLASTX NCBI GI g4586246 BLAST score 362 E value 2.0e-34Match length 150 % identity 47 NCBI Description (AL049640) putative protein [Arabidopsis thaliana] 419797 Seq. No. uC-osrocyp009g10b1 Seq. ID Method BLASTX NCBI GI g5921932 BLAST score 446 E value 3.0e-44Match length 164 57 % identity NCBI Description CYTOCHROME P450 84A1 (FERULATE-5-HYDROXYLASE) (F5H) >gi 1488255 (U38416) ferulate-5-hydroxylase [Arabidopsis thaliana] >gi 2961381 emb CAA18128 (AL022141) ferulate-5-hydroxylase (FAH1) [Arabidopsis thaliana] >gi_3925365 (AF068574) ferulate-5-hydroxylase [Arabidopsis thaliana] 419798 Seq. No. Seq. ID uC-osrocyp009g11a1 Method BLASTX NCBI GI g1084462 BLAST score 160 E value 1.0e-10

```
NCBI Description RCg2 protein - rice >gi_786130 (L27209) RCc2 [Oryza sativa]
                  >gi_786134 (L27210) root-specific protein [Oryza sativa]
                  419799
Seq. No.
Seq. ID
                  uC-osrocyp009g11b1
                  BLASTX
Method
                  q1076746
NCBI GI
                  601
BLAST score
                  2.0e-62
E value
                  131
Match length
                  89
% identity
                  heat shock protein 70 - rice (fragment)
NCBI Description
                  >gi 763160 emb CAA47948 (X67711) heat shock protein 70
                  [Oryza sativa]
                  419800
Seq. No.
Seq. ID
                  uC-osrocyp009g12b1
                  BLASTX
Method
                  g4680193
NCBI GI
BLAST score
                  518
                  1.0e-52
E value
                  164
Match length
                  66
% identity
NCBI Description (AF111710) putative farnesyl pyrophosphate synthase [Oryza
                  sativa subsp. indica]
                  419801
Seq. No.
Seq. ID
                  uC-osrocyp009h02b1
                  BLASTX
Method
NCBI GI
                  q4262142
BLAST score
                  168
E value
                   1.0e-11
                   58
Match length
                   57
% identity
NCBI Description
                  (AC005275) putative alcohol dehydrogenase [Arabidopsis
                   thaliana]
                   419802
Seq. No.
Seq. ID
                   uC-osrocyp009h03a1
Method
                   BLASTX
NCBI GI
                   q520570
BLAST score
                   179
                   5.0e-13
E value
Match length
                   61
                   59
% identity
NCBI Description (U12315) peroxidase [Cenchrus ciliaris]
Seq. No.
                   419803
                   uC-osrocyp009h03b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3176664
BLAST score
                   160
E value
                   1.0e-16
                   106
Match length
                   52
% identity
NCBI Description (AC004393) Contains similarity to beta scruin gb Z47541
                   from Limulus polyphemus. ESTs gb_T04493 and gb_AA585955
```

BLAST score

642

come from this gene. [Arabidopsis thaliana]

419804 Seq. No. Seq. ID uC-osrocyp009h04a1 Method BLASTX g3738288 NCBI GI 165 BLAST score E value 3.0e-11Match length 54 59 % identity (AC005309) auxin-responsive GH3-like protein [Arabidopsis NCBI Description thaliana] 419805 Seq. No. Seq. ID uC-osrocyp009h05a1 Method BLASTX NCBI GI q4666287 BLAST score 439 E value 2.0e-43 Match length 86 98 % identity NCBI Description (D85764) cytosolic monodehydroascorbate reductase [Oryza satival 419806 Seq. No. uC-osrocyp009h05b1 Seq. ID Method BLASTX NCBI GI q3176686 BLAST score 259 E value 3.0e-22 Match length 165 % identity (AC003671) Similar to high affinity potassium transporter, NCBI Description HAK1 protein gb U22945 from Schwanniomyces occidentalis. [Arabidopsis thaliana] Seq. No. 419807 Seq. ID uC-osrocyp009h06a1 Method BLASTX NCBI GI q481477 BLAST score 430 E value 2.0e-42 Match length 89 % identity 17 NCBI Description ubiquitin precursor - rice >qi 416038 emb CAA53665 (X76064) polyubiquitin [Oryza sativa] >gi 1574944 (U37687) polyubiquitin [Oryza sativa] >gi 6013289 gb AAF01315.1 AF184279 1 (AF184279) polyubiquitin [Oryza sativa] >gi 6013291 gb AAF01316.1 AF184280 1 (AF184280) polyubiquitin [Oryza sativa] Seq. No. 419808 uC-osrocyp009h06b1 Seq. ID Method BLASTX NCBI GI q3258575



E value 4.0e-67
Match length 165
% identity 76

NCBI Description (U89959) Hypothetical protein [Arabidopsis thaliana]

Seq. No. 419809

Seq. ID uC-osrocyp009h09b1

Method BLASTX
NCBI GI g283008
BLAST score 860
E value 9.0e-93
Match length 172
% identity 96

NCBI Description sucrose synthase (EC 2.4.1.13) - rice

 $>gi_20366_emb_CAA46017_ (X64770)$ sucrose synthase [Oryza

satīva]

Seq. No. 419810

Seq. ID uC-osrocyp009h10a1

Method BLASTX
NCBI GI g2959370
BLAST score 144
E value 9.0e-09
Match length 62
% identity 42

NCBI Description (AL022117) hypothetical protein [Schizosaccharomyces pombe]

Seq. No. 419811

Seq. ID uC-osrocyp009h11a1

Method BLASTX
NCBI GI g5263310
BLAST score 146
E value 5.0e-09
Match length 34
% identity 74

NCBI Description (AC007727) EST gb_N95925 comes from this gene. [Arabidopsis

thaliana]

Seq. No. 419812

Seq. ID uC-osrocyp009h11b1

Method BLASTX
NCBI GI g464987
BLAST score 363
E value 1.0e-34
Match length 102
% identity 72

NCBI Description UBIQUITIN-CONJUGATING ENZYME E2-17 KD 10 (UBIQUITIN-PROTEIN

LIGASE 10) (UBIQUITIN CARRIER PROTEIN 10)

>gi_421858_pir__S32672 ubiquitin--protein ligase (EC

6.3.2.19) UBC10 - Arabidopsis thaliana

>gi_297878_emb_CAA78715_ (Z14991) ubiquitin conjugating
enzyme [Arabidopsis thaliana] >gi_349213 (L00640) ubiquitin

conjugating enzyme [Arabidopsis thaliana]

Seq. No. 419813

Seq. ID uC-osrocyp009h12b1

Method BLASTX

```
NCBI GI
                   g3283996
BLAST score
                   198
E value
                   4.0e-15
Match length
                   50
% identity
                   72
                   (AF072908) calcium-dependent protein kinase [Nicotiana
NCBI Description
                   419814
Seq. No.
                   uC-osrocyp010a02a1
Seq. ID
Method
                   BLASTN
NCBI GI
                   q3885887
BLAST score
                   450
                   0.0e+00
E value
Match length
                   472
                   99
% identity
                  Oryza sativa high mobility group protein (HMG) mRNA,
NCBI Description
                   complete cds
Seq. No.
                   419815
                   uC-osrocyp010a02b1
Seq. ID
                   BLASTX
Method
NCBI GI
                   g3885888
BLAST score
                   169
                   8.0e-22
E value
Match length
                   109
                   59
% identity
NCBI Description (AF093632) high mobility group protein [Oryza sativa]
Seq. No.
                   419816
                   uC-osrocyp010a04b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   q1617274
BLAST score
                   347
                   6.0e - 33
E value
                   98
Match length
                   64
% identity
NCBI Description
                  (Z72152) AMP-binding protein [Brassica napus]
Seq. No.
                   419817
                   uC-osrocyp010a06b1
Seq. ID
                   BLASTX
Method
NCBI GI
                   q4469023
BLAST score
                   347
E value
                   8.0e-55
                   128
Match length
                   83
% identity
NCBI Description (AL035602) putative protein [Arabidopsis thaliana]
                   419818
Seq. No.
Seq. ID
                   uC-osrocyp010a07a1
Method
                   BLASTX
NCBI GI
                   g2443755
BLAST score
                   250
E value
                   2.0e-21
                   77
Match length
```

62

% identity

NCBI Description (AF020433) cyclophilin [Arabidopsis thaliana]

Seq. No. 419819

Seq. ID uC-osrocyp010a09a1

Method BLASTX
NCBI GI g3876299
BLAST score 149
E value 2.0e-09
Match length 71
% identity 44

NCBI Description (Z71180) similar to BPTI/KUNITZ inhibitor domain; cDNA EST

EMBL:D68293 comes from this gene; cDNA EST yk448h4.5 comes from this gene; cDNA EST yk249e6.5 comes from this gene; cDNA EST yk448h4.3 comes from this gene [Caenorhabdi...

>gi 3880760 emb CAA16311.1 (AL021474) similar to

BPTI/KUNITZ inhibitor domain; cDNA EST EMBL:D68293 comes from this gene; cDNA EST yk448h4.5 comes from this gene; cDNA EST yk249e6.5 comes from this gene; cDNA EST yk248h4.3

comes from this gene [Caenorh

Seq. No. 419820

Seq. ID uC-osrocyp010a09b1

Method BLASTX
NCBI GI g3876299
BLAST score 221
E value 8.0e-18
Match length 86
% identity 47

NCBI Description (Z71180) similar to BPTI/KUNITZ inhibitor domain; cDNA EST

EMBL:D68293 comes from this gene; cDNA EST yk448h4.5 comes from this gene; cDNA EST yk249e6.5 comes from this gene; cDNA EST yk448h4.3 comes from this gene [Caenorhabdi...

>qi 3880760 emb CAA16311.1 (AL021474) similar to

BPTI/KUNITZ inhibitor domain; cDNA EST EMBL:D68293 comes from this gene; cDNA EST yk448h4.5 comes from this gene; cDNA EST yk249e6.5 comes from this gene; cDNA EST yk249e48h4.3

comes from this gene [Caenorh

Seq. No. 419821

Seq. ID uC-osrocyp010a10b1

Method BLASTX
NCBI GI g5091627
BLAST score 157
E value 2.0e-10
Match length 55
% identity 58

NCBI Description (AC007454) Similar to gb_AF082176 auxin response factor 9

from Arabidopsis thaliana

Seq. No. 419822

Seq. ID uC-osrocyp010a12b1

Method BLASTX
NCBI GI g445613
BLAST score 252
E value 8.0e-22
Match length 71
% identity 66



NCBI Description ribosomal protein L7 [Solanum tuberosum]

Seq. No. 419823

Seq. ID uC-osrocyp010b01b1

Method BLASTX
NCBI GI g1350742
BLAST score 310
E value 2.0e-28
Match length 102
% identity 58

NCBI Description PROBABLE 60S RIBOSOMAL PROTEIN L35A >gi_1086831 (U41264) coded for by C. elegans cDNA yk64g10.5; coded for by C.

elegans cDNA yk51f3.5; coded for by C. elegans cDNA

yk115e7.3; coded for by C. elegans cDNA yk99d1.3; coded for by C. elegans cDNA yk99d1.5; coded for by C. elegans cDNA

yk64g1

Seq. No. 419824

Seq. ID uC-osrocyp010b02a1

Method BLASTX
NCBI GI g2833375
BLAST score 342
E value 5.0e-32
Match length 71
% identity 89

NCBI Description DNA-DIRECTED RNA POLYMERASE II 8.2 KD POLYPEPTIDE (RPB10)

(RP10) (ABC10) >gi 533690 (U12133) RNA polymerase II

subunit RPB10 homolog; similar to yeast RNA polymerase II subunit RPB10, Swiss-Prot Accession Number P22139 [Brassica

napus]

Seq. No. 419825

Seq. ID uC-osrocyp010b02b1

Method BLASTX
NCBI GI g2833375
BLAST score 349
E value 8.0e-33
Match length 71
% identity 90

NCBI Description DNA-DIRECTED RNA POLYMERASE II 8.2 KD POLYPEPTIDE (RPB10)

(RP10) (ABC10) >gi_533690 (U12133) RNA polymerase II

subunit RPB10 homolog; similar to yeast RNA polymerase II subunit RPB10, Swiss-Prot Accession Number P22139 [Brassica

napus]

Seq. No. 419826

Seq. ID uC-osrocyp010b03a1

Method BLASTX
NCBI GI g1350986
BLAST score 526
E value 1.0e-53
Match length 107
% identity 100

NCBI Description 40S RIBOSOMAL PROTEIN S3A (CYC07 PROTEIN)

>gi_483431_dbj_BAA05059_ (D26060) cyc07 [Oryza sativa]

Seq. No. 419827

Seq. ID

```
uC-osrocyp010b03b1
Seq. ID
                  BLASTX
Method
                  q1350986
NCBI GI
BLAST score
                  525
                  2.0e-61
E value
Match length
                  125
                  96
% identity
                  40S RIBOSOMAL PROTEIN S3A (CYC07 PROTEIN)
NCBI Description
                  >gi 483431 dbj_BAA05059 (D26060) cyc07 [Oryza sativa]
                  419828
Seq. No.
Seq. ID
                  uC-osrocyp010b05a1
                  BLASTX
Method
                  g1076746
NCBI GI
                   215
BLAST score
                   3.0e-17
E value
                  70
Match length
                   66
% identity
                  heat shock protein 70 - rice (fragment)
NCBI Description
                   >gi 763160 emb_CAA47948 (X67711) heat shock protein 70
                   [Oryza sativa]
                   419829
Seq. No.
Seq. ID
                   uC-osrocyp010b05b1
                   BLASTX
Method
                   g1076746
NCBI GI
                   517
BLAST score
                   8.0e-53
E value
Match length
                   110
                   96
% identity
                   heat shock protein 70 - rice (fragment)
NCBI Description
                   >gi_763160_emb_CAA47948_ (X67711) heat shock protein 70
                   [Oryza sativa]
Seq. No.
                   419830
Seq. ID
                   uC-osrocyp010b07a1
                   BLASTX
Method
NCBI GI
                   g4508082
BLAST score
                   197
E value
                   4.0e-15
Match length
                   56
% identity
                   66
                  (AC005882) Putative RNA polymerase II subunit Rpb10
NCBI Description
                   [Arabidopsis thaliana]
                   419831
Seq. No.
                   uC-osrocyp010b09b1
Seq. ID
                   BLASTN
Method
                   g2062705
NCBI GI
                   34
BLAST score
                   2.0e-10
E value
Match length
                   34
                   100
% identity
NCBI Description Human butyrophilin (BTF5) mRNA, complete cds
                   419832
Seq. No.
                   uC-osrocyp010b11a1
```

Match length

% identity

56 100

```
BLASTN
Method
NCBI GI
                  g5912298
                  88
BLAST score
                  1.0e-41
E value
                  102
Match length
                  97
% identity
NCBI Description Oryza sativa mRNA for gigantea homologue, partial
                  419833
Seq. No.
                  uC-osrocyp010b11b1
Seq. ID
                 BLASTX
Method
NCBI GI
                 g5912299
BLAST score
                  590
E value
                  3.0e-61
                  134
Match length
% identity
                  84
NCBI Description (AJ133787) gigantea homologue [Oryza sativa]
Seq. No.
                  419834
Seq. ID
                  uC-osrocyp010c02b1
Method
                 BLASTX
NCBI GI
                  q82496
BLAST score
                  458
E value
                  6.0e-59
Match length
                  151
% identity
                  81
NCBI Description phenylalanine ammonia-lyase (EC 4.3.1.5) - rice
                  419835
Seq. No.
Seq. ID
                  uC-osrocyp010c03a1
Method
                  BLASTX
                  q3688528
NCBI GI
BLAST score
                  214
                  5.0e-17
E value
Match length
                  59
% identity
NCBI Description (AJ004958) pre-pro-TPE4A protein [Pisum sativum]
                  419836
Seq. No.
Seq. ID
                  uC-osrocyp010c04b1
                  BLASTX
Method
NCBI GI
                  q3560166
BLAST score
                  246
E value
                  9.0e-21
Match length
                  139
% identity
NCBI Description (AL031525) ubiquitin carboxyl-terminal hydrolase
                  [Schizosaccharomyces pombe]
Seq. No.
                  419837
Seq. ID
                  uC-osrocyp010c07a1
Method
               BLASTX
NCBI GI
                 g129591
BLAST score
                  306
                  8.0e-28
E value
```

NCBI GI

E value

BLAST score

NCBI Description PHENYLALANINE AMMONIA-LYASE >gi 295824 emb CAA34226 (X16099) phenylalanine ammonia-lyase [Oryza sativa] Seq. No. 419838 Seq. ID uC-osrocyp010c07b1 Method BLASTX NCBI GI q1076746 BLAST score 604 E value 2.0e-71 Match length 150 96 % identity NCBI Description heat shock protein 70 - rice (fragment) >gi_763160 emb CAA47948 (X67711) heat shock protein 70 [Oryza sativa] Seq. No. 419839 Seq. ID uC-osrocyp010c09a1 Method BLASTX NCBI GI q1350742 BLAST score 177 E value 1.0e-12 Match length 43 % identity 65 NCBI Description PROBABLE 60S RIBOSOMAL PROTEIN L35A >gi 1086831 (U41264) coded for by C. elegans cDNA yk64g10.5; coded for by C. elegans cDNA yk51f3.5; coded for by C. elegans cDNA yk115e7.3; coded for by C. elegans cDNA yk99d1.3; coded for by C. elegans cDNA yk99d1.5; coded for by C. elegans cDNA yk64g1 Seq. No. 419840 uC-osrocyp010c09b1 Seq. ID Method BLASTX NCBI GI g1173630 174 BLAST score 2.0e-12 E value Match length 67 % identity 48 (U34747) cysteine proteinase [Phalaenopsis sp. 'hybrid NCBI Description SM9108'] 419841 Seq. No. uC-osrocyp010c12b1 Seq. ID Method BLASTN NCBI GI g6015437 BLAST score 36 E value 2.0e-10 Match length 36 100 % identity NCBI Description Homo sapiens PEX1 mRNA, complete cds 419842 Seq. No. Seq. ID uC-osrocyp010d02b1 Method BLASTX

55093

g1208496

9.0e-19

```
Match length
                  79
% identity
NCBI Description
                  (D38124) EREBP-3 [Nicotiana tabacum]
Seq. No.
                  419843
                  uC-osrocyp010d03b1
Seq. ID
                  BLASTX
Method
NCBI GI
                  q1351974
BLAST score
                  467
                  1.0e-46
E value
                  98
Match length
                  100
% identity
NCBI Description
                  ADP-RIBOSYLATION FACTOR >gi 1076788 pir S49325
                  ADP-ribosylation factor - maize >gi 1076789 pir
                  ADP-ribosylation factor - maize >gi 556686 emb CAA56351
                   (X80042) ADP-ribosylation factor [Zea mays]
                  419844
Seq. No.
Seq. ID
                  uC-osrocyp010d04a1
                  BLASTX
Method
                  q3063710
NCBI GI
BLAST score
                  321
                  1.0e-29
E value
Match length
                  72
                  76
% identity
NCBI Description (AL022537) putative protein [Arabidopsis thaliana]
                   419845
Seq. No.
Seq. ID
                  uC-osrocyp010d04b1
Method
                  BLASTX
NCBI GI
                   q3063710
BLAST score
                   447
E value
                   1.0e-50
Match length
                   136
% identity
                   68
                  (AL022537) putative protein [Arabidopsis thaliana]
NCBI Description
                   419846
Seq. No.
Seq. ID
                  uC-osrocyp010d05a1
Method
                  BLASTX
NCBI GI
                   q5354158
BLAST score
                   153
                   6.0e-10
E value
                  70
Match length
% identity
                   43
                  (AF149841) digalactosyldiacylglycerol synthase [Arabidopsis
NCBI Description
                   thaliana] >gi 5354160 gb AAD42379.1 AF149842 1 (AF149842)
                   digalactosyldiacylglycerol synthase [Arabidopsis thaliana]
                   >gi 6041825 gb AAF02140.1 AC009918 12 (AC009918)
                   digalactosyldiacylglycerol synthase [Arabidopsis thaliana]
```

Method BLASTX NCBI GI g5354158 BLAST score 237 E value 4.0e-23

BLAST score

156

Match length 143 % identity 45 NCBI Description (AF149841) digalactosyldiacylglycerol synthase [Arabidopsis] thaliana] >qi 5354160 qb AAD42379.1 AF149842 1 (AF149842) digalactosyldiacylglycerol synthase [Arabidopsis thaliana] >gi 6041825 gb AAF02140.1 AC009918 12 (AC009918) digalactosyldiacylglycerol synthase [Arabidopsis thaliana] Seq. No. 419848 Seq. ID uC-osrocyp010d08a1 BLASTX Method NCBI GI g2293566 BLAST score 495 6.0e-50 E value 96 Match length 100 % identity NCBI Description (AF012896) ADP-ribosylation factor 1 [Oryza sativa] Seq. No. 419849 uC-osrocyp010d09a1 Seq. ID Method BLASTX NCBI GI g3641252 BLAST score 264 E value 7.0e-23 143 Match length % identity (AF053127) leucine-rich receptor-like protein kinase [Malus NCBI Description domestica] 419850 Seq. No. uC-osrocyp010d10b1 Seq. ID Method BLASTX g1076809 NCBI GI BLAST score 310 2.0e-28 E value Match length 105 % identity 63 H+-transporting ATPase (EC 3.6.1.35) - maize NCBI Description >gi 758355 emb_CAA59800_ (X85805) H(+)-transporting ATPase [Zea mays] 419851 Seq. No. uC-osrocyp010d12b1 Seq. ID BLASTX Method NCBI GI q5919185 BLAST score 215 2.0e-17 E value 81 Match length 54 % identity (AF183809) arabinogalactan protein Pop14A9 [Populus alba x NCBI Description Populus tremula] 419852 Seq. No. uC-osrocyp010e01b1 Seq. ID Method BLASTX g1076316 NCBI GI

Seq. ID Method

NCBI GI

```
3.0e-10
E value
Match length
                   67
                  37
% identity
                  drought-induced protein Di19 - Arabidopsis thaliana
NCBI Description
                  >gi 469110_emb_CAA55321_ (X78584) Di19 [Arabidopsis
                  thaliana]
                  419853
Seq. No.
Seq. ID
                  uC-osrocyp010e02b1
                  BLASTX
Method
NCBI GI
                  a584706
BLAST score
                  564
                  4.0e-58
E value
Match length
                  113
                  100
% identity
NCBI Description ASPARTATE AMINOTRANSFERASE, CYTOPLASMIC (TRANSAMINASE A)
                  >gi_2130066_pir__JC5124 aspartate transaminase (EC
                   2.6.1.1), cytoplasmic - rice >gi_287298_dbj_BAA03504_
                   (D14673) aspartate aminotransferase [Oryza sativa]
                  419854
Seq. No.
Seq. ID
                  uC-osrocyp010e04b1
                  BLASTX
Method
                  g2230757
NCBI GI
BLAST score
                  453
                  5.0e-45
E value
                  164
Match length
                   60
% identity
NCBI Description (Y11969) dnaJ-like protein [Arabidopsis thaliana]
Seq. No.
                  419855
Seq. ID
                  uC-osrocyp010e05a1
Method
                  BLASTX
NCBI GI
                  a480450
BLAST score
                   349
                   7.0e - 33
E value
                  78
Match length
                   87
% identity
                  ketol-acid reductoisomerase (EC 1.1.1.86) - Arabidopsis
NCBI Description
                   thaliana >gi 402552 emb CAA49506 (X69880) ketol-acid
                  reductoisomerase [Arabidopsis thaliana]
Seq. No.
                   419856
Seq. ID
                  uC-osrocyp010e05b1
                   BLASTX
Method
NCBI GI
                   q419757
BLAST score
                   409
E value
                   1.0e-73
Match length
                   170
                   79
% identity
NCBI Description ketol-acid reductoisomerase (EC 1.1.1.86) precursor -
                  Arabidopsis thaliana
                   419857
Seq. No.
```

55096

uC-osrocyp010e07a1

BLASTX

q584706

Seq. ID Method

NCBI GI

E value

BLAST score

Match length



```
186
BLAST score
E value
                  7.0e-14
                  56
Match length
                  71
% identity
                  ASPARTATE AMINOTRANSFERASE, CYTOPLASMIC (TRANSAMINASE A)
NCBI Description
                  >gi 2130066 pir JC5124 aspartate transaminase (EC
                  2.6.1.1), cytoplasmic - rice >gi 287298_dbj BAA03504
                  (D14673) aspartate aminotransferase [Oryza sativa]
                  419858
Seq. No.
Seq. ID
                  uC-osrocyp010e08a1
                  BLASTX
Method
NCBI GI
                  q5430769
                  505
BLAST score
                  4.0e-51
E value
                  170
Match length
                  57
% identity
NCBI Description (AC007504) Similar to somatic embryogenesis receptor-like
                  kinase [Arabidopsis thaliana]
                  419859
Seq. No.
                  uC-osrocyp010e10a1
Seq. ID
                  BLASTX
Method
NCBI GI
                  g5679845
BLAST score
                  201
                  2.0e-15
E value
                  50
Match length
                  78
% identity
NCBI Description (AJ243961) 11332.9 [Oryza sativa]
                  419860
Seq. No.
                  uC-osrocyp010e10b1
Seq. ID
                  BLASTX
Method
NCBI GI
                  q5679845
BLAST score
                  376
                  9.0e - 46
E value
Match length
                  107
% identity
NCBI Description (AJ243961) 11332.9 [Oryza sativa]
Seq. No.
                   419861
Seq. ID
                  uC-osrocyp010e11a1
                   BLASTX
Method
NCBI GI
                   g1706956
BLAST score
                   261
                   2.0e-22
E value
Match length
                  62
                  76
% identity
NCBI Description (U58283) cellulose synthase [Gossypium hirsutum]
                   419862
Seq. No.
```

160

uC-osrocyp010e12b1

BLASTX

150 2.0e-09

g2911300

E value

2.0e-12

```
% identity
NCBI Description
                   (AF022937) structural polyprotein [Rhopalosiphum padi
                  virus]
                  419863
Seq. No.
                  uC-osrocyp010f01b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g128191
BLAST score
                  534
                  1.0e-54
E value
                  137
Match length
% identity
                  77
NCBI Description NITRATE REDUCTASE [NAD(P)H] >gi 66210 pir RDBHNP nitrate
                  reductase (NAD(P)H) (EC 1.6.6.2) - barley
                  >gi 19065 emb CAA42739 (X60173) nitrate reductase
                  (NAD(P)H) [Hordeum vulgare]
Seq. No.
                  419864
Seq. ID
                  uC-osrocyp010f03a1
Method
                  BLASTX
NCBI GI
                  q913445
BLAST score
                  209
E value
                  2.0e-16
Match length
                  65
% identity
                  58
                  (S75487) alcohol dehydrogenase ADH=alcohol dehydrogenase
NCBI Description
                  homolog {EC 1.1.1.1} [Lycopersicon esculentum=tomatoes, cv.
                  red cherry, Peptide, 389 aa] [Lycopersicon esculentum]
                  419865
Seq. No.
                  uC-osrocyp010f03b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1491615
BLAST score
                  155
                  3.0e-10
E value
Match length
                  45
% identity
                  67
NCBI Description
                  (X99923) male sterility 2-like protein [Arabidopsis
                  thaliana]
                  419866
Seq. No.
                  uC-osrocyp010f04a1
Seq. ID
Method
                  BLASTX
                  g2398829
NCBI GI
BLAST score
                  246
                  8.0e-21
E value
                  51
Match length
% identity
                  (Y11220) mitochondrial uncoupling protein [Solanum
NCBI Description
                  tuberosum]
                  419867
Seq. No.
                  uC-osrocyp010f04b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2398829
BLAST score
                  173
```

```
Match length
                  52
% identity
                  (Y11220) mitochondrial uncoupling protein [Solanum
NCBI Description
                  tuberosum]
                  419868
Seq. No.
                  uC-osrocyp010f05b1
Seq. ID
Method
                  BLASTX
                  g3176664
NCBI GI
BLAST score
                  331
                  1.0e-35
E value
Match length
                  157
% identity
                  54
                  (AC004393) Contains similarity to beta scruin gb Z47541
NCBI Description
                  from Limulus polyphemus. ESTs gb_T04493 and gb_AA585955
                  come from this gene. [Arabidopsis thaliana]
Seq. No.
                  419869
                  uC-osrocyp010f06a1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4454466
BLAST score
                  184
E value
                  2.0e-13
                  57
Match length
                  58
% identity
NCBI Description (AC006234) unknown protein [Arabidopsis thaliana]
Seq. No.
                  419870
Seq. ID
                  uC-osrocyp010f06b1
Method
                  BLASTX
                  q4454466
NCBI GI
                  184
BLAST score
                  2.0e-13
E value
                  57
Match length
% identity
                  58
NCBI Description (AC006234) unknown protein [Arabidopsis thaliana]
Seq. No.
                  419871
                  uC-osrocyp010f07b1
Seq. ID
                  BLASTX
Method
                  g729051
NCBI GI
BLAST score
                  463
E value
                  3.0e-46
                  108
Match length
                  84
% identity
NCBI Description CALTRACTIN (CENTRIN) >gi_444342_prf__1906390A
                  caltractin-like protein [Atriplex nummularia]
                   419872
Seq. No.
Seq. ID
                  uC-osrocyp010f09b1
Method
                  BLASTX
                   q913445
NCBI GI
                   388
BLAST score
E value
                  1.0e-37
Match length
                  117
% identity
                  (S75487) alcohol dehydrogenase ADH=alcohol dehydrogenase
NCBI Description
```

```
red cherry, Peptide, 389 aa] [Lycopersicon esculentum]
Seq. No.
                  419873
                  uC-osrocyp010f10b1
Seq. ID
                  BLASTX
Method
NCBI GI
                  q102506
BLAST score
                  229
                  1.0e-18
E value
Match length
                  97
                  43
% identity
NCBI Description glucose transport protein homolog - Caenorhabditis elegans
                  419874
Seq. No.
                  uC-osrocyp010g01a1
Seq. ID
                  BLASTX
Method
NCBI GI
                  g2827661
BLAST score
                  223
E value
                  5.0e-18
                  87
Match length
                  55
% identity
NCBI Description (AL021637) hyuC-like protein [Arabidopsis thaliana]
Seq. No.
                   419875
                  uC-osrocyp010g02a1
Seq. ID
                  BLASTX
Method
                  g481477
NCBI GI
BLAST score
                   429
E value
                   3.0e-42
Match length
                   90
                   17
% identity
                  ubiquitin precursor - rice >gi_416038 emb_CAA53665
NCBI Description
                   (X76064) polyubiquitin [Oryza sativa] >gi_1574944 (U37687)
                   polyubiquitin [Oryza sativa]
                   >gi_6013289_gb_AAF01315.1_AF184279_1 (AF184279)
                   polyubiquitin [Oryza sativa]
                   >gi 6013291_gb_AAF01316.1_AF184280 1 (AF184280)
                   polyubiquitin [Oryza sativa]
                   419876
Seq. No.
                   uC-osrocyp010g02b1
Seq. ID
Method
                   BLASTX
                   q1747296
NCBI GI
                   461
BLAST score
                   4.0e-46
E value
Match length
                   113
                   81
% identity
                  (D45384) vacuolar H+-pyrophosphatase [Oryza sativa]
NCBI Description
                   >gi_3298476_dbj_BAA31524_ (AB012766) ovp2 [Oryza sativa]
                   419877
Seq. No.
                   uC-osrocyp010g03b1
Seq. ID
                   BLASTX
Method
NCBI GI
                   g4850271
                   249
BLAST score
                   3.0e-21
E value
```

homolog {EC 1.1.1.1} [Lycopersicon esculentum=tomatoes, cv.

55100

90

Match length

NCBI Description

```
% identity
NCBI Description
                   (AJ238244) putative high affinity sulfate transporter
                   [Aegilops tauschii]
Seq. No.
                   419878
Seq. ID
                  uC-osrocyp010g04a1
Method
                  BLASTN
NCBI GI
                  q394735
                   455
BLAST score
                   0.0e + 00
E value
                   455
Match length
                   100
% identity
NCBI Description Rice lip19 mRNA for basic/leucine zipper protein
                   419879
Seq. No.
Seq. ID
                  uC-osrocyp010g04b1
Method
                  BLASTN
NCBI GI
                  g394735
BLAST score
                   439
E value
                   0.0e + 00
Match length
                   525
                   96
% identity
NCBI Description Rice lip19 mRNA for basic/leucine zipper protein
Seq. No.
                   419880
Seq. ID
                   uC-osrocyp010g05b1
Method
                   BLASTX
                   q3047077
NCBI GI
BLAST score
                   384
E value
                   7.0e-37
                   146
Match length
% identity
                  (AF058914) contains similarity to the conserved C-terminal
NCBI Description
                   domain of helicases (Pfam: helicase C.hmm, score: 90.11),
                   similar to DEAD-box helicases [Arabidopsis thaliana]
Seq. No.
                   419881
                   uC-osrocyp010g06b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g6056374
BLAST score
                   255
                   8.0e-22
E value
Match length
                   88
% identity
                   57
NCBI Description
                  (AC009894) Similar to serine/threonine kinases [Arabidopsis
                   thaliana]
                   419882
Seq. No.
                   uC-osrocyp010g07a1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g542059
BLAST score
                   217
E value
                   2.0e-17
Match length
                   47
                   89
% identity
```

inorganic pyrophosphatase (EC 3.6.1.1) - common tobacco

>gi 457744 emb CAA54869 (X77915) inorganic pyrophosphatase

```
[Nicotiana tabacum]
Seq. No.
                  419883
Seq. ID
                  uC-osrocyp010g07b1
Method
                  BLASTX
NCBI GI
                  q2827661
BLAST score
                  267
E value
                  4.0e-24
                  80
Match length
                  74
% identity
NCBI Description (AL021637) hyuC-like protein [Arabidopsis thaliana]
Seq. No.
                  419884
Seq. ID
                  uC-osrocyp010g08b1
                  BLASTX
Method
NCBI GI
                  q2760349
BLAST score
                  685
                  2.0e-72
E value
Match length
                  137
% identity
NCBI Description (U84969) ubiquitin [Arabidopsis thaliana]
Seq. No.
                   419885
                  uC-osrocyp010g09a1
Seq. ID
                  BLASTX
Method
NCBI GI
                  q128191
BLAST score
                   362
                   2.0e-34
E value
Match length
                  78
% identity
                  NITRATE REDUCTASE [NAD(P)H] >gi 66210 pir RDBHNP nitrate
NCBI Description
                   reductase (NAD(P)H) (EC 1.6.6.2) - barley
                   >qi 19065 emb CAA42739 (X60173) nitrate reductase
                   (NAD(P)H) [Hordeum vulgare]
                   419886
Seq. No.
                   uC-osrocyp010g10a1
Seq. ID
Method
                   BLASTX
NCBI GI
                   q3550549
BLAST score
                   270
E value
                   1.0e-23
Match length
                   53
                   98
% identity
NCBI Description (AJ004965) cytosolic pyruvate orthophosphate dikinase
                   [Oryza sativa subsp. indica]
                   419887
Seq. No.
                   uC-osrocyp010g10b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3550549
BLAST score
                   696
```

% identity (AJ004965) cytosolic pyruvate orthophosphate dikinase NCBI Description [Oryza sativa subsp. indica]

6.0e-86

171

99

E value

Match length



```
Seq. No.
                   419888
Seq. ID
                   uC-osrocyp010g12b1
                  BLASTX
Method
NCBI GI
                  g4826682
BLAST score
                   269
                   3.0e-29
E value
                   167
Match length
% identity
                  cystinosis, nephropathic >gi 3036840 emb CAA11021
NCBI Description
                   (AJ222967) cystinosin [Homo sapiens]
                   >gi 3036851_emb_CAA75882_ (Y15924) cystinosin [Homo
                   sapiens]
                   419889
Seq. No.
```

uC-osrocyp010h01b1 Seq. ID BLASTX Method NCBI GI q2213600 BLAST score 208 E value 3.0e-16

95 Match length 46 % identity

(AC000348) T7N9.20 [Arabidopsis thaliana] NCBI Description

Seq. No. 419890 uC-osrocyp010h03a1 Seq. ID BLASTX Method q1129134 NCBI GI BLAST score 190 E value 3.0e-14Match length 41

78 % identity

(X94105) old yellow enzyme NADPH dehydrogenase [Chenopodium NCBI Description

rubrum]

419891 Seq. No.

uC-osrocyp010h04a1 Seq. ID

Method BLASTX NCBI GI g4544402 BLAST score 231 E value 5.0e-19 Match length 150 % identity 27

(AC007047) putative leucine rich repeat protein NCBI Description

[Arabidopsis thaliana]

419892 Seq. No.

uC-osrocyp010h07a1 Seq. ID

Method BLASTX NCBI GI g3152572 BLAST score 268 E value 2.0e-23 114 Match length 51 % identity

NCBI Description (AC002986) Contains homology to DNAJ heatshock protein

gb U32803 from Haemophilus influenzae. [Arabidopsis

thaliana]

```
419893
Seq. No.
Seq. ID
                   uC-osrocyp010h08b1
                   BLASTN
Method
NCBI GI
                   q425794
BLAST score
                   87
                   2.0e-41
E value
                   87
Match length
% identity
                   100
NCBI Description Rice mRNA for heat shock protein 82 (gene name AD167),
                  partial cds
                   419894
Seq. No.
Seq. ID
                   uC-osrocyp010h09b1
                   BLASTX
Method
NCBI GI
                   q4894182
BLAST score
                   658
E value
                   5.0e-69
                   188
Match length
% identity
                   71
                  (AJ242551) 12-oxophytodienoate reductase [Lycopersicon
NCBI Description
                   esculentum]
                   419895
Seq. No.
Seq. ID
                   uC-osrocyp010h10b1
                   BLASTX
Method
NCBI GI
                   q4894182
BLAST score
                   161
                   1.0e-23
E value
Match length
                   116
% identity
NCBI Description
                  (AJ242551) 12-oxophytodienoate reductase [Lycopersicon
                   esculentum]
Seq. No.
                   419896
                   uC-osrocyp010h11a1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2351580
BLAST score
                   315
E value
                   7.0e-29
Match length
                   72
% identity
                   82
                  (U82433) thymidine diphospho-glucose 4-6-dehydratase
NCBI Description
                   homolog [Prunus armeniaca]
                   419897
Seq. No.
                   uC-osrocyp010h11b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3927825
BLAST score
                   419
E value
                   3.0e-52
Match length
                   135
% identity
                   80
NCBI Description
                  (AC005727) putative dTDP-glucose 4-6-dehydratase
                   [Arabidopsis thaliana]
                   419898
Seq. No.
Seq. ID
                   uC-osrocyp010h12a1
```

BLAST score

224

```
Method
                  BLASTX
                  q4574208
NCBI GI
BLAST score
                  301
                  3.0e-27
E value
Match length
                  62
% identity
                  97
NCBI Description (AF093108) histone H3 [Tortula ruralis]
                  419899
Seq. No.
                  uC-osrocyp010h12b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g422606
BLAST score
                  522
E value
                  7.0e-63
Match length
                  134
                  91
% identity
NCBI Description histone H3.1 - African clawed frog >gi 288992 emb CAA51455
                  (X72950) histone H3 [Xenopus laevis]
Seq. No.
                  419900
                  uC-osrocyp011a01b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1710078
BLAST score
                  587
E value
                  9.0e-61
Match length
                  146
% identity
                  73
NCBI Description RAB24 PROTEIN >gi 971280 dbj BAA09947 (D63917) RAB24
                  protein [Oryza sativa]
                  419901
Seq. No.
                  uC-osrocyp011a02a1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g5441876
                  195
BLAST score
                  1.0e-105
E value
                  447
Match length
% identity
                  99
NCBI Description Oryza sativa genomic DNA, chromosome 2, clone:P0437H03
                  (contig b)
                  419902
Seq. No.
                  uC-osrocyp011a02b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1710078
BLAST score
                  579
E value
                  2.0e-61
Match length
                  152
                  76
% identity
NCBI Description RAB24 PROTEIN >gi_971280_dbj_BAA09947_ (D63917) RAB24
                  protein [Oryza sativa]
Seq. No.
                  419903
                  uC-osrocyp011a03b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4586058
```

Match length

38

```
3.0e-18
E value
                  150
Match length
                  39
% identity
NCBI Description (AC007020) unknown protein [Arabidopsis thaliana]
                  419904
Seq. No.
Seq. ID
                  uC-osrocyp011a04a1
                  BLASTX
Method
NCBI GI
                  g549986
                  330
BLAST score
E value
                  1.0e-30
                  69
Match length
                  93
% identity
                  (U13149) possible apospory-associated protein [Pennisetum
NCBI Description
                  ciliare]
                  419905
Seq. No.
Seq. ID
                  uC-osrocyp011a05b1
                  BLASTX
Method
                  g416869
NCBI GI
                  290
BLAST score
                  5.0e-26
E value
Match length
                  132
                  46
% identity
NCBI Description CYSTEINE SYNTHASE, CHLOROPLAST PRECURSOR (O-ACETYLSERINE
                  SULFHYDRYLASE) (O-ACETYLSERINE (THIOL)-LYASE) (CSASE)
                  >gi 303902_dbj_BAA03542_ (D14722) cysteine synthase
                   [Spinacia oleracea]
Seq. No.
                   419906
Seq. ID
                  uC-osrocyp011a06b1
Method
                  BLASTX
                  g2576361
NCBI GI
                   388
BLAST score
E value
                   1.0e-39
                   90
Match length
% identity
NCBI Description (U39782) lysine and histidine specific transporter
                   [Arabidopsis thaliana]
Seq. No.
                   419907
Seq. ID
                   uC-osrocyp011a07a1
                   BLASTN
Method
NCBI GI
                   g20332
BLAST score
                   61
                   2.0e-25
E value
Match length
                   68
                   99
% identity
NCBI Description O.sativa RAc7 gene for actin
                   419908
Seq. No.
                   uC-osrocyp011a07b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3941480
BLAST score
                   150
                   2.0e-09
E value
```

```
% identity
NCBI Description
                   (AF062894) putative transcription factor [Arabidopsis
                   thaliana]
                   419909
Seq. No.
Seq. ID
                   uC-osrocyp011a08a1
Method
                   BLASTX
NCBI GI
                   g2760362
                   200
BLAST score
                   2.0e-15
E value
Match length
                  74
% identity
                   55
                  (AF016511) 15.9 kDa subunit of RNA polymerase II
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                   419910
                   uC-osrocyp011a08b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   q4512685
BLAST score
                   497
                   3.0e-50
E value
Match length
                   165
% identity
                   58
                  (AC006931) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                  >gi 4559325 gb AAD22987.1 AC007087 6 (AC007087)
                   hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   419911
                  uC-osrocyp011a09b1
Seq. ID
Method
                  BLASTX
NCBI GI
                   g3420239
BLAST score
                   649
                   5.0e-68
E value
Match length
                  121
                   98
% identity
NCBI Description (AF059484) actin [Gossypium hirsutum]
Seq. No.
                   419912
Seq. ID
                  uC-osrocyp011a10b1
Method
                  BLASTX
NCBI GI
                   q2262170
BLAST score
                   286
                  2.0e-25
E value
Match length
                  110
% identity
                   57
NCBI Description
                  (AC002329) predicted glycosyl hydrolase [Arabidopsis
                  thaliana]
Seq. No.
                   419913
Seq. ID
                  uC-osrocyp011a11b1
Method
                  BLASTX
NCBI GI
                  q5734704
BLAST score
                   419
E value
                   4.0e-41
Match length
                  140
% identity
                  (AC008075) Contains similarity to gb AF114753 polytropic
NCBI Description
```

```
murine leukamia virus receptor SYG1 from Mus musculus.
                  gb N96331 comes from this gene. [Arabidopsis thaliana]
Seq. No.
                  419914
Seq. ID
                  uC-osrocyp011b01a1
Method
                 BLASTX
NCBI GI
                  q729305
BLAST score
                  153
E value
                  4.0e-10
Match length
                  46
% identity
                  70
NCBI Description
                 PYRUVATE DECARBOXYLASE ISOZYME 3 (PDC)
                  >gi 22765 emb CAA79819 (Z21722) pyruvate decarboxylase
                  [Zea mays] >gi 217972 dbj BAA03354 (D14457) Pyruvate
                  Decarboxylase [Zea mays]
Seq. No.
                  419915
Seq. ID
                  uC-osrocyp011b01b1
Method
                  BLASTX
NCBI GI
                  q5031275
BLAST score
                  568
E value
                  2.0e-58
Match length
                  147
% identity
                  71
NCBI Description (AF139496) unknown [Prunus armeniaca]
Seq. No.
                  419916
Seq. ID
                  uC-osrocyp011b02a1
Method
                 BLASTX
NCBI GI
                  q1710077
BLAST score
                  245
                  1.0e-20
E value
Match length
                  62
                  76
% identity
                 PEROXIREDOXIN (REHYDRIN HOMOLOG) (B15C)
NCBI Description
                  >gi_471321_emb_CAA54066 (X76605) HvB15C [Hordeum vulgare]
                  >gi 1694833_emb_CAA65387_ (X96551) peroxiredoxin [Hordeum
                  vulgare]
                  419917
Seq. No.
                  uC-osrocyp011b02b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g129231
BLAST score
                  650
                  3.0e-68
E value
                  143
Match length
                  88
% identity
NCBI Description ORYZAIN ALPHA CHAIN PRECURSOR >gi 67644 pir KHRZOA oryzain
                  (EC 3.4.22.-) alpha precursor - rice
                  >gi_218181_dbj_BAA14402_ (D90406) oryzain alpha precursor
```

Seq. No. 419918

Seq. ID uC-osrocyp011b03a1

[Oryza sativa]

Method BLASTN NCBI GI g471320

```
BLAST score
                  51
E value
                  1.0e-19
Match length
                  95
% identity
                  88
NCBI Description H.vulgare (cv. Bomi) B15C mRNA
                  419919
Seq. No.
Seq. ID
                  uC-osrocyp011b03b1
Method
                  BLASTX
NCBI GI
                  g1706328
BLAST score
                  437
E value
                  3.0e-73
Match length
                  163
% identity
                  87
NCBI Description
                  PYRUVATE DECARBOXYLASE ISOZYME 2 (PDC) >gi 1009710 (U27350)
                  pyruvate decarboxylase 2 [Oryza sativa] >gi 1777455
                  (U38199) pyruvate decarboxylase 2 [Oryza sativa]
Seq. No.
                  419920
                  uC-osrocyp011b04b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1136122
BLAST score
                  590
E value
                  4.0e-61
Match length
                  110
% identity
                  97
                 (X91807) alfa-tubulin [Oryza sativa]
NCBI Description
Seq. No.
                  419921
                  uC-osrocyp011b05a1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g1835728
                  57
BLAST score
                  4.0e-23
E value
                  96
Match length
                  91
% identity
NCBI Description Oryza sativa ribosomal protein mRNA, complete cds
                   419922
Seq. No.
                  uC-osrocyp011b05b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2341032
BLAST score
                  798
E value
                  2.0e-85
Match length
                  172
                  85
% identity
                  (AC000104) EST gb_ATTS0956 comes from this gene.
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                  419923
Seq. ID
                  uC-osrocyp011b07b1
Method
                  BLASTX
NCBI GI
                   q1644291
BLAST score
                  160
E value
                   1.0e-10
Match length
                  132
% identity
                   35
```

```
NCBI Description (Z73295) receptor-like protein kinase [Catharanthus roseus]
                  419924
Seq. No.
Seq. ID
                  uC-osrocyp011b10a1
Method
                  BLASTX
NCBI GI
                  q2244792
BLAST score
                  176
E value
                  1.0e-12
                  57
Match length
                  54
% identity
NCBI Description (Z97336) ankyrin like protein [Arabidopsis thaliana]
Seq. No.
                  419925
                  uC-osrocyp011b10b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2641211
BLAST score
                  290
                  6.0e-26
E value
Match length
                  74
                  76
% identity
NCBI Description (AF031547) histone-like protein [Fritillaria agrestis]
                  419926
Seq. No.
Seq. ID
                  uC-osrocyp011b11b1
Method
                  BLASTX
                  q3122724
NCBI GI
BLAST score
                  296
                  1.0e-26
E value
Match length
                  63
% identity
                  89
NCBI Description 60S RIBOSOMAL PROTEIN L38 >gi 2289009 (AC002335) ribosomal
                  protein L38 isolog [Arabidopsis thaliana]
Seq. No.
                  419927
Seq. ID
                  uC-osrocyp011c01b1
Method
                  BLASTX
NCBI GI
                  g114420
BLAST score
                  719
E value
                  2.0e-76
Match length
                  143
% identity
                  100
NCBI Description ATP SYNTHASE BETA CHAIN, MITOCHONDRIAL PRECURSOR
                  >qi 100882 pir S11491 H+-transporting ATP synthase (EC
                  3.6.1.34) beta chain, mitochondrial - maize
                  >gi 22173 emb CAA38140 (X54233) ATPase F1 subunit protein
                   [Zea mays] >gi 897618 (M36087) F-1-ATPase subunit 2 [Zea
                  mays]
Seq. No.
                  419928
                  uC-osrocyp011c02a1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g5031275
                  174
BLAST score
                  2.0e-12
E value
                  44
Match length
                  73
% identity
NCBI Description (AF139496) unknown [Prunus armeniaca]
```

```
419929
Seq. No.
Seq. ID
                  uC-osrocyp011c02b1
Method
                  BLASTX
NCBI GI
                  g3757521
BLAST score
                  510
E value
                  1.0e-51
Match length
                  161
                  58
% identity
NCBI Description (AC005167) unknown protein [Arabidopsis thaliana]
                  419930
Seq. No.
Seq. ID
                  uC-osrocyp011c03a1
Method
                  BLASTX
NCBI GI
                  g129231
BLAST score
                  264
E value
                   6.0e-23
Match length
                  52
% identity
                  92
NCBI Description
                  ORYZAIN ALPHA CHAIN PRECURSOR >qi 67644 pir KHRZOA oryzain
                   (EC 3.4.22.-) alpha precursor - rice
                  >gi 218181 dbj BAA14402 (D90406) oryzain alpha precursor
                   [Oryza sativa]
Seq. No.
                   419931
                  uC-osrocyp011c04b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4680496
BLAST score
                  260
                  1.0e-22
E value
Match length
                  52
                   96
% identity
                  (AF119222) putative sugar transporter protein [Oryza
NCBI Description
                  sativa]
                   419932
Seq. No.
                  uC-osrocyp011c07b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4206765
BLAST score
                  157
E value
                  2.0e-10
Match length
                  73
% identity
                   45
                  (AF104329) putative type 1 membrane protein [Arabidopsis
NCBI Description
                  thaliana]
                   419933
Seq. No.
                   uC-osrocyp011c08b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3618312
BLAST score
                   225
                   2.0e-18
E value
                  96
Match length
% identity
                   46
                  (AB001884) zinc finger protein [Oryza sativa]
NCBI Description
```

419934

Seq. No.

```
Seq. ID
                  uC-osrocyp011c10b1
                  BLASTX
Method
NCBI GI
                  q1174162
                  765
BLAST score
                  1.0e-81
E value
                  155
Match length
% identity
                  85
                  (U44976) ubiquitin-conjugating enzyme [Arabidopsis
NCBI Description
                  thaliana] >gi 3746915 (AF091106) E2
                  ubiquitin-conjugating-like enzyme [Arabidopsis thaliana]
Seq. No.
                  419935
                  uC-osrocyp011c12a1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g1136121
BLAST score
                  57
                  2.0e-23
E value
Match length
                  109
                  88
% identity
NCBI Description O.sativa mRNA for alpha-tubulin (clone OSTA-136)
Seq. No.
                  419936
Seq. ID
                  uC-osrocyp011d02a1
Method
                  BLASTX
NCBI GI
                  g231587
BLAST score
                  278
                  2.0e-24
E value
Match length
                  75
% identity
                  76
                  ATP SYNTHASE BETA CHAIN, MITOCHONDRIAL PRECURSOR
NCBI Description
                  >gi_283001_pir__S25304 H+-transporting ATP synthase (EC
                  3.6.1.34) beta chain precursor, mitochondrial - rice
                  >gi 218147 dbj BAA01372 (D10491) mitochondrial F1-ATPase
                  [Oryza sativa]
                  419937
Seq. No.
                  uC-osrocyp011d02b1
Seq. ID
Method
                  BLASTX
                  g3023713
NCBI GI
BLAST score
                  150
                  1.0e-09
E value
                  37
Match length
                  78
% identity
                  ENOLASE (2-PHOSPHOGLYCERATE DEHYDRATASE)
NCBI Description
                   (2-PHOSPHO-D-GLYCERATE HYDRO-LYASE) (OSE1) >gi 780372
                   (U09450) enolase [Oryza sativa]
Seq. No.
                  419938
                  uC-osrocyp011d04b1
Seq. ID
Method
                  BLASTX
                  g2760839
NCBI GI
                  175
BLAST score
E value
                  1.0e-12
                  74
Match length
% identity
                  49
NCBI Description (AC003105) putative receptor kinase [Arabidopsis thaliana]
```

Seq. ID

```
Seq. No.
                  419939
Seq. ID
                  uC-osrocyp011d05b1
Method
                  BLASTN
NCBI GI
                  g6006355
BLAST score
                  494
                  0.0e + 00
E value
                  507
Match length
% identity
                  99
NCBI Description Oryza sativa genomic DNA, chromosome 6, clone:P0493C11
                  419940
Seq. No.
                  uC-osrocyp011d06a1
Seq. ID
Method
                  BLASTN
NCBI GI
                  q4680488
BLAST score
                  82
                  3.0e-38
E value
Match length
                  94
% identity
                  55
NCBI Description Oryza sativa BAC clone 1.H19, complete sequence
                  419941
Seq. No.
                  uC-osrocyp011d06b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2501189
BLAST score
                  393
E value
                  4.0e-38
Match length
                  112
% identity
                  71
NCBI Description
                  THIAMINE BIOSYNTHETIC ENZYME 1-1 PRECURSOR
                  >gi 2130146 pir S61419 thiamine biosynthetic enzyme thi1-1
                   - maize >gi 596078 (U17350) thiamine biosynthetic enzyme
                  [Zea mays]
Seq. No.
                  419942
Seq. ID
                  uC-osrocyp011d07b1
Method
                  BLASTX
NCBI GI
                  g5734462
BLAST score
                  166
E value
                  2.0e-11
Match length
                  128
% identity
                  35
NCBI Description
                  (AL109832) hypothetical protein [Schizosaccharomyces pombe]
                  >gi_5912375 emb CAB55874.1 (Z66568) hypothetical protein
                   [Schizosaccharomyces pombe]
                  419943
Seq. No.
                  uC-osrocyp011d08b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4544450
BLAST score
                  246
                  1.0e-22
E value
Match length
                  150
                  22
% identity
NCBI Description (AC006592) hypothetical protein [Arabidopsis thaliana]
                  419944
Seq. No.
```

55113

uC-osrocyp011d09b1

Method

NCBI GI BLAST score

E value

BLASTX q4587584

245 1.0e-20

```
BLASTX
Method
NCBI GI
                  g2894607
BLAST score
                  453
                  5.0e-45
E value
Match length
                  128
                  63
% identity
                  (ALO21889) NAM (no apical meristem)-like protein
NCBI Description
                  [Arabidopsis thaliana]
                  419945
Seq. No.
                  uC-osrocyp011d10b1
Seq. ID
                  BLASTX
Method
NCBI GI
                  q2493318
BLAST score
                  234
E value
                  2.0e-19
                  99
Match length
                  47
% identity
NCBI Description BLUE COPPER PROTEIN PRECURSOR >gi 562779 emb CAA80963
                   (Z25471) blue copper protein [Pisum sativum]
                  >gi 1098264 prf 2115352A blue Cu protein [Pisum sativum]
                  419946
Seq. No.
                  uC-osrocyp011d11b1
Seq. ID
                  BLASTX
Method
NCBI GI
                  g5262154
                  217
BLAST score
                  3.0e-17
E value
                  135
Match length
                  39
% identity
NCBI Description (AL080237) putative protein [Arabidopsis thaliana]
                   419947
Seq. No.
                  uC-osrocyp011e01a1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3126967
BLAST score
                   460
                   7.0e-46
E value
                  150
Match length
                   12
% identity
NCBI Description (AF061807) polyubiquitin [Elaeagnus umbellata]
Seq. No.
                   419948
Seq. ID
                   uC-osrocyp011e02b1
Method
                   BLASTX
NCBI GI
                   q1684855
BLAST score
                   808
E value
                   1.0e-86
Match length
                   164
                   26
% identity
NCBI Description (U77939) ubiquitin-like protein [Phaseolus vulgaris]
                   419949
Seq. No.
Seq. ID
                   uC-osrocyp011e03b1
```

```
165
Match length
                  35
% identity
                  (AC007232) unknown protein [Arabidopsis thaliana]
NCBI Description
                  419950
Seq. No.
Seq. ID
                  uC-osrocyp011e04b1
                  BLASTX
Method
NCBI GI
                  q3608481
                  309
BLAST score
                  2.0e-28
E value
Match length
                  78
                  67
% identity
                  (AF088913) ribosomal protein L27a [Petunia x hybrida]
NCBI Description
                  419951
Seq. No.
Seq. ID
                  uC-osrocyp011e05b1
                  BLASTX
Method
                  g2499709
NCBI GI
BLAST score
                  498
                  2.0e-50
E value
                  94
Match length
                  99
% identity
NCBI Description PHOSPHOLIPASE D 1 PRECURSOR (PLD 1) (CHOLINE PHOSPHATASE 1)
                  (PHOSPHATIDYLCHOLINE-HYDROLYZING PHOSPHOLIPASE D 1)
                  >qi 1020415 dbj BAA11136 (D73411) phospholipase D [Oryza
                  satīva] >gi_1902903_dbj_BAA19467_ (AB001920) phospholipase
                  D [Oryza sativa]
                  419952
Seq. No.
Seq. ID
                  uC-osrocyp011e06a1
                  BLASTN
Method
                  q6006355
NCBI GI
BLAST score
                  90
                  7.0e-43
E value
Match length
                  138
                  91
% identity
NCBI Description Oryza sativa genomic DNA, chromosome 6, clone:P0493C11
Seq. No.
                   419953
                  uC-osrocyp011e06b1
Seq. ID
Method
                  BLASTX
                  g3258575
NCBI GI
                   325
BLAST score
                  5.0e - 30
E value
                  159
Match length
% identity
                   48
NCBI Description (U89959) Hypothetical protein [Arabidopsis thaliana]
                   419954
Seq. No.
                  uC-osrocyp011e09b1
Seq. ID
                  BLASTX
Method
NCBI GI
                   g5734759
                   337
BLAST score
                   2.0e-31
E value
                  108
Match length
                   55
% identity
```

NCBI Description (AC007651) Similar to Cytochrome P450 [Arabidopsis

E value

Match length

% identity

thaliana] 419955 Seq. No. Seq. ID uC-osrocyp011e10b1 BLASTX Method NCBI GI q585661 303 BLAST score 2.0e-27 E value 124 Match length 48 % identity PEROXIDASE PRECURSOR >gi 287401 dbj BAA03644 (D14997) NCBI Description peroxidase [Oryza sativa] 419956 Seq. No. Seq. ID uC-osrocyp011e11b1 BLASTX Method g3941480 NCBI GI 146 BLAST score 5.0e-09 E value Match length 38 71 % identity (AF062894) putative transcription factor [Arabidopsis NCBI Description thaliana] 419957 Seq. No. Seq. ID uC-osrocyp011e12a1 BLASTX Method NCBI GI g5262154 BLAST score 159 1.0e-10 E value 43 Match length 72 % identity (AL080237) putative protein [Arabidopsis thaliana] NCBI Description Seq. No. 419958 uC-osrocyp011e12b1 Seq. ID BLASTX Method q4836914 NCBI GI BLAST score 158 E value 2.0e-10 114 Match length % identity (AC007153) 68961 [Arabidopsis thaliana] NCBI Description Seq. No. 419959 Seq. ID uC-osrocyp011f03b1 Method BLASTX NCBI GI g1657621 BLAST score 398

NCBI Description (U72505) G6p [Arabidopsis thaliana] >gi_3068711 (AF049236) putative acyl-coA dehydrogenase [Arabidopsis thaliana]

>gi_5478795_dbj_BAA82478.1_ (AB017643) Short-chain acyl CoA

oxidase [Arabidopsis thaliana]

1.0e-38

122

```
Seq. No.
                  419960
                  uC-osrocyp011f05a1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3608481
BLAST score
                  157
                  2.0e-10
E value
Match length
                  44
% identity
                  70
                  (AF088913) ribosomal protein L27a [Petunia x hybrida]
NCBI Description
                  419961
Seq. No.
                  uC-osrocyp011f05b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g571484
BLAST score
                  350
                  5.0e-33
E value
Match length
                  87
% identity
                  72
                  (U16727) peroxidase precursor [Medicago truncatula]
NCBI Description
                  419962
Seq. No.
Seq. ID
                  uC-osrocyp011f06a1
                  BLASTX
Method
NCBI GI
                  g2499709
BLAST score
                  190
                   3.0e-14
E value
Match length
                  40
                   90
% identity
NCBI Description
                  PHOSPHOLIPASE D 1 PRECURSOR (PLD 1) (CHOLINE PHOSPHATASE 1)
                   (PHOSPHATIDYLCHOLINE-HYDROLYZING PHOSPHOLIPASE D 1)
                   >gi 1020415 dbj BAA11136 (D73411) phospholipase D [Oryza
                   sativa] >qi 1902903 dbj BAA19467 (AB001920) phospholipase
                   D [Oryza sativa]
                   419963
Seq. No.
                  uC-osrocyp011f07b1
Seq. ID
Method
                  BLASTX
                  g5880464
NCBI GI
BLAST score
                   475
                   1.0e-55
E value
Match length
                  167
% identity
                   64
                  (AF088901) actin bundling protein ABP135 [Lilium
NCBI Description
                   longiflorum]
                   419964
Seq. No.
                   uC-osrocyp011f08a1
Seq. ID
                  BLASTX
Method
NCBI GI
                   g1350986
BLAST score
                   330
E value
                   1.0e-30
Match length
                   68
                   99
% identity
NCBI Description 40S RIBOSOMAL PROTEIN S3A (CYC07 PROTEIN)
                   >gi_483431_dbj_BAA05059_ (D26060) cyc07 [Oryza sativa]
```

419965

Seq. No.

```
Seq. ID
                   uC-osrocyp011f08b1
Method
                   BLASTX
NCBI GI
                   q5596468
BLAST score
                   185
                   1.0e-13
E value
Match length
                   51
% identity
                   61
                   (AL096882) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   419966
                   uC-osrocyp011f09b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   q1350986
BLAST score
                   651
                   3.0e-68
E value
Match length
                   125
                   100
% identity
NCBI Description
                   40S RIBOSOMAL PROTEIN S3A (CYC07 PROTEIN)
                   >gi 483431 dbj BAA05059 (D26060) cyc07 [Oryza sativa]
                   419967
Seq. No.
                   uC-osrocyp011f10a1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g4887022
BLAST score
                   246
                   9.0e-21
E value
Match length
                   50
                   90
% identity
                   (AF123509) Nt-iaa4.1 deduced protein [Nicotiana tabacum]
NCBI Description
                   419968
Seq. No.
                   uC-osrocyp011f10b1
Seq. ID
                   BLASTX
Method
NCBI GI
                   g1353516
                    409
BLAST score
                    6.0e-40
E value
                   113
Match length
                    70
% identity
NCBI Description
                   (U38651) sugar transporter [Medicago truncatula]
                    419969
Seq. No.
                   uC-osrocyp011f12a1
Seq. ID
Method
                   BLASTX
                    g1710077
NCBI GI
BLAST score
                    175
                    2.0e-12
E value
                    51
Match length
                    71
% identity
                   PEROXIREDOXIN (REHYDRIN HOMOLOG) (B15C)
NCBI Description
                    >gi 2130029 pir S60285 B15C protein - barley
                   >gi_471321_emb_CAA54066 (X76605) HvB15C [Hordeum vulgare]
>gi_1694833_emb_CAA65387 (X96551) peroxiredoxin [Hordeum
                    vulgare]
Seq. No.
                    419970
                   uC-osrocyp011g02a1
Seq. ID
Method
                   BLASTX
```

```
NCBI GI
                  g4580466
BLAST score
                  362
E value
                  2.0e-39
Match length
                  121
% identity
                  70
                  (AC006081) putative 50S ribosomal protein L4 [Arabidopsis
NCBI Description
                  thaliana]
                  419971
Seq. No.
                  uC-osrocyp011g04a1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g6063540
BLAST score
                  897
                  5.0e-97
E value
Match length
                  180
% identity
                  96
                  (AP000615) similar to OsMlo-h1. (Z95353) [Oryza sativa]
NCBI Description
Seq. No.
                  419972
                  uC-osrocyp011g06b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g6063540
BLAST score
                  312
                  2.0e-59
E value
Match length
                  120
% identity
                  99
                  (APO00615) similar to OsMlo-h1. (Z95353) [Oryza sativa]
NCBI Description
Seq. No.
                  419973
                  uC-osrocyp011g07a1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1854378
                  225
BLAST score
E value
                  2.0e-18
                  50
Match length
                  84
% identity
                  (AB001338) Sucrose-Phosphate Synthase [Saccharum
NCBI Description
                  officinarum]
                  419974
Seq. No.
                  uC-osrocyp011g07b1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g1132482
BLAST score
                  40
                  4.0e-13
E value
                  108
Match length
% identity
                  84
NCBI Description Rice mRNA for ADP-ribosylation factor, complete cds
                   419975
Seq. No.
                  uC-osrocyp011g08b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1854378
BLAST score
                   614
                   6.0e-64
E value
Match length
                  142
% identity
                  84
```

NCBI Description

```
officinarum]
Seq. No.
                  419976
Seq. ID
                  uC-osrocyp011g10a1
                  BLASTX
Method
NCBI GI
                  g1346109
BLAST score
                  486
                  7.0e-49
E value
Match length
                  90
                  100
% identity
                  GUANINE NUCLEOTIDE-BINDING PROTEIN BETA SUBUNIT-LIKE
NCBI Description
                  PROTEIN (GPB-LR) (RWD) >gi_540535_dbj_BAA07404_ (D38231)
                  RWD [Oryza sativa]
                  419977
Seq. No.
Seq. ID
                  uC-osrocyp011g10b1
                  BLASTX
Method
NCBI GI
                  q4678943
BLAST score
                  204
                  7.0e-16
E value
Match length
                  83
                  52
% identity
                  (AL049711) putative protein [Arabidopsis thaliana]
NCBI Description
                  419978
Seq. No.
                  uC-osrocyp011g11a1
Seq. ID
                  BLASTX
Method
NCBI GI
                   g99758
BLAST score
                  179
                   7.0e-13
E value
Match length
                   46
                  72
% identity
                  monosaccharid transport protein STP4 - Arabidopsis thaliana
NCBI Description
                  >gi 16524 emb CAA47325_ (X66857) sugar transport protein
                   [Arabidopsis thaliana]
                   419979
Seq. No.
Seq. ID
                  uC-osrocyp011g11b1
Method
                  BLASTX
                   q2739431
NCBI GI
                   238
BLAST score
                   6.0e-21
E value
Match length
                   149
                   42
% identity
NCBI Description (U70368) hematopoietic-specific IL-2 deubiquitinating
                   enzyme [Mus musculus]
                   419980
Seq. No.
                   uC-osrocyp011g12b1
Seq. ID
Method
                   BLASTX
                   g1346109
NCBI GI
BLAST score
                   403
E value
                   5.0e-52
                   107
Match length
                   100
% identity
NCBI Description GUANINE NUCLEOTIDE-BINDING PROTEIN BETA SUBUNIT-LIKE
                                       55120
```

(AB001338) Sucrose-Phosphate Synthase [Saccharum

NCBI Description

```
RWD [Oryza sativa]
Seq. No.
                   419981
Seq. ID
                  uC-osrocyp011h01b1
                  BLASTX
Method
NCBI GI
                  q1255951
BLAST score
                  200
E value
                  2.0e-15
Match length
                  50
% identity
                  76
NCBI Description
                  (X96932) PS60 [Nicotiana tabacum]
Seq. No.
                   419982
Seq. ID
                  uC-osrocyp011h02b1
Method
                  BLASTX
NCBI GI
                  g1709620
BLAST score
                   358
E value
                   2.0e-36
Match length
                  128
                   62
% identity
NCBI Description
                  PROTEIN DISULFIDE ISOMERASE PRECURSOR (PDI) >gi 508975
                   (U11496) protein disulfide isomerase [Triticum aestivum]
                  >gi 1094851 prf 2106410A protein disulfide isomerase
                   [Triticum aestivum]
Seq. No.
                   419983
Seq. ID
                  uC-osrocyp011h03a1
Method
                  BLASTX
NCBI GI
                   g1546696
BLAST score
                   265
                   4.0e-23
E value
                  74
Match length
                  68
% identity
NCBI Description
                  (X98807) peroxidase ATP21a [Arabidopsis thaliana]
                   419984
Seq. No.
                  uC-osrocyp011h04b1
Seq. ID
Method
                   BLASTN
NCBI GI
                   g5441876
BLAST score
                   157
                   9.0e-83
E value
                   489
Match length
% identity
                   100
                  Oryza sativa genomic DNA, chromosome 2, clone:P0437H03
NCBI Description
                   (contig b)
                   419985
Seq. No.
                  uC-osrocyp011h05a1
Seq. ID
Method
                  BLASTX
NCBI GI
                   g3746568
BLAST score
                   495
E value
                   6.0e-50
Match length
                  114
% identity
                   78
```

PROTEIN (GPB-LR) (RWD) >gi 540535 dbj BAA07404 (D38231)

55121

beta subunit [Arabidopsis thaliana]

(AF061638) branched-chain alpha-keto acid decarboxylase E1

Seq. No.

419991

```
Seq. No.
                  419986
Seq. ID
                  uC-osrocyp011h06b1
Method
                  BLASTN
NCBI GI
                  g166671
BLAST score
                  37
E value
                   4.0e-11
Match length
                  65
                  89
% identity
NCBI Description A.thaliana middle repetative sequence
                  419987
Seq. No.
Seq. ID
                  uC-osrocyp011h09b1
Method
                  BLASTX
NCBI GI
                  q1402906
BLAST score
                  335
E value
                  3.0e-31
Match length
                  83
% identity
                  73
                  (X98314) peroxidase [Arabidopsis thaliana]
NCBI Description
                  >gi_4468977_emb_CAB38291_ (AL035605) peroxidase, prxr2
                   [Arabidopsis thaliana]
Seq. No.
                   419988
Seq. ID
                  uC-osrocyp011h10b1
Method
                  BLASTX
NCBI GI
                  g2760362
BLAST score
                   434
E value
                  8.0e-43
Match length
                  132
% identity
                   65
                  (AF016511) 15.9 kDa subunit of RNA polymerase II
NCBI Description
                   [Arabidopsis thaliana]
                   419989
Seq. No.
                  uC-osrocyp011h11b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1167955
BLAST score
                  176
E value
                  1.0e-12
Match length
                  78
                   44
% identity
                   (U43497) putative 32.7 kDa jasmonate-induced protein
NCBI Description
                   [Hordeum vulgare] >gi 2465428 (AF021257) 32 kDa protein
                   [Hordeum vulgare]
                   419990
Seq. No.
                  uC-osrocyp011h12b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3551245
BLAST score
                  313
E value
                  1.0e-28
                  115
Match length
                  58
% identity
                  (AB012702) P40-like protein [Daucus carota]
NCBI Description
```

```
uC-osrocyp012a01a1
Seq. ID
Method
                  BLASTX
                  g5902444
NCBI GI
BLAST score
                  264
                  5.0e-23
E value
                  132
Match length
                  49
% identity
                  (AB030283) GAG-POL precursor [Oryza sativa]
NCBI Description
                  419992
Seq. No.
Seq. ID
                  uC-osrocyp012a01b1
                  BLASTX
Method
NCBI GI
                  g5902444
BLAST score
                  481
                  1.0e-51
E value
Match length
                  158
                  72
% identity
                  (AB030283) GAG-POL precursor [Oryza sativa]
NCBI Description
Seq. No.
                  419993
                  uC-osrocyp012a02b1
Seq. ID
Method
                  BLASTX
                  q4455256
NCBI GI
BLAST score
                   502
                  1.0e-50
E value
                  114
Match length
                   77
% identity
                  (AL035523) protein-methionine-S-oxide reductase
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                   419994
Seq. ID
                   uC-osrocyp012a03a1
Method
                   BLASTX
NCBI GI
                   q3377950
BLAST score
                   251
                   2.0e-21
E value
Match length
                   71
% identity
                   56
NCBI Description
                  (AJ009830) cysteine proteinase precursor, AN11 [Ananas
                   comosus]
                   419995
Seq. No.
                   uC-osrocyp012a03b1
Seq. ID
Method
                  BLASTX
NCBI GI
                   q3377950
                   214
BLAST score
                   5.0e-17
E value
Match length
                   135
                   41
% identity
                   (AJ009830) cysteine proteinase precursor, AN11 [Ananas
NCBI Description
                   comosus]
                   419996
Seq. No.
                   uC-osrocyp012a05b1
Seq. ID
Method
                   BLASTX
                   g2088647
NCBI GI
```

BLAST score

2.0e-12 E value Match length 67 48 % identity NCBI Description (AF002109) hypothetical protein [Arabidopsis thaliana] >qi 3158394 (AF036340) LRR-containing F-box protein [Arabidopsis thaliana] 419997 Seq. No. Seq. ID uC-osrocyp012a06b1 BLASTX Method q4104457 NCBI GI 422 BLAST score 2.0e-41 E value 132 Match length 61 % identity (AF036172) 2-oxoglutarate/malate translocator [Zea mays] NCBI Description 419998 Seq. No. Seq. ID uC-osrocyp012a07b1 Method BLASTX NCBI GI q5922631 189 BLAST score 1.0e-14 E value Match length 53 74 % identity (AP000492) ESTs C26347(C12145), AU078074(C12145) correspond NCBI Description to a region of the predicted gene.; similar to prpol; Zea mays retrotransposon Cinful-1. (AF049110) [Oryza sativa] >gi 6016864 dbj BAA85207.1 (AP000570) ESTs $C26\overline{3}47(C121\overline{4}5)$, $\overline{A}U078074(C12145)$ correspond to a region of the predicted gene.; Similar to prpol; Zea mays retrotransposon Cinful-1. (AF049110) [Oryza sativa] Seq. No. 419999 uC-osrocyp012a09a1 Seq. ID Method BLASTX g3789942 NCBI GI 330 BLAST score E value 9.0e-31 66 Match length % identity 20 (AF093505) polyubiquitin [Saccharum hybrid cultivar NCBI Description H32-8560] 420000 Seq. No. uC-osrocyp012a09b1 Seq. ID Method BLASTX g100934 NCBI GI BLAST score 708 6.0e-75 E value Match length 142

polyubiquitin(ubiquitin) [maize, Peptide, 533 aa] [Zea

Seq. No.

Seq. ID

420006

uC-osrocyp012a12b1

```
mays]
                  420001
Seq. No.
Seq. ID
                  uC-osrocyp012a10a1
Method
                  BLASTX
                  g1781336
NCBI GI
                  149
BLAST score
                  2.0e-09
E value
Match length
                  54
                  56
% identity
                  (Y10469) peroxidase [Spinacia oleracea]
NCBI Description
                  420002
Seq. No.
Seq. ID
                  uC-osrocyp012a10b1
Method
                  BLASTX
                  g1781336
NCBI GI
BLAST score
                  500
                  2.0e-50
E value
                  164
Match length
                  60
% identity
                 (Y10469) peroxidase [Spinacia oleracea]
NCBI Description
                  420003
Seq. No.
                  uC-osrocyp012a11a1
Seq. ID
                  BLASTN
Method
                  g473983
NCBI GI
BLAST score
                  196
                  1.0e-106
E value
                  302
Match length
% identity
                  91
NCBI Description Rice mRNA, partial homologous to heat shock protein 82 gene
                   420004
Seq. No.
Seq. ID
                  uC-osrocyp012a11b1
Method
                  BLASTX
                   q417154
NCBI GI
BLAST score
                  755
                   2.0e-80
E value
                   170
Match length
% identity
                  HEAT SHOCK PROTEIN 82 >gi 100685 pir S25541 heat shock
NCBI Description
                  protein 82 - rice (strain Taichung Native One)
                  >gi_20256_emb_CAA77978_ (Z11920) heat shock protein 82
                   (HSP82) [Oryza sativa]
Seq. No.
                   420005
Seq. ID
                   uC-osrocyp012a12a1
Method
                   BLASTN
NCBI GI
                   g20280
BLAST score
                   340
                   0.0e + 00
E value
Match length
                   369
                   99
% identity
NCBI Description Rice gene for phenylalanine ammonia-lyase (EC 4.3.1.5)
```

```
BLASTX
Method
NCBI GI
                  g82496
                  703
BLAST score
                  2.0e-74
E value
                  153
Match length
                  90
% identity
NCBI Description phenylalanine ammonia-lyase (EC 4.3.1.5) - rice
                  420007
Seq. No.
Seq. ID
                  uC-osrocyp012b01a1
                  BLASTX
Method
NCBI GI
                  q829283
BLAST score
                  232
                  3.0e-19
E value
                  58
Match length
                  83
% identity
NCBI Description (Z15018) heat shock protein hsp82 [Oryza sativa]
Seq. No.
                  420008
Seq. ID
                  uC-osrocyp012b01b1
Method
                  BLASTX
NCBI GI
                  q417154
                  379
BLAST score
                  1.0e-36
E value
Match length
                  100
                  77
% identity
NCBI Description HEAT SHOCK PROTEIN 82 >gi_100685 pir S25541 heat shock
                  protein 82 - rice (strain Taichung Native One)
                  >gi_20256_emb_CAA77978_ (Z11920) heat shock protein 82
                   (HSP82) [Oryza sativa]
                  420009
Seq. No.
                  uC-osrocyp012b03a1
Seq. ID
                  BLASTN
Method
NCBI GI
                  g2196541
BLAST score
                  149
                  4.0e-78
E value
Match length
                  300
                  86
% identity
NCBI Description Oryza sativa glycine-rich protein mRNA, complete cds
Seq. No.
                  420010
Seq. ID
                  uC-osrocyp012b03b1
Method
                  BLASTN
NCBI GI
                  g2196541
BLAST score
                  233
E value
                  1.0e-128
Match length
                  233
% identity
                  100
NCBI Description Oryza sativa glycine-rich protein mRNA, complete cds
                  420011
Seq. No.
                  uC-osrocyp012b04b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1723239
BLAST score
                  339
```

1.0e-31

E value

```
Match length
                  157
% identity
                  42
                  HYPOTHETICAL 35.7 KD PROTEIN C26A3.11 IN CHROMOSOME I
NCBI Description
                  >gi 1177358 emb CAA93234 (Z69240) putative amidohydrolase
                  [Schizosaccharomyces pombe]
                  420012
Seq. No.
Seq. ID
                  uC-osrocyp012b06b1
Method
                  BLASTX
                  q4836876
NCBI GI
                  730
BLAST score
                  2.0e-77
E value
Match length
                  165
                  83
% identity
                  (ACO07260) Similar to dTDP-D-glucose 4,6-dehydratase
NCBI Description
                  [Arabidopsis thaliana]
                  420013
Seq. No.
Seq. ID
                  uC-osrocyp012b07b1
                  BLASTX
Method
                  q3395431
NCBI GI
BLAST score
                  234
                  2.0e-19
E value
Match length
                  93
% identity
                  48
                  (AC004683) unknown protein [Arabidopsis thaliana]
NCBI Description
                  420014
Seq. No.
Seq. ID
                  uC-osrocyp012b11a1
Method
                  BLASTX
NCBI GI
                  g4102839
BLAST score
                  220
E value
                  2.0e-20
Match length
                  93
                  52
% identity
                 (AF016713) LeOPT1 [Lycopersicon esculentum]
NCBI Description
                  420015
Seq. No.
Seq. ID
                  uC-osrocyp012b11b1
Method
                  BLASTX
NCBI GI
                  g4102839
BLAST score
                  340
E value
                  8.0e-32
Match length
                  102
% identity
                   62
                  (AF016713) LeOPT1 [Lycopersicon esculentum]
NCBI Description
                  420016
Seq. No.
                  uC-osrocyp012c02a1
Seq. ID
Method
                  BLASTX
```

Method BLASTX
NCBI GI g2880042
BLAST score 150
E value 1.0e-09
Match length 42
% identity 64

NCBI Description (AC002340) putative 3-hydroxyisobutyryl-coenzyme A

hydrolase [Arabidopsis thaliana]

Method

BLASTX

```
420017
Seq. No.
Seq. ID
                   uC-osrocyp012c03b1
Method
                  BLASTX
NCBI GI
                   g4572676
BLAST score
                   145
E value
                  7.0e-09
Match length
                   93
                   35
% identity
NCBI Description (AC006954) unknown protein [Arabidopsis thaliana]
Seq. No.
                   420018
                  uC-osrocyp012c04b1
Seq. ID
Method
                  BLASTX
NCBI GI
                   g1076748
BLAST score
                   217
E value
                   2.0e-17
Match length
                   87
% identity
                   51
                  major intrinsic protein - rice >gi_440869 dbj BAA04257
NCBI Description
                   (D17443) major intrinsic protein [Oryza sativa]
Seq. No.
                   420019
                  uC-osrocyp012c05a1
Seq. ID
Method
                  BLASTN
NCBI GI
                   g20191
                   375
BLAST score
E value
                   0.0e + 00
Match length
                  390
                   99
% identity
NCBI Description O.sativa mRNA for catalase
Seq. No.
                   420020
                  uC-osrocyp012c05b1
Seq. ID
Method
                  BLASTX
NCBI GI
                   g2130069
BLAST score
                   913
E value
                   6.0e-99
                  169
Match length
% identity
                   97
NCBI Description catalase (EC 1.11.1.6) catA - rice
                  >gi_1261858 dbj BAA06232 (D29966) catalase [Oryza sativa]
                   420021
Seq. No.
                  uC-osrocyp012c06a1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3080415
BLAST score
                  194
E value
                  8.0e-15
                  40
Match length
% identity
                  82
                  (AL022604) cysteine proteinase-like protein [Arabidopsis
NCBI Description
                  thaliana]
                   420022
Seq. No.
Seq. ID
                  uC-osrocyp012c06b1
```

Match length

```
NCBI GI
                  g641905
BLAST score
                  187
                   9.0e-14
E value
Match length
                  80
% identity
                   47
NCBI Description (U19267) cysteine proteinase [Zinnia elegans]
                  420023
Seq. No.
Seq. ID
                  uC-osrocyp012c07b1
Method
                  BLASTX
                  g4454050
NCBI GI
BLAST score
                  159
E value
                  1.0e-10
                  75
Match length
                  51
% identity
NCBI Description (AL035394) putative protein [Arabidopsis thaliana]
Seq. No.
                  420024
Seq. ID
                  uC-osrocyp012c08b1
Method
                  BLASTX
NCBI GI
                  q118497
                   503
BLAST score
                   6.0e-51
E value
Match length
                  150
% identity
                   63
NCBI Description ALDEHYDE DEHYDROGENASE, CYTOSOLIC 1 (ALDH CLASS 1) (ALHDII)
                   (ALDH-E1) >gi_91935_pir__A32616 aldehyde dehydrogenase
                   (NAD+) (EC 1.2.1.3) PB, cytosolic - rat >gi_202846 (M23995)
                   aldehyde dehydrogenase (EC 1.2.1.3) [Rattus norvegicus]
                   420025
Seq. No.
                  uC-osrocyp012c10a1
Seq. ID
                  BLASTN
Method
NCBI GI
                  q20280
BLAST score
                   241
E value
                   1.0e-133
Match length
                   324
                   94
% identity
NCBI Description Rice gene for phenylalanine ammonia-lyase (EC 4.3.1.5)
Seq. No.
                   420026
                  uC-osrocyp012c10b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   q82496
BLAST score
                   521
                   4.0e-53
E value
                   125
Match length
% identity
                   82
NCBI Description phenylalanine ammonia-lyase (EC 4.3.1.5) - rice
                   420027
Seq. No.
                   uC-osrocyp012c11b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g1001649
BLAST score
                   526
                   1.0e-53
E value
                   157
```

```
% identity
NCBI Description
                   (D64002) DNA gyrase A subunit [Synechocystis sp.]
Seq. No.
                   420028
Seq. ID
                  uC-osrocyp012d01b1
                  BLASTX
Method
NCBI GI
                   q1076809
BLAST score
                   717
                   6.0e-76
E value
                   152
Match length
                   93
% identity
                  H+-transporting ATPase (EC 3.6.1.35) - maize
NCBI Description
                  >gi 758355 emb CAA59800 (X85805) H(+)-transporting ATPase
                   [Zea mays]
                   420029
Seq. No.
Seq. ID
                  uC-osrocyp012d02b1
                  BLASTX
Method
NCBI GI
                   a3150410
BLAST score
                   208
E value
                   3.0e-16
                  160
Match length
% identity
                   29
NCBI Description (AC004165) unknown protein [Arabidopsis thaliana]
                   420030
Seq. No.
                   uC-osrocyp012d04b1
Seq. ID
                  BLASTX
Method
NCBI GI
                   q4056507
BLAST score
                   358
                   7.0e - 34
E value
Match length
                   98
                   73
% identity
NCBI Description
                   (AC005896) putative RNA binding protein [Arabidopsis
                   thaliana]
                   420031
Seq. No.
                   uC-osrocyp012d05a1
Seq. ID
```

Method BLASTN NCBI GI q6016845 BLAST score 69 4.0e-31 E value 85 Match length 95 % identity

NCBI Description Oryza sativa genomic DNA, chromosome 1, clone:P0711E10

420032 Seq. No.

uC-osrocyp012d05b1 Seq. ID

Method BLASTN NCBI GI g6016845 BLAST score 213 E value 1.0e-116 434 Match length 97 % identity

NCBI Description Oryza sativa genomic DNA, chromosome 1, clone:P0711E10

420033 Seq. No.

uC-osrocyp012d07b1 Seq. ID Method BLASTX NCBI GI g5732432 BLAST score 466 E value 2.0e-46 170 Match length 54 % identity NCBI Description (AF177535) contains similarity to Pfam family PF01331 mRNA capping enzyme; score=24.3, E=1.3e-11, E=1 [Arabidopsis thaliana] 420034 Seq. No. Seq. ID uC-osrocyp012d08b1 Method BLASTX NCBI GI q2245125 BLAST score 156 E value 3.0e-10 Match length 52 % identity 60

NCBI Description (Z97343) hypothetical protein [Arabidopsis thaliana]

420035 Seq. No.

Seq. ID uC-osrocyp012d09b1

Method BLASTX NCBI GI g4519615 BLAST score 147 4.0e-09 E value 78 Match length % identity 45

NCBI Description (AB017594) RPE65 [Gallus gallus]

420036 Seq. No.

Seq. ID uC-osrocyp012d10a1

Method BLASTN NCBI GI g2196541 BLAST score 230 E value 1.0e-126 Match length 348 % identity 96

NCBI Description Oryza sativa glycine-rich protein mRNA, complete cds

Seq. No. 420037

Seq. ID uC-osrocyp012d10b1

Method BLASTX NCBI GI g2293480 BLAST score 432 1.0e-42E value Match length 84 100 % identity

NCBI Description (AF011331) glycine-rich protein [Oryza sativa]

Seq. No. 420038

uC-osrocyp012d11b1 Seq. ID

Method BLASTX NCBI GI q5262154 BLAST score 159 E value 1.0e-10

Match length 33 % identity NCBI Description (AL080237) putative protein [Arabidopsis thaliana] Seq. No. 420039 Seq. ID uC-osrocyp012d12b1 Method BLASTX NCBI GI q3298547 BLAST score 218 E value 2.0e-17 Match length 104 49 % identity NCBI Description (AC004681) putative condensin protein [Arabidopsis thaliana] 420040 Seq. No. Seq. ID uC-osrocyp012e01b1 Method BLASTX NCBI GI q1351136 BLAST score 411 E value 2.0e-46 Match length 126 75 % identity NCBI Description SUCROSE SYNTHASE 2 (SUCROSE-UDP GLUCOSYLTRANSFERASE 2) >gi_514946 (L22296) UDP-glucose:D-fructose 2-glucosyl-transferase [Zea mays] >gi_533252 (L33244) sucrose synthase 2 [Zea mays] Seq. No. 420041 uC-osrocyp012e03a1 Seq. ID Method BLASTX NCBI GI g4960156 BLAST score 276 E value 2.0e-24 Match length 55 % identity 95 NCBI Description (AF153284) putative progesterone-binding protein homolog [Arabidopsis thaliana] 420042 Seq. No. uC-osrocyp012e05b1 Seq. ID Method BLASTX NCBI GI g4204265 BLAST score 182 E value 3.0e-13 59 Match length % identity 59 NCBI Description (AC005223) 45643 [Arabidopsis thaliana] 420043 Seq. No.

Seq. ID uC-osrocyp012e06b1

Method BLASTX
NCBI GI g4455246
BLAST score 290
E value 7.0e-26
Match length 106
% identity 59

```
NCBI Description (AL035523) putative protein [Arabidopsis thaliana]
Seq. No.
                  420044
Seq. ID
                  uC-osrocyp012e10b1
Method
                  BLASTX
NCBI GI
                  g3258575
                  525
BLAST score
                  2.0e-53
E value
Match length
                  141
% identity
                  70
NCBI Description
                 (U89959) Hypothetical protein [Arabidopsis thaliana]
                  420045
Seq. No.
Seq. ID
                  uC-osrocyp012f01a1
Method
                  BLASTX
                  g4574139
NCBI GI
BLAST score
                  170
                  4.0e-12
E value
Match length
                  39
% identity
                  90
NCBI Description (AF073697) cysteine synthase [Oryza sativa]
                  420046
Seq. No.
Seq. ID
                  uC-osrocyp012f01b1
Method
                  BLASTX
                  q4574139
NCBI GI
BLAST score
                  426
                  4.0e-42
E value
Match length
                  88
% identity
                  97
NCBI Description (AF073697) cysteine synthase [Oryza sativa]
Seq. No.
                  420047
Seq. ID
                  uC-osrocyp012f05b1
Method
                  BLASTX
NCBI GI
                  g1168537
BLAST score
                  556
                  4.0e-57
E value
Match length
                  133
% identity
                  82
NCBI Description ASPARTIC PROTEINASE PRECURSOR >gi 82458 pir JS0732
                  aspartic proteinase (EC 3.4.23.-) - rice
                  >gi 218143 dbj BAA02242 (D12777) aspartic proteinase
                  [Oryza sativa]
                  420048
Seq. No.
                  uC-osrocyp012f06b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2244797
BLAST score
                  232
E value
                  4.0e-19
```

Match length 152 38 % identity

NCBI Description (Z97336) hypothetical protein [Arabidopsis thaliana]

420049 Seq. No.

Seq. ID uC-osrocyp012f07b1



```
BLASTX
Method
NCBI GI
                  g2213629
                  397
BLAST score
                  1.0e-38
E value
Match length
                  103
% identity
                  67
NCBI Description (AC000103) F21J9.21 [Arabidopsis thaliana]
Seq. No.
                  420050
Seq. ID
                  uC-osrocyp012f08b1
Method
                  BLASTX
NCBI GI
                  g2984709
BLAST score
                  466
E value
                  1.0e-46
                  109
Match length
                  83
% identity
NCBI Description (AF053468) DnaJ-related protein ZMDJ1 [Zea mays]
Seq. No.
                  420051
Seq. ID
                  uC-osrocyp012f09a1
Method
                  BLASTN
                  g5051932
NCBI GI
BLAST score
                  42
                  3.0e-14
E value
Match length
                  143
% identity
                  81
NCBI Description Oryza sativa MADS-box protein FDRMADS8 mRNA, complete cds
                  420052
Seq. No.
Seq. ID
                  uC-osrocyp012f10a1
Method
                  BLASTX
                  q1076746
NCBI GI
BLAST score
                  207
                  2.0e-16
E value
Match length
                  70
% identity
                  64
                  heat shock protein 70 - rice (fragment)
NCBI Description
                  >gi_763160 emb CAA47948 (X67711) heat shock protein 70
                  [Oryza sativa]
Seq. No.
                  420053
Seq. ID
                  uC-osrocyp012f10b1
Method
                  BLASTX
NCBI GI
                  q1076746
BLAST score
                  741
E value
                  9.0e-79
Match length
                  172
                  85
% identity
NCBI Description
                  heat shock protein 70 - rice (fragment)
                  >gi_763160 emb CAA47948_ (X67711) heat shock protein 70
```

[Oryza sativa]

Seq. No. 420054

uC-osrocyp012f11a1 Seq. ID

Method BLASTX NCBI GI q4678268 BLAST score 239

```
4.0e-20
E value
Match length
                  51
                  82
% identity
NCBI Description (AL049660) putative protein [Arabidopsis thaliana]
                  420055
Seq. No.
Seq. ID
                  uC-osrocyp012f11b1
                  BLASTX
Method
NCBI GI
                  q4678268
BLAST score
                  361
                  3.0e - 34
E value
                  77
Match length
                  79
% identity
NCBI Description (AL049660) putative protein [Arabidopsis thaliana]
                  420056
Seq. No.
Seq. ID
                  uC-osrocyp012f12b1
Method
                  BLASTX
NCBI GI
                  q113261
                  723
BLAST score
                  1.0e-76
E value
Match length
                  148
% identity
                  96
NCBI Description ACTIN 7 >gi 71637 pir ATRZ7 actin 7 - rice
                  >gi 20333 emb CAA33872 (X15863) actin [Oryza sativa]
                  420057
Seq. No.
Seq. ID
                  uC-osrocyp012g01b1
                  BLASTX
Method
NCBI GI
                  q4581155
BLAST score
                  192
                  1.0e-14
E value
                  137
Match length
% identity
NCBI Description (AC006919) putative receptor kinase [Arabidopsis thaliana]
                  420058
Seq. No.
                  uC-osrocyp012g02b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q5596468
BLAST score
                  182
E value
                  2.0e-13
Match length
                  78
% identity
NCBI Description (AL096882) putative protein [Arabidopsis thaliana]
Seq. No.
                  420059
                  uC-osrocyp012g05b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2494165
BLAST score
                  252
                  2.0e-21
E value
Match length
                  69
                  71
% identity
                  DNA LIGASE (POLYDEOXYRIBONUCLEOTIDE SYNTHASE [ATP])
NCBI Description
                  >gi 2129574 pir S71278 DNA ligase - Arabidopsis thaliana
```

>gi 1359495 emb CAA66599 (X97924) DNA ligase [Arabidopsis

% identity

thaliana]

```
420060
Seq. No.
                  uC-osrocyp012g06b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2760317
BLAST score
                  210
                  2.0e-16
E value
                  69
Match length
                  62
% identity
                 (AC002130) F1N21.1 [Arabidopsis thaliana]
NCBI Description
                  420061
Seq. No.
                  uC-osrocyp012g08b1
Seq. ID
Method
                  BLASTN
NCBI GI
                  q444046
                  59
BLAST score
                  3.0e-24
E value
                  95
Match length
                  91
% identity
NCBI Description Z.mays OBF1 mRNA for ocs-element binding factor
Seq. No.
                  420062
                  uC-osrocyp012g09b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1351877
BLAST score
                  159
E value
                  1.0e-10
Match length
                  83
                  45
% identity
                 ALCOHOL DEHYDROGENASE II >gi 82845 pir S20911 alcohol
NCBI Description
                  dehydrogenase (EC 1.1.1.1) II - yeast (Kluyveromyces
                  marxianus var. lactis) >gi_2833_emb_CAA45739 (X64397)
                  Alcohol Dehydrogenase II [Kluyveromyces lactis]
                  420063
Seq. No.
Seq. ID
                  uC-osrocyp012g11a1
Method
                  BLASTX
NCBI GI
                  q121349
                  447
BLAST score
                  1.0e-44
E value
                  84
Match length
% identity
                  100
NCBI Description GLUTAMINE SYNTHETASE SHOOT ISOZYME (GLUTAMATE--AMMONIA
                  LIGASE) (CLONE LAMBDA-GS28) >gi_20368_emb_CAA32461
                  (X14245) cytosolic glutamine synthetase (AA 1-356) [Oryza
                  sativa]
                  420064
Seq. No.
                  uC-osrocyp012g11b1
Seq. ID
                  BLASTX
Method
NCBI GI
                  q121349
BLAST score
                  801
                  7.0e-86
E value
Match length
                  148
```

NCBI Description GLUTAMINE SYNTHETASE SHOOT ISOZYME (GLUTAMATE--AMMONIA

Seq. No.

Seq. ID Method

NCBI GI

E value

Seq. No.

Seq. ID Method

NCBI GI

E value

Seq. No.

Seq. ID Method

NCBI GI

E value

Seq. No. Seq. ID

Method

NCBI GI

E value

BLAST score

Match length

% identity

```
LIGASE) (CLONE LAMBDA-GS28) >gi 20368 emb CAA32461
                  (X14245) cytosolic glutamine synthetase (AA 1-356) [Oryza
                  sativa]
                  420065
                  uC-osrocyp012g12b1
                  BLASTX
                  g4678280
                  239
                  6.0e-20
                  155
                  35
NCBI Description (AL049660) zinc finger-like protein [Arabidopsis thaliana]
                  420066
                  uC-osrocyp012h01b1
                  BLASTX
                  g419781
                  198
                  6.0e-21
                  86
                  61
NCBI Description
                  probable cysteine proteinase precursor (clone CYP-7) -
                  common tobacco >gi 19849 emb CAA78361 (Z13959) tobacco
                  pre-pro-cysteine proteinase [Nicotiana tabacum]
                  420067
                  uC-osrocyp012h04a1
                  BLASTX
                  g902584
                  171
                  4.0e-12
                  34
                  15
NCBI Description
                 (U29159) polyubiquitin containing 7 ubiquitin monomers [Zea
                  mays]
                  420068
                  uC-osrocyp012h04b1
                  BLASTX
                  q418854
                  888
                  5.0e-96
                  184
                  18
NCBI Description
                  ubiquitin precursor - parsley >gi 288112 emb CAA45621
                  (X64344) polyubiquitin [Petroselinum crispum]
                  >gi_288114_emb_CAA45622_ (X64345) polyubiquitin
                  [Petroselinum crispum]
```

Seq. No. 420069

Seq. ID uC-osrocyp012h05a1

Method BLASTN NCBI GI g1132482 BLAST score 366 E value 0.0e+00Match length 390

```
% identity
 NCBI Description Rice mRNA for ADP-ribosylation factor, complete cds
                   420070
 Seq. No.
                   uC-osrocyp012h05b1
 Seq. ID
Method
                   BLASTX
NCBI GI
                   g1703380
 BLAST score
                   618
E value
                   2.0e-64
Match length
                   122
 % identity
                   99
NCBI Description ADP-RIBOSYLATION FACTOR >gi 1132483 dbj BAA04607 (D17760)
                   ADP-ribosylation factor [Oryza sativa]
Seq. No.
                   420071
                   uC-osrocyp012h07a1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3757522
BLAST score
                   154
E value
                   4.0e-10
                   41
Match length
 % identity
                   68
NCBI Description (AC005167) putative splicing factor [Arabidopsis thaliana]
                   420072
Seq. No.
Seq. ID
                   uC-osrocyp012h07b1
Method
                   BLASTX
NCBI GI
                   g3757522
BLAST score
                   455
E value
                   3.0e-45
Match length
                   124
                   73
 % identity
NCBI Description (AC005167) putative splicing factor [Arabidopsis thaliana]
                   420073
Seq. No.
                   uC-osrocyp012h09b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g4138583
BLAST score
                   289
E value
                   9.0e-26
                   70
Match length
 % identity
NCBI Description (Y10821) plastidic ATP/ADP-transporter [Solanum tuberosum]
Seq. No.
                   420074
Seq. ID
                   uC-osrocyp012h11b1
Method
                   BLASTX
NCBI GI
                   g4678362
BLAST score
                   217
E value
                   3.0e-19
Match length
                   99
 % identity
                   52
NCBI Description
                   (AL049659) protein kinase-like protein [Arabidopsis
                   thaliana]
Seq. No.
                   420075
Seq. ID
                   uC-osrocyp013a01b1
```

NCBI Description

420080

Seq. No.

```
Method
                  BLASTX
NCBI GI
                  g3421413
BLAST score
                   212
                   4.0e-22
E value
                  86
Match length
                  75
% identity
                   (AF081922) protein phosphatase 2A 55 kDa B regulatory
NCBI Description
                   subunit [Oryza sativa] >gi 3421415 (AF081923) protein
                  phosphatase 2A 55 kDa B regulatory subunit [Oryza sativa]
                   420076
Seq. No.
                  uC-osrocyp013a07b1
Seq. ID
Method
                  BLASTX
NCBI GI
                   q129591
BLAST score
                   324
                   4.0e-30
E value
                  95
Match length
% identity
                   68
                  PHENYLALANINE AMMONIA-LYASE >gi 295824 emb CAA34226
NCBI Description
                   (X16099) phenylalanine ammonia-lyase [Oryza sativa]
                   420077
Seq. No.
Seq. ID
                   uC-osrocyp013a09b1
Method
                  BLASTX
NCBI GI
                   q4103987
BLAST score
                   519
                   8.0e-53
E value
Match length
                   137
% identity
                   73
NCBI Description
                  (AF030516) 5,10-methylenetetrahydrofolate
                  dehydrogenase-5,10-methenyltetrahydrofolate cyclohydrolase
                   [Pisum sativum] >gi 6002383 emb CAB56756.1 (AJ011589)
                   5,10-methylenetetrahydrofolate dehydrogenase:
                   5,10-methenyltetrahydrofolate cyclohydrolase [Pisum
                   sativum]
Seq. No.
                   420078
Seq. ID
                   uC-osrocyp013a10b1
Method
                   BLASTX
NCBI GI
                   g1944573
BLAST score
                   436
                   3.0e-43
E value
Match length
                   123
% identity
                  (Z49146) phenylalanine ammonia-lyase [Hordeum vulgare]
NCBI Description
                   420079
Seq. No.
Seq. ID
                   uC-osrocyp013a12b1
Method
                   BLASTX
NCBI GI
                   q3337361
BLAST score
                   176
                   3.0e-13
E value
Match length
                   70
% identity
                   49
```

55139

(AC004481) ankyrin-like protein [Arabidopsis thaliana]

Method

NCBI GI

E value

BLAST score

Match length

BLASTX

372

115

q4490309

1.0e-35

```
Seq. ID
                  uC-osrocyp013b01b1
Method
                  BLASTX
NCBI GI
                  g3075400
BLAST score
                  261
E value
                  1.0e-22
Match length
                  74
                  65
% identity
NCBI Description
                  (AC004484) putative thromboxane-A synthase [Arabidopsis
                  thaliana] >gi 3413720 (AC004747) putative thromboxin-A
                  synthase [Arabidopsis thaliana]
Seq. No.
                  420081
Seq. ID
                  uC-osrocyp013b04b1
                  BLASTX
Method
NCBI GI
                  q1362086
BLAST score
                  434
E value
                  7.0e-48
Match length
                  116
% identity
                  91
                  5-methyltetrahydropteroyltriglutamate--homocysteine
NCBI Description
                  S-methyltransferase (EC 2.1.1.14) - Madagascar periwinkle
                  >gi 2129919 pir S65957
                  5-methyltetrahydropteroyltriglutamate--homocysteine
                  S-methyltransferase (EC 2.1.1.14) - Madagascar periwinkle
                  >gi_886471_emb_CAA58474_ (X83499) methionine synthase
                  [Catharanthus roseus]
Seq. No.
                  420082
Seq. ID
                  uC-osrocyp013b07b1
Method
                  BLASTX
                  g417154
NCBI GI
BLAST score
                  747
                  1.0e-79
E value
Match length
                  157
                  94
% identity
                 HEAT SHOCK PROTEIN 82 >gi 100685 pir S25541 heat shock
NCBI Description
                  protein 82 - rice (strain Taichung Native One)
                  >gi 20256 emb CAA77978 (Z11920) heat shock protein 82
                   (HSP82) [Oryza sativa]
                  420083
Seq. No.
                  uC-osrocyp013c01b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2642443
BLAST score
                  184
E value
                  2.0e-17
                  87
Match length
                  48
% identity
NCBI Description
                  (AC002391) putative cytochrome P450 [Arabidopsis thaliana]
                  420084
Seq. No.
                  uC-osrocyp013c02b1
Seq. ID
```

```
% identity
NCBI Description
                   (AL035678) peroxidase ATP17a-like protein [Arabidopsis
                   thaliana]
Seq. No.
                   420085
                  uC-osrocyp013c07b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3540180
BLAST score
                  165
E value
                  2.0e-11
Match length
                  93
% identity
                  41
NCBI Description (AC004122) Unknown protein [Arabidopsis thaliana]
Seq. No.
                  420086
Seq. ID
                  uC-osrocyp013c08b1
Method
                  BLASTX
NCBI GI
                  q2791806
BLAST score
                  246
E value
                  9.0e-21
Match length
                  73
% identity
NCBI Description (AF041433) bet3 [Mus musculus]
Seq. No.
                  420087
Seq. ID
                  uC-osrocyp013d02b1
Method
                  BLASTX
NCBI GI
                  g1076746
BLAST score
                  726
                  4.0e-77
E value
Match length
                  148
% identity
                  99
NCBI Description
                  heat shock protein 70 - rice (fragment)
                  >gi 763160 emb CAA47948 (X67711) heat shock protein 70
                   [Oryza sativa]
Seq. No.
                  420088
Seq. ID
                  uC-osrocyp013d04b1
Method
                  BLASTX
NCBI GI
                  g123620
                  502
BLAST score
E value
                  2.0e-54
Match length
                  117
% identity
                  90
                 HEAT SHOCK COGNATE 70 KD PROTEIN 2 >gi_100224_pir__S14950
NCBI Description
                  heat shock cognate protein 70 - tomato
                  >gi_19258_emb_CAA37971_ (X54030) heat shock protein cognate
                  70 [Lycopersicon esculentum]
                  420089
Seq. No.
Seq. ID
                  uC-osrocyp013d05b1
Method
                  BLASTX
NCBI GI
                  g1084461
BLAST score
                  196
E value
                  6.0e-15
Match length
                  44
% identity
                  84
```

E value

Match length

6.0e-09

42

NCBI Description RCc3 protein - rice >gi_786132 (L27208) RCc3 [Oryza sativa] Seq. No. 420090 Seq. ID uC-osrocyp013d06b1 Method BLASTX NCBI GI q3087888 BLAST score 328 E value 1.0e-30 113 Match length % identity 59 NCBI Description (X94302) hexokinase [Solanum tuberosum] Seq. No. 420091 Seq. ID uC-osrocyp013d07b1 Method BLASTX NCBI GI g1702996 BLAST score 466 3.0e-63 E value Match length 149 % identity 87 PROTEIN PHOSPHATASE PP2A, 65 KD REGULATORY SUBUNIT, ALPHA NCBI Description ISOFORM (PROTEIN PHOSPHATASE PP2A SUBUNIT A, ALPHA ISOFORM) (PR65-ALPHA) >gi_510469_emb_CAA84414_ (Z34955) protein phosphatase 2A 65 kDa regulatory subunit, alpha isoform [Sus scrofa] >gi_4514639 dbj_BAA75478.1 (AB021743) PR65 [Mus musculus] Seq. No. 420092 Seq. ID uC-osrocyp013d08b1 Method BLASTX NCBI GI q100665 BLAST score 341 E value 2.0e-35 Match length 80 % identity 55 NCBI Description calmodulin 2 (clone lambda DASH) - rice >gi 20190 emb CAA78288 (Z12828) calmodulin [Oryza sativa] >gi_310313 (L18914) calmodulin [Oryza sativa] Seq. No. 420093 Seq. ID uC-osrocyp013e02b1 Method BLASTX NCBI GI q2979565 BLAST score 431 E value 2.0e-42 Match length 112 % identity 74 NCBI Description (AC003680) putative sin3 associated polypeptide (SAP18) [Arabidopsis thaliana] Seq. No. 420094 Seq. ID uC-osrocyp013e11b1 Method BLASTX NCBI GI g1170767 BLAST score 144

BLAST score

E value

395

3.0e-38

```
% identity
NCBI Description
                  26S PROTEASE REGULATORY SUBUNIT 8 HOMOLOG (LET1 PROTEIN)
                  >gi_626074_pir__S45176 transcription factor SUG1 homolog -
                  fission yeast (Schizosaccharomyces pombe) >qi 406051
                  (U02280) Let1 [Schizosaccharomyces pombe]
                  >gi 4106689 emb CAA22628.1 (AL035065) 26s protease
                  regulatory subunit 8 homolog [Schizosaccharomyces pombe]
Seq. No.
                  420095
Seq. ID
                  uC-osrocyp013f03b1
Method
                  BLASTX
                  g2655098
NCBI GI
BLAST score
                  293
                  2.0e-26
E value
                  120
Match length
% identity
                  53
NCBI Description (AF023472) peptide transporter [Hordeum vulgare]
Seq. No.
                  420096
Seq. ID
                  uC-osrocyp013f06b1
Method
                  BLASTN
                  g3287498
NCBI GI
BLAST score
                  41
E value
                  1.0e-13
Match length
                  49
% identity
                  96
NCBI Description Oryza sativa gene for importin alpha, complete cds
Seq. No.
                  420097
Seq. ID
                  uC-osrocyp013f08b1
Method
                  BLASTX
                  g3219969
NCBI GI
BLAST score
                  157
E value
                  2.0e-10
Match length
                  56
                  48
% identity
NCBI Description
                 HYPOTHETICAL 22.4 KD PROTEIN C6G10.10C IN CHROMOSOME I
                  >gi_2330874_emb_CAB11296.1_ (Z98603) hypothetical protein
                  [Schizosaccharomyces pombe]
Seq. No.
                  420098
Seq. ID
                  uC-osrocyp013f11b1
Method
                  BLASTN
NCBI GI
                  q5091496
BLAST score
                  36
E value
                  1.0e-10
Match length
                  36
% identity
                  100
NCBI Description Oryza sativa genomic DNA, chromosome 6, clone P0680A03,
                  complete sequence
Seq. No.
                  420099
Seq. ID
                  uC-osrocyp013f12b1
Method
                  BLASTX
NCBI GI
                  g1416514
```



```
99
Match length
                  75
% identity
                  (D63168) CTP:phosphocholine cytidylyltransferase [Brassica
NCBI Description
                  napus]
Seq. No.
                  420100
Seq. ID
                  uC-osrocyp013g02b1
                  BLASTX
Method
NCBI GI
                  q1076746
BLAST score
                  315
E value
                  5.0e-29
                  111
Match length
                  62
% identity
                  heat shock protein 70 - rice (fragment)
NCBI Description
                  >gi_763160_emb_CAA47948_ (X67711) heat shock protein 70
                   [Oryza sativa]
                  420101
Seq. No.
Seq. ID
                  uC-osrocyp013g03b1
Method
                  BLASTN
NCBI GI
                  q20280
BLAST score
                  127
                  5.0e-65
E value
                  223
Match length
% identity
                  90
NCBI Description Rice gene for phenylalanine ammonia-lyase (EC 4.3.1.5)
                   420102
Seq. No.
Seq. ID
                  uC-osrocyp013g04b1
Method
                  BLASTX
                  q445126
NCBI GI
BLAST score
                   429
E value
                   4.0e-47
Match length
                   116
% identity
                   82
NCBI Description heat shock protein HSP81-1 [Arabidopsis thaliana]
Seq. No.
                   420103
Seq. ID
                   uC-osrocyp013g07b1
Method
                  BLASTX
NCBI GI
                  g1136122
BLAST score
                   546
                   4.0e-56
E value
Match length
                   102
% identity
                   97
NCBI Description (X91807) alfa-tubulin [Oryza sativa]
                   420104
Seq. No.
                   uC-osrocyp013g09b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g4585985
```

NCBI GI g4585985
BLAST score 156
E value 1.0e-10
Match length 80
% identity 38

NCBI Description (AC005287) Hypothetical protein [Arabidopsis thaliana]

Seq. No. 420105 Seq. ID uC-osrocyp013g10b1 Method BLASTX NCBI GI g2501353 BLAST score 496 9.0e-57 E value 120 Match length % identity 95 TRANSKETOLASE, CHLOROPLAST (TK) >gi_1084440_pir__\$54300 NCBI Description transketolase (EC 2.2.1.1) 3 - Craterostigma plantagineum $(fragment) > gi_664901_emb_CAA86607_ (Z46646) transketolase$ [Craterostigma plantagineum] 420106 Seq. No. uC-osrocyp013g11b1 Seq. ID Method BLASTX NCBI GI q4836950 BLAST score 233 3.0e-19 E value 123 Match length % identity 44 NCBI Description (AC006085) Hypothetical protein [Arabidopsis thaliana] Seq. No. 420107 uC-osrocyp013h01b1 Seq. ID Method BLASTX NCBI GI q3928092 BLAST score 173 E value 3.0e-12 Match length 53 58 % identity NCBI Description (AC005770) unknown protein [Arabidopsis thaliana] Seq. No. 420108 uC-osrocyp013h02b1 Seq. ID Method BLASTX NCBI GI g3334349 BLAST score 417 E value 3.0e-41Match length 100 % identity 78 NCBI Description GLYCYL-TRNA SYNTHETASE (GLYCINE--TRNA LIGASE) (GLYRS) >gi_2564215_emb CAA05162 (AJ002062) glycyl-tRNA synthetase [Arabidopsis thaliana] 420109 Seq. No. Seq. ID uC-osrocyp013h05b1 Method BLASTX NCBI GI g5031281 BLAST score 286 E value 1.0e-25

75 Match length % identity 71

NCBI Description (AF139499) unknown [Prunus armeniaca]

Seq. No. 420110

Seq. ID uC-osrocyp013h07b1

Match length

% identity

```
Method
                 BLASTX
NCBI GI
                 g6063540
BLAST score
                 490
E value
                 6.0e-68
                 147
Match length
                 92
% identity
NCBI Description (AP000615) similar to OsMlo-h1. (Z95353) [Oryza sativa]
                 420111
Seq. No.
Seq. ID
                 uC-osrocyp013h08b1
                 BLASTX
Method
                 g1703380
NCBI GI
BLAST score
                 844
E value
                 7.0e-91
                 165
Match length
                 99
% identity
NCBI Description ADP-RIBOSYLATION FACTOR >gi 1132483 dbj BAA04607 (D17760)
                 ADP-ribosylation factor [Oryza sativa]
Seq. No.
                 420112
Seq. ID
                 uC-osrocyp013h09b1
                 BLASTX
Method
NCBI GI
                 g2293480
BLAST score
                 424
                 1.0e-41
E value
                 89
Match length
                 94
% identity
NCBI Description (AF011331) glycine-rich protein [Oryza sativa]
Seq. No.
                 420113
Seq. ID
                 uC-osrocyp013h10b1
Method
                 BLASTX
                 a1853974
NCBI GI
BLAST score
                 423
E value
                 1.0e-41
Match length
                 137
                 65
% identity
NCBI Description (D14481) putative peroxidase [Oryza sativa]
Seq. No.
                 420114
Seq. ID
                 uC-osrocyp013h11b1
Method
                 BLASTX
NCBI GI
                 q2570503
BLAST score
                 145
E value
                 6.0e-17
Match length
                81
% identity
                 63
NCBI Description (AF022734) zinc inducible protein [Oryza sativa]
Seq. No.
                 420115
                 uC-osrocyp013h12b1
Seq. ID
Method
                 BLASTX
                 NCBI GI
BLAST score
                 395
E value
                 3.0e-38
```

```
(AB016065) mitochondrial phosphate transporter [Oryza
NCBI Description
                  sativa]
Seq. No.
                  420116
Seq. ID
                  uC-osrocyp014a01a1
Method
                  BLASTX
NCBI GI
                  q133999
BLAST score
                  161
                  2.0e-20
E value
                  68
Match length
                  87
% identity
NCBI Description CHLOROPLAST 30S RIBOSOMAL PROTEIN S7 >gi 70904 pir R3RZ7
                  ribosomal protein S7 - rice chloroplast
                  >gi_12037_emb_CAA33942_ (X15901) ribosomal protein S7
                  [Oryza sativa] >gi 12065 emb CAA33919 (X15901) ribosomal
                  protein S7 [Oryza sativa] >gi 226657 prf 1603356CH
                  ribosomal protein S7 [Oryza sativa]
Seq. No.
                  420117
                  uC-osrocyp014a02a1
Seq. ID
Method
                  BLASTN
NCBI GI
                  q5381215
BLAST score
                  226
E value
                  1.0e-124
Match length
                  393
% identity
                  89
NCBI Description Oryza sativa rwc-2 mRNA for water channel protein, partial
                  cds
Seq. No.
                  420118
Seq. ID
                  uC-osrocyp014a04b1
Method
                  BLASTX
NCBI GI
                  q2267006
BLAST score
                  709
E value
                  4.0e-75
Match length
                  147
% identity
                  97
NCBI Description (AF006825) endosperm lumenal binding protein [Oryza sativa]
Seq. No.
                  420119
Seq. ID
                  uC-osrocyp014a05a1
Method
                  BLASTN
NCBI GI
                  g871929
BLAST score
                  35
E value
                  3.0e-10
Match length
                  63
% identity
                  89
NCBI Description Rice mRNA EN486, partial sequence
                  420120
Seq. No.
Seq. ID
                  uC-osrocyp014a05b1
Method
                  BLASTX
NCBI GI 😘
                  g2293480
BLAST score
                  424
                  9.0e-42
E value
Match length
                  85
% identity
                  96
```

Seq. No.

420126

```
NCBI Description
                  (AF011331) glycine-rich protein [Oryza sativa]
                  420121
Seq. No.
Seq. ID
                  uC-osrocyp014a06a1
Method
                  BLASTN
NCBI GI
                  q5091597
BLAST score
                  69
E value
                  3.0e - 30
Match length
                  109
                  91
% identity
NCBI Description
                  Oryza sativa chromosome 1 BAC 10A19I, complete sequence
Seq. No.
                  420122
Seq. ID
                  uC-osrocyp014a06b1
Method
                  BLASTX
NCBI GI
                  q2984709
BLAST score
                  473
                  2.0e-47
E value
Match length
                  93
                  97
% identity
                  (AF053468) DnaJ-related protein ZMDJ1 [Zea mays]
NCBI Description
Seq. No.
                  420123
Seq. ID
                  uC-osrocyp014a07b1
Method
                  BLASTX
NCBI GI
                  q4587520
BLAST score
                  246
E value
                  6.0e-21
Match length
                  119
% identity
                  50
                  (AC007060) Strong similarity to gb X71057 protein kinase
NCBI Description
                  from Nicotiana tabacum and contains PF 00069 eukaryotic
                  protein kinase domain. [Arabidopsis thaliana]
                  420124
Seq. No.
                  uC-osrocyp014a08a1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3617770
BLAST score
                  241
                  3.0e-20
E value
                  85
Match length
                  59
% identity
NCBI Description
                  (Y14329) threonyl-tRNA synthetase [Arabidopsis thaliana]
                  420125
Seq. No.
                  uC-osrocyp014a08b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4587520
BLAST score
                  501
E value
                  1.0e-50
Match length
                  151
% identity
                  66
NCBI Description
                  (AC007060) Strong similarity to gb X71057 protein kinase
                  from Nicotiana tabacum and contains PF 00069 eukaryotic
                  protein kinase domain. [Arabidopsis thaliana]
```

```
uC-osrocyp014a10a1
Seq. ID
Method
                  BLASTX
                  g2642159
NCBI GI
BLAST score
                  478
E value
                   5.0e-48
                  95
Match length
                  92
% identity
                  (AC003000) putative mannose-1-phosphate quanyltransferase
NCBI Description
                   [Arabidopsis thaliana] >gi 3598958 (AF076484) GDP-mannose
                  pyrophosphorylase [Arabidopsis thaliana] >gi 4151925
                   (AF108660) CYT1 protein [Arabidopsis thaliana]
                   420127
Seq. No.
Seq. ID
                  uC-osrocyp014a11a1
Method
                  BLASTN
NCBI GI
                  g871929
BLAST score
                  161
E value
                  3.0e-85
Match length
                  290
% identity
                  90
NCBI Description Rice mRNA EN486, partial sequence
                   420128
Seq. No.
Seq. ID
                  uC-osrocyp014b01b1
Method
                  BLASTX
                  g3142698
NCBI GI
BLAST score
                   361
                   2.0e-34
E value
Match length
                   104
% identity
                   67
                   (AF064542) protein farnesyltransferase subunit A
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                   420129
                   uC-osrocyp014b05b1
Seq. ID
Method
                  BLASTN
NCBI GI
                   g6006355
```

Method BLASTN
NCBI GI g6006355
BLAST score 246
E value 1.0e-136
Match length 254
% identity 99

NCBI Description Oryza sativa genomic DNA, chromosome 6, clone:P0493C11

Seq. No. 420130

Seq. ID uC-osrocyp014b06b1

Method BLASTX
NCBI GI g549063
BLAST score 690
E value 8.0e-73
Match length 139
% identity 96

NCBI Description TRANSLATIONALLY CONTROLLED TUMOR PROTEIN HOMOLOG (TCTP) >gi_1072464_pir__A38958 IgE-dependent histamine-releasing

factor homolog - rice >gi_303835_dbj_BAA02151_ (D12626)

21kd polypeptide [Oryza sativa]

Seq. No. 420131

```
Seq. ID
                  uC-osrocyp014b07b1
Method
                  BLASTX
NCBI GI
                  g1718097
BLAST score
                  376
                  4.0e-36
E value
Match length
                  109
% identity
                  61
                  VACUOLAR ATP SYNTHASE SUBUNIT AC39 (V-ATPASE AC39 SUBUNIT)
NCBI Description
                   (41 KD ACCESSORY PROTEIN) (DVA41) >qi 626048 pir A55016
                  lysosomal membrane protein DVA41 - slime mold
                   (Dictyostelium discoideum) >qi 532733 (U13150) vacuolar
                  ATPase subunit DVA41 [Dictyostelium discoideum]
Seq. No.
                  420132
Seq. ID
                  uC-osrocyp014b08b1
Method
                  BLASTX
NCBI GI
                  q3395431
BLAST score
                  249
E value
                  3.0e-21
Match length
                  69
% identity
                  67
NCBI Description (AC004683) unknown protein [Arabidopsis thaliana]
Seq. No.
                  420133
Seq. ID
                  uC-osrocyp014b09a1
Method
                  BLASTN
NCBI GI
                  q5091597
BLAST score
                  70
E value
                  6.0e-31
Match length
                  127
% identity
                  89
NCBI Description Oryza sativa chromosome 1 BAC 10A19I, complete sequence
Seq. No.
                  420134
                  uC-osrocyp014b09b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4455194
BLAST score
                  257
E value
                  3.0e-22
Match length
                  67
% identity
                  70
NCBI Description (AL035440) putative protein [Arabidopsis thaliana]
Seq. No.
                  420135
                  uC-osrocyp014b10b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g119958
BLAST score
                  470
E value
                  5.0e-47
Match length
                  135
% identity
                  70
NCBI Description FERREDOXIN III PRECURSOR (FD III) >gi 168473 (M73831)
```

Fd III [Zea mays] >gi_444686_prf__1907324C ferredoxin:ISOTYPE=III [Zea mays]

420136

Seq. No.

ferredoxin [Zea mays] >gi_1864001_dbj_BAA19251_ (AB001387)

Match length

92

```
Seq. ID
                  uC-osrocyp014b11b1
Method
                  BLASTN
NCBI GI
                  q433815
BLAST score
                  87
E value
                  4.0e-41
                  210
Match length
% identity
                  45
NCBI Description O.sativa gene for hydroxyproline-rich glycoprotein
                  420137
Seq. No.
Seq. ID
                  uC-osrocyp014c01b1
Method
                  BLASTX
NCBI GI
                  q5733089
BLAST score
                  160
E value
                  9.0e-11
Match length
                  59
% identity
                  53
NCBI Description (AF172681) amine oxidase [Canavalia lineata]
Seq. No.
                  420138
Seq. ID
                  uC-osrocyp014c02b1
Method
                  BLASTX
                  g2293480
NCBI GI
BLAST score
                  449
                  1.0e-44
E value
Match length
                  89
                  98
% identity
NCBI Description (AF011331) glycine-rich protein [Oryza sativa]
Seq. No.
                  420139
Seq. ID
                  uC-osrocyp014c05a1
Method
                  BLASTN
NCBI GI
                  g1519250
BLAST score
                  223
E value
                  1.0e-122
Match length
                  323
                  92
% identity
NCBI Description Oryza sativa GF14-c protein mRNA, complete cds
Seq. No.
                  420140
Seq. ID
                  uC-osrocyp014c05b1
Method
                  BLASTX
NCBI GI
                  g2493147
BLAST score
                  391
E value
                  8.0e-38
Match length
                  85
% identity
                  93
NCBI Description VACUOLAR ATP SYNTHASE 16 KD PROTEOLIPID SUBUNIT >gi 857574
                  (U27098) H+-ATPase [Oryza sativa]
Seq. No.
                  420141
Seq. ID
                  uC-osrocyp014c06a1
Method
                  BLASTX
NCBI GI
                  g4218144
BLAST score
                  146
E value
                  1.0e-17
```

% identity

NCBI Description

54

thaliana]



```
% identity
NCBI Description
                   (AJ132398) glutathione transferase, GST 10b [Arabidopsis
                   thaliana]
Seq. No.
                   420142
                   uC-osrocyp014c06b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3212865
BLAST score
                   604
E value
                   8.0e-63
Match length
                   140
% identity
                   81
NCBI Description (AC004005) unknown protein [Arabidopsis thaliana]
Seq. No.
                   420143
Seq. ID
                   uC-osrocyp014c07b1
Method
                   BLASTX
NCBI GI
                   q3377820
BLAST score
                   298
                   3.0e-27
E value
Match length
                   97
                   61
% identity
NCBI Description
                   (AF076275) contains similarity to coatomer zeta chains
                   [Arabidopsis thaliana]
Seq. No.
                   420144
Seq. ID
                   uC-osrocyp014c09a1
Method
                   BLASTX
NCBI GI
                   g4115383
BLAST score
                   209
E value
                   2.0e-16
Match length
                   48
% identity
                   81
NCBI Description
                   (AC005967) receptor-like protein kinase [Arabidopsis
                   thaliana]
Seq. No.
                   420145
Seq. ID
                   uC-osrocyp014c09b1
Method
                  BLASTX
NCBI GI
                   g3420055
BLAST score
                   250
                   3.0e-36
E value
                   93
Match length
                   84
% identity
NCBI Description
                  (AC004680) cyclophilin [Arabidopsis thaliana]
Seq. No.
                   420146
Seq. ID
                  uC-osrocyp014c10a1
Method
                  BLASTX
NCBI GI
                   g4454039
BLAST score
                   404
E value
                   2.0e-39
Match length
                  147
```

(AL035394) putative Na+/H+-exchanging protein [Arabidopsis

```
Seq. No.
                  420147
Seq. ID
                  uC-osrocyp014c11a1
Method
                  BLASTX
NCBI GI
                  q5689170
BLAST score
                  611
E value
                  1.0e-63
Match length
                  150
% identity
                  71
NCBI Description
                 (AB023781) cathepsin Y [Rattus norvegicus]
Seq. No.
                  420148
Seq. ID
                  uC-osrocyp014c12a1
Method
                  BLASTX
NCBI GI
                  g1362086
BLAST score
                  242
                  2.0e-20
E value
Match length
                  51
                  94
% identity
NCBI Description
                  5-methyltetrahydropteroyltriglutamate--homocysteine
                  S-methyltransferase (EC 2.1.1.14) - Madagascar periwinkle
                  >gi 2129919 pir S65957
                  5-methyltetrahydropteroyltriglutamate--homocysteine
                  S-methyltransferase (EC 2.1.1.14) - Madagascar periwinkle
                  >gi_886471_emb_CAA58474_ (X83499) methionine synthase
                  [Catharanthus roseus]
Seq. No.
                  420149
                  uC-osrocyp014c12b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2801538
BLAST score
                  417
E value
                  3.0e-41
Match length
                  114
% identity
                  79
NCBI Description (AF039532) harpin induced gene 1 homolog [Oryza sativa]
                  420150
Seq. No.
                  uC-osrocyp014d01a1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g3600088
BLAST score
                  65
E value
                  6.0e-28
                  89
Match length
                  93
% identity
NCBI Description Oryza sativa unknown mRNA
                  420151
Seq. No.
                  uC-osrocyp014d01b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g129591
BLAST score
                  418
                  4.0e-41
E value
                  101
Match length
                  81
% identity
NCBI Description PHENYLALANINE AMMONIA-LYASE >gi 295824 emb CAA34226
```

(X16099) phenylalanine ammonia-lyase [Oryza sativa]

```
420152
Seq. No.
Seq. ID
                  uC-osrocyp014d02b1
Method
                  BLASTX
NCBI GI
                  q1002800
BLAST score
                  353
                  2.0e-33
E value
                  94
Match length
                  69
% identity
                  (U33917) Cpm7 [Craterostigma plantagineum]
NCBI Description
                  420153
Seq. No.
Seq. ID
                  uC-osrocyp014d03b1
                  BLASTX
Method
NCBI GI
                  g485518
                  347
BLAST score
                  9.0e-33
E value
                  70
Match length
                  94
% identity
                  ubiquitin / ribosomal protein CEP52 - rice
NCBI Description
                  >gi 303857 dbj BAA02154 (D12629) ubiquitin/ribosomal
                  polyprotein [Oryza sativa]
                  420154
Seq. No.
                  uC-osrocyp014d04b1
Seq. ID
                  BLASTX
Method
                  g4539422
NCBI GI
BLAST score
                  261
                  1.0e-22
E value
Match length
                  97
% identity
                  56
NCBI Description (AL049171) putative protein [Arabidopsis thaliana]
                   420155
Seq. No.
Seq. ID
                  uC-osrocyp014d05b1
Method
                  BLASTX
NCBI GI
                   g4455349
BLAST score
                  158
                  1.0e-10
E value
Match length
                  72
% identity
                   44
NCBI Description (AL035524) putative protein [Arabidopsis thaliana]
```

420156 Seq. No.

uC-osrocyp014d07b1 Seq. ID

Method BLASTX g1705629 NCBI GI 823 BLAST score 2.0e-88 E value Match length 154 98 % identity

NCBI Description CATALASE ISOZYME B (CAT-B) >gi_516839_dbj_BAA05494_

(D26484) catalase [Oryza sativa]

420157 Seq. No.

uC-osrocyp014d09a1 Seq. ID

BLASTX Method NCBI GI g283008

```
BLAST score
                  182
E value
                  8.0e-27
                  65
Match length
% identity
                  100
NCBI Description
                  sucrose synthase (EC 2.4.1.13) - rice
                  >gi 20366 emb CAA46017 (X64770) sucrose synthase [Oryza
                  sativa]
                  420158
Seq. No.
                  uC-osrocyp014d09b1
Seq. ID
Method
                  BLASTX
                  q585661
NCBI GI
BLAST score
                  354
                  1.0e-33
E value
Match length
                  82
% identity
                  84
NCBI Description PEROXIDASE PRECURSOR >gi_287401_dbj_BAA03644_ (D14997)
                  peroxidase [Oryza sativa]
Seq. No.
                  420159
Seq. ID
                  uC-osrocyp014d10a1
Method
                  BLASTX
NCBI GI
                  q5031281
BLAST score
                  146
E value
                  4.0e-09
Match length
                  33
% identity
                  82
NCBI Description (AF139499) unknown [Prunus armeniaca]
Seq. No.
                  420160
                  uC-osrocyp014d10b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q5929928
BLAST score
                  442
E value
                   6.0e-44
Match length
                  106
% identity
                  82
                  (AF178950) voltage-dependent anion channel protein 1a [Zea
NCBI Description
                  mays]
Seq. No.
                   420161
                  uC-osrocyp014d11b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4056506
BLAST score
                  225
                  2.0e-18
E value
Match length
                  122
% identity
                  35
NCBI Description (AC005896) nodulin-like protein [Arabidopsis thaliana]
```

Seq. No. 420162

Seq. ID uC-osrocyp014d12b1

Method BLASTX
NCBI GI g2293480
BLAST score 274
E value 3.0e-32
Match length 89

```
% identity
NCBI Description (AF011331) glycine-rich protein [Oryza sativa]
Seq. No.
                  420163
Seq. ID
                  uC-osrocyp014e01b1
                  BLASTN
Method
NCBI GI
                  g6015437
BLAST score
                  35
E value
                  4.0e-10
                  35
Match length
                  100
% identity
NCBI Description Homo sapiens PEX1 mRNA, complete cds
                  420164
Seq. No.
Seq. ID
                  uC-osrocyp014e03a1
Method
                  BLASTX
NCBI GI
                  g1172553
BLAST score
                  317
E value
                  3.0e-29
Match length
                  72
                  88
% identity
NCBI Description OUTER MITOCHONDRIAL MEMBRANE PROTEIN PORIN
                  (VOLTAGE-DEPENDENT ANION-SELECTIVE CHANNEL PROTEIN) (VDAC)
                  >gi 456672 emb CAA54788 (X77733) voltage dependent anion
                  channel (VDAC) [Triticum aestivum]
                  420165
Seq. No.
Seq. ID
                  uC-osrocyp014e03b1
Method
                  BLASTX
NCBI GI
                  q5031281
BLAST score
                  312
                  2.0e-28
E value
Match length
                  103
% identity
                  61
NCBI Description (AF139499) unknown [Prunus armeniaca]
Seq. No.
                  420166
Seq. ID
                  uC-osrocyp014e04a1
Method
                  BLASTN
NCBI GI
                  g287400
BLAST score
                  345
E value
                  0.0e + 00
Match length
                  396
% identity
                  96
NCBI Description Rice mRNA for peroxidase, complete cds
Seq. No.
                  420167
Seq. ID
                  uC-osrocyp014e04b1
Method
                  BLASTX
NCBI GI
                  g283008
BLAST score
                  688
                  1.0e-72
E value
Match length
                  154
% identity
                  88
NCBI Description sucrose synthase (EC 2.4.1.13) - rice
                  >gi 20366 emb CAA46017 (X64770) sucrose synthase [Oryza
                  sativa]
```

Seq. No.

420173

```
Seq. No.
                   420168
Seq. ID
                  uC-osrocyp014e06a1
Method
                  BLASTN
NCBI GI
                  q20280
BLAST score
                   41
                  1.0e-13
E value
Match length
                   93
                  86
% identity
NCBI Description Rice gene for phenylalanine ammonia-lyase (EC 4.3.1.5)
                   420169
Seq. No.
Seq. ID
                  uC-osrocyp014e07b1
Method
                  BLASTX
NCBI GI
                  q1168537
BLAST score
                   673
E value
                  8.0e-71
Match length
                  166
% identity
                  72
NCBI Description ASPARTIC PROTEINASE PRECURSOR >gi 82458 pir JS0732
                  aspartic proteinase (EC 3.4.23.-) - rice
                  >gi_218143_dbj_BAA02242 (D12777) aspartic proteinase
                   [Oryza sativa]
                   420170
Seq. No.
Seq. ID
                  uC-osrocyp014e08b1
Method
                  BLASTX
                  q439879
NCBI GI
BLAST score
                  222
E value
                   6.0e-18
Match length
                   46
                  85
% identity
NCBI Description
                  (L15194) [Golden delicious apple fruit expressed mRNA,
                  complete cds.], gene product [Malus domestica]
Seq. No.
                   420171
                  uC-osrocyp014e09a1
Seq. ID
Method
                  BLASTX
NCBI GI
                   g4539422
BLAST score
                   368
E value
                   4.0e-35
                  83
Match length
                  81
% identity
                 (AL049171) putative protein [Arabidopsis thaliana]
NCBI Description
                  420172
Seq. No.
                  uC-osrocyp014e12a1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g129591
BLAST score
                  240
E value
                  4.0e-20
Match length
                  44
                  100
% identity
NCBI Description PHENYLALANINE AMMONIA-LYASE >qi 295824 emb CAA34226
                   (X16099) phenylalanine ammonia-lyase [Oryza sativa]
```

```
Seq. ID
                  uC-osrocyp014e12b1
Method
                  BLASTX
                  q3929647
NCBI GI
BLAST score
                  163
E value
                  4.0e-11
                  92
Match length
                  50
% identity
NCBI Description (AJ004881) Immutans protein [Arabidopsis thaliana]
                  420174
Seq. No.
Seq. ID
                  uC-osrocyp014f01a1
Method
                  BLASTN
NCBI GI
                  g2801537
BLAST score
                  359
E value
                  0.0e+00
                  375
Match length
                  99
% identity
                  Oryza sativa harpin induced gene 1 homolog (Hin1) mRNA,
NCBI Description
                  complete cds
                  420175
Seq. No.
Seq. ID
                  uC-osrocyp014f01b1
Method
                  BLASTX
NCBI GI
                  g1362086
BLAST score
                  556
                  7.0e-61
E value
Match length
                  151
% identity
NCBI Description
                  5-methyltetrahydropteroyltriglutamate--homocysteine
                  S-methyltransferase (EC 2.1.1.14) - Madagascar periwinkle
                  >gi 2129919 pir S65957
                  5-methyltetrahydropteroyltriglutamate--homocysteine
                  S-methyltransferase (EC 2.1.1.14) - Madagascar periwinkle
                  >gi_886471_emb_CAA58474_ (X83499) methionine synthase
                  [Catharanthus roseus]
Seq. No.
                  420176
                  uC-osrocyp014f02b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q5019548
BLAST score
                  434
E value
                  7.0e-43
                  95
Match length
                  77
% identity
NCBI Description
                  (AJ242663) cathepsin Z [Mus musculus]
                  420177
Seq. No.
                  uC-osrocyp014f07b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4049401
BLAST score
                  329
                  1.0e-30
E value
                  83
Match length
% identity
                  73
NCBI Description
                  (AJ131580) glutathione transferase AtGST 10 [Arabidopsis
```

thaliana]

Seq. ID Method

```
420178
Seq. No.
Seq. ID
                  uC-osrocyp014f08a1
Method
                   BLASTN
NCBI GI
                   g857573
                   74
BLAST score
                   3.0e-33
E value
                   126
Match length
                   90
% identity
                  Oryza sativa vacuolar H+-ATPase (vatp-P1) mRNA, complete
NCBI Description
                   cds
                   420179
Seq. No.
Seq. ID
                   uC-osrocyp014f08b1
                   BLASTX
Method
                   g1519251
NCBI GI
                   604
BLAST score
                   8.0e-63
E value
Match length
                   122
                   100
% identity
NCBI Description (U65957) GF14-c protein [Oryza sativa]
                   420180
Seq. No.
Seq. ID
                   uC-osrocyp014f09b1
                   BLASTX
Method
NCBI GI
                   g3157949
BLAST score
                   169
                   6.0e-12
E value
                   110
Match length
                   36
% identity
                  (AC002131) Similar to glucan endo-1,3-beta-D-glucosidase
NCBI Description
                   precursor gb Z28697 from Nicotiana tabacum. ESTs gb Z18185
                   and gb_AA605362 come from this gene. [Arabidopsis thaliana]
                   420181
Seq. No.
Seq. ID
                   uC-osrocyp014f11a1
Method
                   BLASTN
NCBI GI
                   q2331130
BLAST score
                   194
                   1.0e-105
E value
Match length
                   222
                   97
% identity
NCBI Description Oryza sativa glycine-rich protein (OSGRP1) mRNA, complete
Seq. No.
                   420182
                   uC-osrocyp014f11b1
Seq. ID
Method
                   BLASTN
NCBI GI
                   g3821780
BLAST score
                   34
E value
                   2.0e-09
Match length
                   34
                   100
% identity
NCBI Description Xenopus laevis cDNA clone 27A6-1
                   420183
Seq. No.
```

55159

uC-osrocyp014f12a1

BLASTX

```
NCBI GI
                   q5281040
 BLAST score
                   282
 E value
                   4.0e-25
                   59
 Match length
                   83
 % identity
                   (AL080318) copper amine oxidase-like protein [Arabidopsis
 NCBI Description
                   thaliana]
                    420184
 Seq. No.
 Seq. ID
                   uC-osrocyp014g02a1
                   BLASTN
 Method
                   g433815
 NCBI GI
 BLAST score
                   183
                   2.0e-98
 E value
                   244
 Match length
                   98
 % identity
 NCBI Description O.sativa gene for hydroxyproline-rich glycoprotein
 Seq. No.
                    420185
                   uC-osrocyp014g03a1
 Seq. ID
 Method
                   BLASTX
 NCBI GI
                   q119958
 BLAST score
                    526
                    1.0e-53
 E value
 Match length
                    105
                    92
 % identity
                   FERREDOXIN III PRECURSOR (FD III) >gi 168473 (M73831)
 NCBI Description
                    ferredoxin [Zea mays] >gi 1864001 dbj BAA19251 (AB001387)
                    Fd III [Zea mays] >gi 444686 prf 1907324C
                    ferredoxin:ISOTYPE=III [Zea mays]
                    420186
 Seq. No.
                    uC-osrocyp014g03b1
 Seq. ID
 Method
                    BLASTX
 NCBI GI
                    g2244876
 BLAST score
                    381
                    1.0e-36
 E value
 Match length
                    126
 % identity
                    63
 NCBI Description (Z97338) hypothetical protein [Arabidopsis thaliana]
                    420187
 Seq. No.
                    uC-osrocyp014g04b1
 Seq. ID
 Method
                    BLASTN
 NCBI GI
                    q5091597
 BLAST score
                    66
                    2.0e-28
 E value
                    127
 Match length
 % identity
                    88
 NCBI Description Oryza sativa chromosome 1 BAC 10A19I, complete sequence
· Seq. No.
                    420188
                    uC-osrocyp014g05b1
 Seq. ID
 Method
                    BLASTX
                    g2894599
 NCBI GI
 BLAST score
                    262
```

55160

6.0e-24

E value

Seq. ID

```
Match length
                  71
% identity
                  (AL021889) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  420189
                  uC-osrocyp014g06b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3036805
BLAST score
                  340
                  7.0e-32
E value
                  123
Match length
% identity
                  54
NCBI Description (AL022373) thaumatin-like protein [Arabidopsis thaliana]
                  420190
Seq. No.
Seq. ID
                  uC-osrocyp014g07b1
Method
                  BLASTX
NCBI GI
                  q4887131
BLAST score
                  478
                  4.0e-48
E value
                  112
Match length
                  78
% identity
NCBI Description (AF134732) 60S ribosomal protein L1 [Prunus armeniaca]
Seq. No.
                  420191
Seq. ID
                  uC-osrocyp014g08a1
Method
                  BLASTN
NCBI GI
                  g6006355
BLAST score
                  57
E value
                  2.0e-23
Match length
                  192
                  83
% identity
NCBI Description Oryza sativa genomic DNA, chromosome 6, clone:P0493C11
Seq. No.
                  420192
Seq. ID
                  uC-osrocyp014g09a1
Method
                  BLASTX
NCBI GI
                  g829283
BLAST score
                  337
                  2.0e-31
E value
Match length
                  80
                  88
% identity
NCBI Description (Z15018) heat shock protein hsp82 [Oryza sativa]
                  420193
Seq. No.
                  uC-osrocyp014g10b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2191193
BLAST score
                  200
                  2.0e-15
E value
Match length
                  134
% identity
                  37
                 (AF007271) contain similarity to type 1 inositol
NCBI Description
                  1,4,5-triphosphate receptors [Arabidopsis thaliana]
                  420194
Seq. No.
```

55161

uC-osrocyp014g11a1

```
Method
                  BLASTX
NCBI GI
                  q4926830
BLAST score
                  180
                  4.0e-13
E value
                  82
Match length
                  43
% identity
                  (AC004135) T17H7.15 [Arabidopsis thaliana]
NCBI Description
                  420195
Seq. No.
                  uC-osrocyp014g12a1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2246442
BLAST score
                  146
                  4.0e-09
E value
Match length
                  81
% identity
                  35
                  (U63298) farnesyltransferase alpha subunit [Pisum sativum]
NCBI Description
                  420196
Seq. No.
                  uC-osrocyp014g12b1
Seq. ID
Method
                  BLASTX
                  g4490309
NCBI GI
BLAST score
                  297
                  6.0e-27
E value
Match length
                  83
% identity
                  65
                  (AL035678) peroxidase ATP17a-like protein [Arabidopsis
NCBI Description
                  thaliana]
                  420197
Seq. No.
                  uC-osrocyp014h02b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3914685
BLAST score
                  662
                  1.0e-69
E value
Match length
                  140
                  91
% identity
NCBI Description 60S RIBOSOMAL PROTEIN L17 >gi_2668748 (AF034948) ribosomal
                  protein L17 [Zea mays]
                  420198
Seq. No.
Seq. ID
                  uC-osrocyp014h05b1
Method
                  BLASTX
NCBI GI
                  g2501064
BLAST score
                  387
                  1.0e-37
E value
Match length
                  99
% identity
                  71
NCBI Description PROBABLE THREONYL-TRNA SYNTHETASE, CYTOPLASMIC
                   (THREONINE--TRNA LIGASE) (THRRS) >gi_2191162 (AF007270)
                  Similar to threonyl-tRNA synthetase; coded for by A.
                  thaliana cDNA R65376 [Arabidopsis thaliana]
                  420199
Seq. No.
                  uC-osrocyp014h06b1
Seq. ID
```

Method BLASTX NCBI GI g5107831



BLAST score 192 E value 2.0e-14 Match length 110 % identity 41

NCBI Description (AF149413) contains similarity to protein kinase domains (Pfam F00069, Score=162.6, E=6.8e-45, N=1) and leucien rich

repeats (Pfam PF00560, Score=210.7, E=2.2e-59, N=10)

The bidencie the line of

[Arabidopsis thaliana]

Seq. No. 420200

Seq. ID uC-osrocyp014h07b1

Method BLASTX
NCBI GI g3169012
BLAST score 359
E value 5.0e-34
Match length 103
% identity 67

NCBI Description (AJ002610) putative calmodulin binding transporter protein

[Hordeum vulgare]

Seq. No. 420201

Seq. ID uC-osrocyp014h08a1

Method BLASTN
NCBI GI g2331130
BLAST score 217
E value 1.0e-118
Match length 270
% identity 99

NCBI Description Oryza sativa glycine-rich protein (OSGRP1) mRNA, complete

cds

Seq. No. 420202

Seq. ID uC-osrocyp014h09a1

Method BLASTN
NCBI GI g2267005
BLAST score 273
E value 1.0e-152
Match length 410
% identity 99

NCBI Description Oryza sativa endosperm lumenal binding protein (BiP) mRNA,

complete cds

Seq. No. 420203

Seq. ID uC-osrocyp014h11b1

Method BLASTX
NCBI GI g3135543
BLAST score 790
E value 1.0e-84
Match length 153
% identity 98

NCBI Description (AF062393) aquaporin [Oryza sativa]

Seq. No. 420204

Seq. ID uC-osrocyp014h12a1

Method BLASTX NCBI GI g1665817 BLAST score 187

NCBI GI

E value

BLAST score

g82734

453 4.0e-45



```
6.0e-14
E value
                  78
Match length
                  50
% identity
                  (D87466) Similar to S.cerevisiae hypothetical protein L3111
NCBI Description
                  (S59316) [Homo sapiens]
                  420205
Seq. No.
Seq. ID
                  uC-osrocyp014h12b1
Method
                  BLASTX
                  g133748
NCBI GI
BLAST score
                  628
E value
                  1.0e-65
                  124
Match length
                  99
% identity
NCBI Description
                  CHLOROPLAST 30S RIBOSOMAL PROTEIN S12 >gi 70961 pir R3RZ12
                  ribosomal protein S12 - rice chloroplast
                  >gi_1213603_emb_CAA33929_ (X15901) ribosomal protein S12
                  [Oryza sativa] >gi_226658_prf__1603356CJ ribosomal protein
                  S12 [Oryza sativa]
                  420206
Seq. No.
Seq. ID
                  uC-osrocyp015a01a1
                  BLASTX
Method
                  q4972075
NCBI GI
BLAST score
                  164
                  3.0e-11
E value
                  37
Match length
                  84
% identity
NCBI Description (AL078467) proton pump interactor [Arabidopsis thaliana]
Seq. No.
                  420207
Seq. ID
                  uC-osrocyp015a01b1
Method
                  BLASTX
                  a4972075
NCBI GI
BLAST score
                  211
                  1.0e-16
E value
                  82
Match length
% identity
                  48
NCBI Description (AL078467) proton pump interactor [Arabidopsis thaliana]
                  420208
Seq. No.
Seq. ID
                  uC-osrocyp015a02b1
                  BLASTX
Method
NCBI GI
                  q2290382
BLAST score
                  216
E value
                  3.0e-17
Match length
                  108
% identity
NCBI Description
                  (U89985) serine/threonine protein phosphatase PPT1
                  [Neurospora crassa]
Seq. No.
                  420209
Seq. ID
                  uC-osrocyp015a03a1
Method
                  BLASTX
```

```
Match length
                   91
% identity
                   29
NCBI Description
                  ubiquitin precursor - maize (fragment)
                  >gi_226763_prf__1604470A poly-ubiquitin [Zea mays]
                   420210
Seq. No.
                  uC-osrocyp015a03b1
Seq. ID
Method
                  BLASTX
                  q1304128
NCBI GI
BLAST score
                   439
                   2.0e-43
E value
                   137
Match length
% identity
                   9
NCBI Description (D63791) polyubiquitin [Homo sapiens]
                   420211
Seq. No.
Seq. ID
                  uC-osrocyp015a04a1
                  BLASTN
Method
NCBI GI
                  q2599091
BLAST score
                   56
                   2.0e-22
E value
Match length
                   100
                   89
% identity
NCBI Description Arabidopsis thaliana WD-40 repeat protein MSI4 (MSI4) mRNA,
                   complete cds
Seq. No.
                   420212
Seq. ID
                   uC-osrocyp015a04b1
Method
                   BLASTX
NCBI GI
                   q4191782
BLAST score
                   577
                   1.0e-59
E value
                   133
Match length
% identity
                   80
NCBI Description (AC005917) WD-40 repeat protein [Arabidopsis thaliana]
                   420213
Seq. No.
                   uC-osrocyp015a06b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g4586021
                   501
BLAST score
                   1.0e-50
E value
                   107
Match length
                   88
% identity
                  (AC007170) putative cytoplasmic aconitate hydratase
NCBI Description
                   [Arabidopsis thaliana]
                   420214
Seq. No.
Seq. ID
                   uC-osrocyp015a07b1
Method
                   BLASTX
NCBI GI
                   g2984709
BLAST score
                   464
E value
                   2.0e-46
Match length
                   88
                   99
% identity
```

NCBI Description (AF053468) DnaJ-related protein ZMDJ1 [Zea mays]

Seq. No. 420215 uC-osrocyp015a09a1 Seq. ID Method BLASTN NCBI GI g1041711 BLAST score 239 1.0e-132 E value Match length 415 % identity 89 NCBI Description Oryza sativa expansin Os-EXP3 (Os-EXP3) mRNA, complete cds Seq. No. 420216 Seq. ID uC-osrocyp015a09b1 Method BLASTX NCBI GI q1041712 BLAST score 598 E value 4.0e-62 Match length 141 % identity 81 NCBI Description (U30479) expansin Os-EXP3 [Oryza sativa] Seq. No. 420217 uC-osrocyp015a10b1 Seq. ID Method BLASTX NCBI GI g2623297 BLAST score 489 E value 3.0e-49Match length 170 % identity 57 NCBI Description (AC002409) unknown protein [Arabidopsis thaliana] >gi 3790583 (AF079180) RING-H2 finger protein RHCla [Arabidopsis thaliana] Seq. No. 420218 uC-osrocyp015a11a1 Seq. ID Method BLASTX NCBI GI g5903045 BLAST score 294 E value 2.0e-26 Match length 60 92 % identity (AC008016) Similar to gb AF108945 signal peptidase 18 kDa NCBI Description subunit from Homo sapiens. ESTs gb H76629, gb H76949 and gb H76216 come from this gene. [Arabidopsis thaliana] 420219 Seq. No. uC-osrocyp015a11b1 Seq. ID Method BLASTX NCBI GI g5903045 BLAST score 436 E value 5.0e-43Match length 103 % identity 82 NCBI Description (AC008016) Similar to gb AF108945 signal peptidase 18 kDa subunit from Homo sapiens. ESTs gb_H76629, gb_H76949 and

Seq. No. 420220

gb_H76216 come from this gene. [Arabidopsis thaliana]

```
Seq. ID
                  uC-osrocyp015b01a1
Method
                  BLASTX
                  g481477
NCBI GI
BLAST score
                  316
                  5.0e-29
E value
Match length
                  77
% identity
                  15
                  ubiquitin precursor - rice >gi_416038_emb CAA53665
NCBI Description
                   (X76064) polyubiquitin [Oryza sativa] >gi 1574944 (U37687)
                  polyubiquitin [Oryza sativa]
                  >gi 6013289 gb AAF01315.1 AF184279 1 (AF184279)
                  polyubiquitin [Oryza sativa]
                  >gi 6013291 gb AAF01316.1 AF184280 1 (AF184280)
                  polyubiquitin [Oryza sativa]
Seq. No.
                  420221
Seq. ID
                  uC-osrocyp015b01b1
Method
                  BLASTX
NCBI GI
                  q1332579
BLAST score
                  704
E value
                  2.0e-74
Match length
                  156
% identity
                  9
NCBI Description (X98063) polyubiquitin [Pinus sylvestris]
                  420222
Seq. No.
Seq. ID
                  uC-osrocyp015b02a1
Method
                  BLASTX
NCBI GI
                  g2078350
BLAST score
                  539
                  4.0e-55
E value
Match length
                  133
% identity
                  74
NCBI Description (U95923) transaldolase [Solanum tuberosum]
                  420223
Seq. No.
Seq. ID
                  uC-osrocyp015b05b1
Method
                  BLASTX
NCBI GI
                  g3980417
BLAST score
                  281
E value
                  8.0e-25
Match length
                  63
% identity
                  87
NCBI Description (AC004561) pumilio-like protein [Arabidopsis thaliana]
                  420224
Seq. No.
Seq. ID
                  uC-osrocyp015b06b1
Method
                  BLASTX
NCBI GI
                  q4567250
BLAST score
                  190
E value
                  3.0e-14
Match length
                  110
% identity
                  41
NCBI Description
                 (AC007070) hypothetical protein [Arabidopsis thaliana]
Seq. No.
Seq. ID
                  uC-osrocyp015b08b1
```

```
Method
                  BLASTX
NCBI GI
                  q5304835
BLAST score
                  354
                   4.0e-36
E value
Match length
                  136
                  56
% identity
NCBI Description (AJ243439) ATP citrate lyase [Cyanophora paradoxa]
Seq. No.
                  420226
Seq. ID
                  uC-osrocyp015b09b1
Method
                  BLASTX
NCBI GI
                  g2623297
BLAST score
                  149
                  3.0e-21
E value
Match length
                  144
                  41
% identity
NCBI Description
                  (AC002409) unknown protein [Arabidopsis thaliana]
                  >gi 3790583 (AF079180) RING-H2 finger protein RHC1a
                   [Arabidopsis thaliana]
Seq. No.
                  420227
Seq. ID
                  uC-osrocyp015b10b1
Method
                  BLASTX
NCBI GI
                  g623586
BLAST score
                  531
E value
                  4.0e-54
Match length
                  117 <
                  93
% identity
NCBI Description (L29273) putative [Nicotiana tabacum]
                  420228
Seq. No.
Seq. ID
                  uC-osrocyp015b12b1
Method
                  BLASTX
NCBI GI
                  g5923675
BLAST score
                  470
E value
                  5.0e-47
Match length
                  169
% identity
                  56
NCBI Description
                  (AC009326) putative mRNA capping enzyme, RNA
                  guanylyltransferase [Arabidopsis thaliana]
Seq. No.
                  420229
Seq. ID
                  uC-osrocyp015c01b1
Method
                  BLASTX
NCBI GI
                  g5031275
BLAST score
                  515
E value
                  3.0e-52
Match length
                  130
% identity
                  72
NCBI Description (AF139496) unknown [Prunus armeniaca]
Seq. No.
                  420230
Seq. ID
                  uC-osrocyp015c02a1
Method
                  BLASTN
NCBI GI
                  g2267592
BLAST score
                  196
E value
                  1.0e-106
```



```
Match length
                   366
                   98
% identity
NCBI Description
                  Oryza sativa glycine-rich RNA-binding protein mRNA,
                   complete cds
Seq. No.
                   420231
Seq. ID
                  uC-osrocyp015c02b1
Method
                  BLASTX
NCBI GI
                  g2293480
BLAST score
                   432
                  1.0e-42
E value
Match length
                  84
% identity
                  100
                 (AF011331) glycine-rich protein [Oryza sativa]
NCBI Description
Seq. No.
                   420232
Seq. ID
                  uC-osrocyp015c04a1
Method
                  BLASTN
NCBI GI
                   g485815
BLAST score
                  83
E value
                  1.0e-38
Match length
                  143
                   90
% identity
NCBI Description Wheat mRNA for WZF1, complete cds
Seq. No.
                   420233
Seq. ID
                  uC-osrocyp015c04b1
Method
                  BLASTX
NCBI GI
                  g542176
                   219
BLAST score
                  1.0e-17
E value
Match length
                  113
                   45
% identity
                  probable finger protein WZF1 - wheat
NCBI Description
                  >gi_485814_dbj_BAA03901 (D16415) WZF1 [Triticum aestivum]
                   >gi_485816_dbj_BAA03902 (D16416) WZF1 [Triticum aestivum]
Seq. No.
                   420234
                  uC-osrocyp015c05a1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g218184
BLAST score
                   34
E value
                   2.0e-09
                   69
Match length
                   89
% identity
NCBI Description Rice mRNA for oryzain gamma (EC 3.4.22)
                   420235
Seq. No.
                  uC-osrocyp015c05b1
Seq. ID
Method
                  BLASTX
```

Method BLASTX
NCBI GI g129233
BLAST score 725
E value 8.0e-77
Match length 156
% identity 96

NCBI Description ORYZAIN GAMMA CHAIN PRECURSOR >gi_67646_pir__KHRZOG oryzain

(EC 3.4.22.-) gamma precursor - rice

E value

Match length

% identity

5.0e-42

114 75

```
>gi 218185 dbj BAA14404 (D90408) oryzain gamma precursor
                   [Oryza sativa]
                  420236
Seq. No.
                  uC-osrocyp015c06b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q136640
                  675
BLAST score
                  3.0e-71
E value
Match length
                  129
                  95
% identity
NCBI Description
                  UBIQUITIN-CONJUGATING ENZYME E2-17 KD (UBIQUITIN-PROTEIN
                  LIGASE) (UBIQUITIN CARRIER PROTEIN) >gi 170785 (M62720)
                  ubiquitin carrier protein [Triticum aestivum]
Seq. No.
                  420237
                  uC-osrocyp015c08b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1399277
BLAST score
                  159
                  2.0e-10
E value
                  94
Match length
% identity
                  39
                  (U31836) calmodulin-domain protein kinase CDPK isoform 7
NCBI Description
                   [Arabidopsis thaliana]
                  420238
Seq. No.
Seq. ID
                  uC-osrocyp015c09b1
Method
                  BLASTX
NCBI GI
                  g2467088
BLAST score
                  165
                  3.0e-11
E value
                  41
Match length
                  73
% identity
NCBI Description (AJ001911) putative Ckc2 [Arabidopsis thaliana]
                  420239
Seq. No.
Seq. ID
                  uC-osrocyp015c11a1
Method
                  BLASTN
                  g2864607
NCBI GI
BLAST score
                  36
E value
                  2.0e-10
Match length
                  68
                  88
% identity
                  Arabidopsis thaliana DNA chromosome 4, BAC clone F10M6
NCBI Description
                   (ESSAII project)
Seq. No.
                  420240
Seq. ID
                  uC-osrocyp015c11b1
Method
                  BLASTX
NCBI GI
                  g399940
             ¥427.
BLAST score
                            · ...
```

55170

>gi_100004_pir__S25005 heat shock protein, 70K - kidney

NCBI Description HEAT SHOCK 70 KD PROTEIN, MITOCHONDRIAL PRECURSOR

```
bean >gi 22636 emb CAA47345 (X66874) 70 kDa heat shock
protein [Phaseolus vulgaris]
```

420241 Seq. No. uC-osrocyp015d03b1 Seq. ID Method BLASTX NCBI GI q3924615 674 BLAST score 6.0e-71 E value Match length 178 % identity 70

NCBI Description (AF069442) hypothetical protein [Arabidopsis thaliana]

Seq. No. 420242

Seq. ID uC-osrocyp015d04b1

Method BLASTX NCBI GI q4508079 BLAST score 397 2.0e-38 E value Match length 143 % identity 62

NCBI Description (AC005882) 66284 [Arabidopsis thaliana]

Seq. No. 420243

Seq. ID uC-osrocyp015d07b1

Method BLASTX NCBI GI g2760834 BLAST score 158 E value 2.0e-10 Match length 84 40 % identity

(AC003105) putative nitrate transporter [Arabidopsis NCBI Description

thaliana]

420244 Seq. No.

uC-osrocyp015d08b1 Seq. ID

Method BLASTX NCBI GI q416966 BLAST score 198 4.0e-15 E value Match length 152 37 % identity

NCBI Description ERYTHRONOLIDE SYNTHASE, MODULES 3 AND 4 (ORF 2)

(6-DEOXYERYTHRONOLIDE B SYNTHASE II) (DEBS 2) >gi 152694

(M63677) eryA ORF2 encoding modules 3 & 4 for

6-deoxyerythronolide B formation6-deoxyerythronolide B

formation; putative [Saccharopolyspora erythraea]

Seq. No. 420245

Seq. ID uC-osrocyp015d11b1

Method BLASTX g451193 NCBI GI BLAST score 370 E value 3.0e - 35Match length 98 77 % identity

(L28008) wali7 [Triticum aestivum] NCBI Description

```
>gi 1090845 prf__2019486B wali7 gene [Triticum aestivum]
Seq. No.
                   420246
Seq. ID
                  uC-osrocyp015d12a1
Method
                  BLASTX
NCBI GI
                  g1944573
BLAST score
                  393
                  5.0e-38
E value
Match length
                  87
                  85
% identity
NCBI Description
                  (Z49146) phenylalanine ammonia-lyase [Hordeum vulgare]
Seq. No.
                   420247
Seq. ID
                  uC-osrocyp015d12b1
Method
                  BLASTX
NCBI GI
                  g82496
BLAST score
                  609
E value
                  2.0e-63
Match length
                  149
                  81
% identity
NCBI Description phenylalanine ammonia-lyase (EC 4.3.1.5) - rice
Seq. No.
                  420248
Seq. ID
                  uC-osrocyp015e01a1
Method
                  BLASTX
NCBI GI
                  g129591
BLAST score
                  178
E value
                  7.0e-13
Match length
                  37
% identity
                  84
NCBI Description PHENYLALANINE AMMONIA-LYASE >qi 295824 emb CAA34226
                  (X16099) phenylalanine ammonia-lyase [Oryza sativa]
                  420249
Seq. No.
                  uC-osrocyp015e01b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g82496
BLAST score
                  624
E value
                  5.0e-65
Match length
                  151
% identity
                  81
NCBI Description phenylalanine ammonia-lyase (EC 4.3.1.5) - rice
Seq. No.
                  420250
                  uC-osrocyp015e02b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g5031281
BLAST score
                  552
E value
                  1.0e-56
                  158
Match length
% identity
                  66
NCBI Description (AF139499) unknown [Prunus armeniaca]
Seq. No.
                  420251
Seq. ID
                  uC-osrocyp015e03a1
Method
                  BLASTX
NCBI GI
                  g1370603
```

```
BLAST score
                   280
                   8.0e-25
E value
Match length
                   84
                   73
% identity
NCBI Description (X98245) annexin p35 [Zea mays]
                   420252
Seq. No.
                  uC-osrocyp015e03b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1370603
BLAST score
                  430
E value
                   2.0e-42
Match length
                  129
% identity
                   66
NCBI Description (X98245) annexin p35 [Zea mays]
                   420253
Seq. No.
Seq. ID
                  uC-osrocyp015e05b1
Method
                  BLASTX
NCBI GI
                  q4432814
BLAST score
                  222
E value
                  6.0e-18
Match length
                  128
% identity
                  38
NCBI Description (AC006593) unknown protein [Arabidopsis thaliana]
                  420254
Seq. No.
Seq. ID
                  uC-osrocyp015e07a1
Method
                  BLASTX
NCBI GI
                  g3860274
BLAST score
                  304
E value
                  1.0e-27
Match length
                  133
% identity
                  44
NCBI Description
                  (AC005824) unknown protein [Arabidopsis thaliana]
                  >gi_4314397 gb AAD15607 (AC006232) putative zinc finger
                  protein [Arabidopsis thaliana]
Seq. No.
                  420255
Seq. ID
                  uC-osrocyp015e07b1
Method
                  BLASTX
NCBI GI
                  g4586109
BLAST score
                  208
E value
                  3.0e-16
                  90
Match length
                  42
% identity
NCBI Description (AL049638) putative protein [Arabidopsis thaliana]
Seq. No.
                  420256
Seq. ID
                  uC-osrocyp015e08a1
Method
                  BLASTX
NCBI GI
                  g4514635
BLAST score
                  266
E value
                  3.0e-23
Match length
                  68
% identity
                  75
NCBI Description
                  (AB021175) root cap protein 1 [Zea mays]
```

```
Seq. No.
                   420257
Seq. ID
                   uC-osrocyp015e08b1
Method
                   BLASTX
NCBI GI
                   q4514635
BLAST score
                   463
E value
                   3.0e-46
Match length
                   123
                   66
% identity
NCBI Description
                  (AB021175) root cap protein 1 [Zea mays]
                   420258
Seq. No.
Seq. ID
                   uC-osrocyp015e09a1
Method
                   BLASTX
NCBI GI
                   q4406814
BLAST score
                   327
E value
                   3.0e-30
Match length
                   101
% identity
                   62
NCBI Description
                   (AC006201) putative peptidyl-prolyl isomerase [Arabidopsis
                   thaliana]
Seq. No.
                   420259
Seq. ID
                   uC-osrocyp015e09b1
Method
                   BLASTX
NCBI GI
                   q4406814
BLAST score
                   387
                   3.0e-37
E value
Match length
                   115
% identity
NCBI Description
                   (AC006201) putative peptidyl-prolyl isomerase [Arabidopsis
                   thaliana]
Seq. No.
                   420260
                   uC-osrocyp015e10a1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2498732
BLAST score
                   268
E value
                   2.0e-23
                   95
Match length
                   51
% identity
NCBI Description
                  PROBABLE NADP-DEPENDENT OXIDOREDUCTASE P2
                   >gi 1362014 pir S57612 zeta-crystallin homolog -
                   Arabidopsis thaliana >gi 886430 emb CAA89262 (Z49268)
                   zeta-crystallin homologue [Arabidopsis thaliana]
                   420261
Seq. No.
                   uC-osrocyp015e10b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2498731
BLAST score
                   369
E value
                   3.0e - 35
Match length
                   142
                   51
% identity
NCBI Description
                  PROBABLE NADP-DEPENDENT OXIDOREDUCTASE P1
                   >gi 1362013 pir S57611 zeta-crystallin homolog -
```

Arabidopsis thaliana >gi 886428 emb CAA89838 (Z49768)



zeta-crystallin homologue [Arabidopsis thaliana]

```
Seq. No.
                  420262
Seq. ID
                  uC-osrocyp015e11b1
Method
                  BLASTX
NCBI GI
                  g1706318
BLAST score
                  727
E value
                  3.0e-77
                  163
Match length
% identity
                  81
                  GLUTAMATE DECARBOXYLASE (GAD) (ERT D1)
NCBI Description
                  >gi 1362098 pir S56177 probable glutamate decarboxylase -
                  tomato >gi_995555_emb_CAA56812_ (X80840) homology to
                  pyroxidal-5'-phosphate-dependant glutamate decarboxylases;
                  putative start codon [Lycopersicon esculentum]
Seq. No.
                  420263
                  uC-osrocyp015e12a1
Seq. ID
Method
                  BLASTX
                  q267056
NCBI GI
                  453
BLAST score
E value
                  5.0e-45
Match length
                  87
% identity
                  98
NCBI Description
                  SUCROSE SYNTHASE 1 (SUCROSE-UDP GLUCOSYLTRANSFERASE 1)
                  >gi 100710 pir S25526 sucrose synthase (EC 2.4.1.13) -
                  rice >gi_20374_emb_CAA78747_ (Z15028) sucrose synthase
                  [Oryza sativa]
Seq. No.
                  420264
                  uC-osrocyp015f02a1
Seq. ID
                  BLASTX
Method
NCBI GI
                  q4510348
BLAST score
                  165
E value
                  2.0e-11
Match length
                  48
% identity
                  56
NCBI Description (AC006921) unknown protein [Arabidopsis thaliana]
Seq. No.
                  420265
Seq. ID
                  uC-osrocyp015f02b1
Method
                  BLASTX
NCBI GI
                  q4510348
BLAST score
                  322
E value
                  1.0e-29
Match length
                  122
% identity
                  51
NCBI Description (AC006921) unknown protein [Arabidopsis thaliana]
Seq. No.
                  420266
                  uC-osrocyp015f03a1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g20280
BLAST score
                  365
E value
                  0.0e + 00
                  377
Match length
```

55175

99

% identity

```
NCBI Description Rice gene for phenylalanine ammonia-lyase (EC 4.3.1.5)
Seq. No.
                  420267
Seq. ID
                  uC-osrocyp015f03b1
Method
                  BLASTX
NCBI GI
                  q82496
BLAST score
                  633
E value
                  4.0e-66
Match length
                  153
                  83
% identity
NCBI Description phenylalanine ammonia-lyase (EC 4.3.1.5) - rice
                  420268
Seq. No.
Seq. ID
                  uC-osrocyp015f04a1
                  BLASTN
Method
NCBI GI
                  g21692
BLAST score
                  51
E value
                  2.0e-19
                  83
Match length
% identity
                  90
NCBI Description T.aestivum mRNA 1 for cathepsin B (2529)
                  420269
Seq. No.
Seq. ID
                  uC-osrocyp015f04b1
                  BLASTX
Method
                  g21693
NCBI GI
BLAST score
                  739
                  1.0e-78
E value
Match length
                  174
% identity
                  76
NCBI Description (X66012) cathepsin B [Triticum aestivum]
                  420270
Seq. No.
                  uC-osrocyp015f05b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4938477
BLAST score
                  202
                  1.0e-15
E value
Match length
                  72
% identity
                  56
NCBI Description (AL078464) putative protein [Arabidopsis thaliana]
Seq. No.
                  420271
                  uC-osrocyp015f06a1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q5596468
BLAST score
                  242
                  3.0e-20
E value
Match length
                  81
% identity
                  58
NCBI Description (AL096882) putative protein [Arabidopsis thaliana]
Seq. No.
                  420272
                  uC-osrocyp015f07b1
Seq. ID
Method
                  BLASTN
NCBI GI
                  q4589439
BLAST score
                  55
```



```
E value
                  7.0e-22
Match length
                  107
% identity
                  88
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MQM1, complete sequence
                  420273
Seq. No.
```

Seq. ID uC-osrocyp015g05b1

Method BLASTX NCBI GI q1706318 BLAST score 778 4.0e-83 E value 179 Match length 82 % identity

NCBI Description GLUTAMATE DECARBOXYLASE (GAD) (ERT D1)

>gi_1362098 pir S56177 probable glutamate decarboxylase tomato >gi 995555 emb CAA56812 (X80840) homology to pyroxidal-5'-phosphate-dependant glutamate decarboxylases;

putative start codon [Lycopersicon esculentum]

420274 Seq. No. Seq. ID uC-osrocyp015g09b1

Method BLASTX NCBI GI g3258575 BLAST score 570 9.0e-59 E value

152 Match length % identity 70

NCBI Description (U89959) Hypothetical protein [Arabidopsis thaliana]

Seq. No. 420275

Seq. ID uC-osrocyp015g10a1

Method BLASTX NCBI GI a5921187 BLAST score 254 1.0e-21 E value Match length 90 54 % identity

NCBI Description CYTOCHROME P450 71C2 >gi 550438 emb CAA57423 (X81829) cytochrome P450 [Zea mays] >gi 1870201 emb CAA72208

(Y11404) cytochrome p450 [Zea mays]

Seq. No. 420276 Seq. ID uC-osrocyp015g10b1

Method BLASTX NCBI GI q5921189 BLAST score 329 E value 2.0e-30 Match length 95 % identity 62

NCBI Description CYTOCHROME P450 71C4 >gi 550542 emb CAA57425 (X81831)

cytochrome P450 [Zea mays] >gi 1850903 emb CAA72196

(Y11368) cytochrome p450 [Zea mays]

420277 Seq. No.

uC-osrocyp015g11b1 Seq. ID

Method BLASTX



NCBI GI g3249064 BLAST score 559 E value 2.0e-57 Match length 173 % identity 58

NCBI Description (AC004473) Strong similarity to trehalose-6-phosphate synthase homolog gb_2245136 from A. thaliana chromosome 4

contig gb Z97344. [Arabidopsis thaliana]

Seq. No. 420278

Seq. ID uC-osrocyp015g12a1

Method BLASTX
NCBI GI g130718
BLAST score 351
E value 4.0e-33
Match length 119
% identity 59

NCBI Description ACID PHOSPHATASE PRECURSOR 1 >gi_170370 (M83211) acid

phosphatase type 1 [Lycopersicon esculentum] >gi_170372
(M67474) acid phosphatase type 5 [Lycopersicon esculentum]
>gi_445121_prf__1908427A acid phosphatase 1 [Lycopersicon

esculentum]

Seq. No. 420279

Seq. ID uC-osrocyp015h01b1

Method BLASTN
NCBI GI g4959460
BLAST score 34
E value 2.0e-09
Match length 34
% identity 100

NCBI Description Zea mays RACB small GTP binding protein mRNA, complete cds

Seq. No. 420280

Seq. ID uC-osrocyp015h02b1

Method BLASTX
NCBI GI g6056204
BLAST score 288
E value 1.0e-25
Match length 139
% identity 45

NCBI Description (AC009400) hypothetical protein [Arabidopsis thaliana]

Seq. No. 420281

Seq. ID uC-osrocyp015h05a1

Method BLASTX
NCBI GI g5042155
BLAST score 176
E value 1.0e-12
Match length 54
% identity 63

NCBI Description (AL078620) putative protein [Arabidopsis thaliana]

Seq. No. 420282

Seq. ID uC-osrocyp015h06b1

Method BLASTX NCBI GI g6063552

E value

3.0e-17

```
BLAST score
                   490
                   2.0e-49
E value
Match length
                   113
% identity
                   94
NCBI Description
                   (AP000615) ESTs AU065232(E60855), C23624(S1554),
                  AU078241(E60855) correspond to a region of the predicted
                   gene.; similar to putative adenylate kinase. (AC005896)
                   [Oryza sativa]
Seq. No.
                   420283
Seq. ID
                  uC-osrocyp015h07a1
Method
                  BLASTN
NCBI GI
                  g2331130
BLAST score
                   204
E value
                   1.0e-111
Match length
                  208
% identity
                   100
                  Oryza sativa glycine-rich protein (OSGRP1) mRNA, complete
NCBI Description
Seq. No.
                   420284
Seq. ID
                  uC-osrocyp015h07b1
Method
                  BLASTX
NCBI GI
                  g2293480
BLAST score
                  431
E value
                  2.0e-42
Match length
                  85
% identity
                   98
NCBI Description
                  (AF011331) glycine-rich protein [Oryza sativa]
                   420285
Seq. No.
                  uC-osrocyp015h09b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3738284
BLAST score
                  272
E value
                   9.0e-24
                  92
Match length
% identity
                  60
NCBI Description
                  (AC005309) unknown protein [Arabidopsis thaliana]
                  420286
Seq. No.
                  uC-osrocyp015h11b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1076748
BLAST score
                  241
E value
                  3.0e-20
                  98
Match length
                  51
% identity
NCBI Description
                  major intrinsic protein - rice >gi_440869_dbj_BAA04257_
                  (D17443) major intrinsic protein [Oryza sativa]
                  420287
Seq. No.
                  uC-osrocyp015h12b1
Seq. ID
Method
                  BLASTX
                  g2827559
NCBI GI
BLAST score
                  215
```



Match length 137 % identity 31

NCBI Description (AL021635) predicted protein [Arabidopsis thaliana] >gi_3292808_emb_CAA19798.1 (AL031018) putative protein

[Arabidopsis thaliana]

Seq. No. 420288

Seq. ID uC-osrocyp016a02b1

Method BLASTX
NCBI GI g5123836
BLAST score 483
E value 1.0e-48
Match length 122
% identity 80

NCBI Description (AJ006974) NAD-malate dehydrogenase [Nicotiana tabacum]

Seq. No. 420289

Seq. ID uC-osrocyp016a04b1

Method BLASTX
NCBI GI g4646217
BLAST score 556
E value 1.0e-72
Match length 145
% identity 93

NCBI Description (AC007290) putative phosphoprotein phosphatase [Arabidopsis

thaliana]

Seq. No. 420290

Seq. ID uC-osrocyp016a06b1

Method BLASTX
NCBI GI g3258575
BLAST score 292
E value 8.0e-33
Match length 143
% identity 52

NCBI Description (U89959) Hypothetical protein [Arabidopsis thaliana]

Seq. No. 420291

Seq. ID uC-osrocyp016a07a1

Method BLASTX
NCBI GI g282994
BLAST score 320
E value 4.0e-30
Match length 67
% identity 87

NCBI Description Sip1 protein - barley >gi 167100 (M77475) seed imbibition

protein [Hordeum vulgare]

Seq. No. 420292

Seq. ID uC-osrocyp016a07b1

Method BLASTX
NCBI GI g3290004
BLAST score 404
E value 3.0e-39
Match length 102
% identity 74

NCBI Description (U82200) pathogenesis related protein-1 [Zea mays]

```
Seq. No.
                  420293
Seq. ID
                  uC-osrocyp016a08b1
Method
                  BLASTX
NCBI GI
                  q4539404
BLAST score
                  428
                  3.0e-42
E value
Match length
                  131
% identity
                  58
                  (AL049524) putative protein [Arabidopsis thaliana]
NCBI Description
                  420294
Seq. No.
Seq. ID
                  uC-osrocyp016a09a1
                  BLASTN
Method
NCBI GI
                  q6016845
BLAST score
                  57
E value
                  2.0e-23
                  125
Match length
% identity
                  86
NCBI Description Oryza sativa genomic DNA, chromosome 1, clone:P0711E10
                  420295
Seq. No.
Seq. ID
                  uC-osrocyp016a09b1
Method
                  BLASTX
                  q4538911
NCBI GI
BLAST score
                  196
                  3.0e-21
E value
Match length
                  120
% identity
                  43
NCBI Description
                  (AL049482) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  420296
Seq. ID
                  uC-osrocyp016a10a1
Method
                  BLASTX
NCBI GI
                  g4646217
BLAST score
                  269
                  3.0e-24
E value
Match length
                  62
% identity
                  84
NCBI Description
                  (AC007290) putative phosphoprotein phosphatase [Arabidopsis
                  thaliana]
                  420297
Seq. No.
                  uC-osrocyp016b02b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4538939
BLAST score
                  499
                  2.0e-50
E value
Match length
                  109
% identity
                  84
NCBI Description
                  (AL049483) Col-0 casein kinase I-like protein [Arabidopsis
                  thaliana]
                  420298
Seq. No.
Seq. ID
                  uC-osrocyp016b04b1
Method
                  BLASTX
NCBI GI
                  g168643
```

BLAST score 232 E value 2.0e-26 Match length 121 % identity 55

NCBI Description (L02540) NADPH HC-toxin reductase [Zea mays]

Seq. No.

Seq. ID uC-osrocyp016b05b1

420299

Method BLASTX
NCBI GI g3252868
BLAST score 252
E value 2.0e-21
Match length 85
% identity 53

NCBI Description (AF033536) putative zinc transporter [Arabidopsis thaliana]

Seq. No. 420300

Seq. ID uC-osrocyp016b06a1

Method BLASTN
NCBI GI g728629
BLAST score 178
E value 1.0e-95
Match length 186
% identity 99

NCBI Description O.sativa mRNA for PCR clone D

Seq. No. 420301

Seq. ID uC-osrocyp016b07b1

Method BLASTX
NCBI GI g4263721
BLAST score 289
E value 7.0e-26
Match length 132
% identity 45

NCBI Description (AC006223) putative DNA repair protein RAD50 [Arabidopsis

thaliana]

Seq. No. 420302

Seq. ID uC-osrocyp016b08b1

Method BLASTX
NCBI GI g5882731
BLAST score 464
E value 2.0e-46
Match length 129
% identity 66

NCBI Description (AC008263) Similar to gb_AF000132 betaine aldehyde dehydrogenase from Amaranthus hypochondriacus. ESTs

gb_T20662, gb R90254, gb AA651436 and gb AA586226 come from

this gene. [Arabidopsis thaliana]

Seq. No. 420303

Seq. ID uC-osrocyp016b11b1

Method BLASTX
NCBI GI g1419090
BLAST score 254
E value 8.0e-22
Match length 49

```
% identity
NCBI Description
                  (X94968) 37kDa chloroplast inner envelope membrane
                  polypeptide precursor [Nicotiana tabacum]
Seq. No.
                  420304
                  uC-osrocyp016c01b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q5689136
BLAST score
                  441
                  8.0e-44
E value
                  94
Match length
% identity
                  46
NCBI Description (AB023479) transcription factor Ntlim1 [Nicotiana tabacum]
                  420305
Seq. No.
Seq. ID
                  uC-osrocyp016c02b1
Method
                  BLASTX
NCBI GI
                  q2894599
BLAST score
                  418
E value
                  7.0e-41
Match length
                  112
% identity
                  69
NCBI Description (AL021889) putative protein [Arabidopsis thaliana]
Seq. No.
                  420306
Seq. ID
                  uC-osrocyp016c03b1
Method
                  BLASTX
NCBI GI
                  g4234955
BLAST score
                  275
E value
                  4.0e-24
                  124
Match length
% identity
                  40
NCBI Description (AF098971) NBS-LRR-like protein cD8 [Phaseolus vulgaris]
Seq. No.
                  420307
Seq. ID
                  uC-osrocyp016c05a1
Method
                  BLASTN
NCBI GI
                  g20280
BLAST score
                  174
E value
                  2.0e-93
Match length
                  178
% identity
                  99
NCBI Description Rice gene for phenylalanine ammonia-lyase (EC 4.3.1.5)
Seq. No.
                  420308
                  uC-osrocyp016c05b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2293480
BLAST score
                  438
E value
                  2.0e-43
Match length
                  88
% identity
                  97
NCBI Description (AF011331) glycine-rich protein [Oryza sativa]
Seq. No.
                  420309
                  uC-osrocyp016c06b1
Seq. ID
Method
                  BLASTX
```



```
NCBI GI
                  g1053047
BLAST score
                  543
E value
                  1.0e-55
                  112
Match length
                  97
% identity
                  (U38425) histone H3 [Glycine max] >gi 1053049 (U38426)
NCBI Description
                  histone H3 [Glycine max] >gi 1053051 (U38427) histone H3
                  [Glycine max]
                  420310
Seq. No.
                  uC-osrocyp016c10b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g82496
BLAST score
                  543
E value
                  1.0e-55
Match length
                  127
                  83
% identity
NCBI Description
                  phenylalanine ammonia-lyase (EC 4.3.1.5) - rice
Seq. No.
                  420311
                  uC-osrocyp016c11a1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g2331130
BLAST score
                  128
                  7.0e-66
E value
Match length
                  128
% identity
                  100
NCBI Description
                  Oryza sativa glycine-rich protein (OSGRP1) mRNA, complete
                   420312
Seq. No.
                  uC-osrocyp016c11b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4262154
BLAST score
                   367
                   3.0e-35
E value
                  107
Match length
% identity
                   68
                   (AC005275) putative protein phosphatase regulatory subunit
NCBI Description
                   [Arabidopsis thaliana]
                   420313
Seq. No.
Seq. ID
                  uC-osrocyp016c12b1
Method
                  BLASTX
NCBI GI
                   g2982458
BLAST score
                   573
E value
                   3.0e-59
Match length
                   139
```

79 % identity

NCBI Description (AL022223) putative protein [Arabidopsis thaliana]

420314 Seq. No.

Seq. ID uC-osrocyp016d01b1

Method BLASTX NCBI GI q2501555 BLAST score 231 E value 5.0e-19

Match length 46 % identity 93

NCBI Description POSSIBLE APOSPORY-ASSOCIATED PROTEIN C >gi_549984 (U13148) possible apospory-associated protein [Pennisetum ciliare]

Seq. No. 420315

Seq. ID uC-osrocyp016d02a1

Method BLASTN
NCBI GI g20378
BLAST score 174
E value 2.0e-93
Match length 178
% identity 99

NCBI Description Oryza sativa mRNA for alpha 1 tubulin

Seq. No. 420316

Seq. ID uC-osrocyp016d02b1

Method BLASTX
NCBI GI g417103
BLAST score 662
E value 1.0e-69
Match length 136
% identity 98

NCBI Description HISTONE H3.2, MINOR >gi_282871_pir__S24346 histone

H3.3-like protein - Arabidopsis thaliana

>gi_16324_emb_CAA42957_ (X60429) histone H3.3 like protein [Arabidopsis thaliana] >gi_404825_emb_CAA42958_ (X60429) histone H3.3 like protein [Arabidopsis thaliana] >gi_488563 (U09458) histone H3.2 [Medicago sativa] >gi_488567 (U09460) histone H3.2 [Medicago sativa] >gi_488569 (U09461) histone H3.2 [Medicago sativa] >gi_488575 (U09464) histone H3.2

[Medicago sativa] $>gi_4885\overline{77}$ (U09465) histone H3.2

[Medicago sativa] >gi_510911_emb_CAA56153 (X79714) histone

H3 [Lolium temulentum] >gi_1435157_emb_CAA58445_ (X83422) histone H3 variant H3.3 [Lycopersicon esculentum] >gi_2558944 (AF024716) histone 3 [Gossypium hirsutum] >gi_3273350_dbj_BAA31218_ (AB015760) histone H3 [Nicotiana tabacum] >gi_3885890 (AF093633) histone H3 [Oryza sativa] >gi_4038469_gb_AAC97380_ (AF109910) histone H3 [Porteresia coarctata] >gi_4490754_emb_CAB38916.1_ (AL035708) histone H3.3 [Arabidopsis thaliana] >gi_4490755 emb_CAB38917.1

(AL035708) Histon H3 [Arabidopsis thaliana]

>gi_6006364_dbj_BAA84794.1_ (AP000559) EST D15300(C0425) corresponds to a region of the predicted gene.; Similar to

histone H3 (AB015760) [Oryza sativa]

Seq. No. 420317

Seq. ID uC-osrocyp016d04b1

Method BLASTX
NCBI GI g1076746
BLAST score 524
E value 2.0e-53
Match length 107
% identity 93

NCBI Description heat shock protein 70 - rice (fragment)

>gi 763160 emb CAA47948 (X67711) heat shock protein 70

[Oryza sativa]

```
Seq. No.
                   420318
                   uC-osrocyp016d06b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3334320
BLAST score
                   526
                   1.0e-53
E value
Match length
                   106
                   94
% identity
NCBI Description 40S RIBOSOMAL PROTEIN SA (P40) >gi 2444420 (AF020553)
                   ribosome-associated protein p40 [Glycine max]
                   420319
Seq. No.
Seq. ID
                   uC-osrocyp016d07b1
Method
                  BLASTX
NCBI GI
                   g135399
BLAST score
                   711
                   3.0e-75
E value
Match length
                   134
                   99
% identity
                  TUBULIN ALPHA-1 CHAIN >gi 100716 pir S20758 tubulin
NCBI Description
                   alpha-1 chain - rice >gi 20379 emb CAA77988 (Z11931) alpha
                   1 tubulin [Oryza sativa] >gi 1136124 emb CAA62918 (X91808)
                   alfa-tubulin [Oryza sativa]
Seq. No.
                   420320
Seq. ID
                   uC-osrocyp016d09b1
Method
                  BLASTX
NCBI GI
                  g5031275
BLAST score
                   213
                   4.0e - 31
E value
Match length
                   116
% identity
                   66
NCBI Description (AF139496) unknown [Prunus armeniaca]
Seq. No.
                   420321
Seq. ID
                   uC-osrocyp016d10b1
Method
                  BLASTX
NCBI GI
                   q3786016
BLAST score
                   223
E value
                   3.0e-18
Match length
                   117
% identity
                   46
NCBI Description
                   (AC005499) putative elongation factor [Arabidopsis
                   thaliana]
Seq. No.
                   420322
Seq. ID
                  uC-osrocyp016e02b1
Method
                  BLASTX
NCBI GI
                  g2842480
BLAST score
                   543
E value
                   1.0e-55
Match length
                   135
% identity
NCBI Description
                   (AL021749) ADP, ATP carrier-like protein [Arabidopsis
```

thaliana]

```
420323
Seq. No.
Seq. ID
                  uC-osrocyp016e03b1
Method
                  BLASTX
                  g417154
NCBI GI
BLAST score
                  763
                  2.0e-91
E value
                  175
Match length
                  97
% identity
                  HEAT SHOCK PROTEIN 82 >gi 100685 pir S25541 heat shock
NCBI Description
                  protein 82 - rice (strain Taichung Native One)
                  >gi 20256 emb CAA77978 (Z11920) heat shock protein 82
                  (HSP82) [Oryza sativa]
                  420324
Seq. No.
Seq. ID
                  uC-osrocyp016e04b1
                  BLASTX
Method
                  g4406820
NCBI GI
BLAST score
                  350
                  4.0e-33
E value
Match length
                  118
                  57
% identity
                  (AC006201) putative ras superfamily member [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  420325
Seq. ID
                  uC-osrocyp016e05a1
Method
                  BLASTN
NCBI GI
                  g425794
BLAST score
                  137
E value
                  2.0e-71
                  153
Match length
                  97
% identity
NCBI Description Rice mRNA for heat shock protein 82 (gene name AD167),
                  partial cds
                  420326
Seq. No.
                  uC-osrocyp016e08b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2501011
BLAST score
                  201
                  2.0e-15
E value
Match length
                  65
                  55
% identity
                  ISOLEUCYL-TRNA SYNTHETASE (ISOLEUCINE--TRNA LIGASE) (ILERS)
NCBI Description
                  >qi 1652625 dbj BAA17545 (D90907) isoleucyl-tRNA
                  synthetase [Synechocystis sp.]
Seq. No.
                   420327
                  uC-osrocyp016e10b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g417154
BLAST score
                   688
E value
                  1.0e-72
Match length
                  144
                   97
% identity
NCBI Description HEAT SHOCK PROTEIN 82 >gi 100685 pir S25541 heat shock
                  protein 82 - rice (strain Taichung Native One)
```

Match length

% identity

136

87

```
>gi_20256_emb_CAA77978_ (Z11920) heat shock protein 82
                   (HSP82) [Oryza sativa]
                  420328
Seq. No.
Seq. ID
                  uC-osrocyp016e12b1
Method
                  BLASTX
NCBI GI
                  g479696
BLAST score
                  250
E value
                  2.0e-21
                  58
Match length
                  93
% identity
NCBI Description oxidase lip19 - rice >gi 394736 emb CAA40596 (X57325)
                  basic/leucine zipper protein [Oryza sativa]
                  420329
Seq. No.
Seq. ID
                  uC-osrocyp016f01a1
Method
                  BLASTX
NCBI GI
                  g3135251
BLAST score
                  214
E value
                  1.0e-17
                  63
Match length
                  60
% identity
NCBI Description
                  (AC003058) putative receptor protein kinase [Arabidopsis
                  thaliana] >gi 3176719 (AC002392) putative protein kinase
                   [Arabidopsis thaliana]
                  420330
Seq. No.
Seq. ID
                  uC-osrocyp016f02b1
Method
                  BLASTX
NCBI GI
                  g2190550
BLAST score
                  407
E value
                  6.0e-40
                  103
Match length
% identity
                  77
                 (ACO01229) ESTs gb_T45673,gb_N37512 come from this gene.
NCBI Description
                  [Arabidopsis thaliana]
Seq. No.
                  420331
Seq. ID
                  uC-osrocyp016f03b1
Method
                  BLASTX
NCBI GI
                  q2493053
BLAST score
                  273
E value
                  4.0e-24
Match length
                  62
                  81
% identity
NCBI Description ATP SYNTHASE EPSILON CHAIN, MITOCHONDRIAL >qi 639793
                  (L39120) mitochondrial F1F0 ATP synthase epsilon subunit
                  [Zea mays]
Seq. No.
                  420332
Seq. ID
                  uC-osrocyp016f04b1
Method
                  BLASTX
NCBI GI
                  g3914685
BLAST score
                  574
                  5.0e-61
E value
```

```
NCBI Description
                  60S RIBOSOMAL PROTEIN L17 >gi 2668748 (AF034948) ribosomal
                  protein L17 [Zea mays]
Seq. No.
                   420333
Seq. ID
                  uC-osrocyp016f06a1
Method
                  BLASTN
NCBI GI
                  g5042437
BLAST score
                  104
E value
                  1.0e-51
Match length
                  188
% identity
                  44
NCBI Description Oryza sativa BAC T49B20 genomic sequence, complete sequence
                  420334
Seq. No.
Seq. ID
                  uC-osrocyp016f09b1
Method
                  BLASTX
NCBI GI
                  q225901
BLAST score
                  143
E value
                  7.0e-18
Match length
                  79
% identity
                  59
NCBI Description ribosomal protein S6 [Rattus norvegicus]
Seq. No.
                  420335
Seq. ID
                  uC-osrocyp016f10a1
Method
                  BLASTN
NCBI GI
                  q871929
BLAST score
                  88
E value
                  5.0e-42
Match length
                  144
% identity
                  91
NCBI Description Rice mRNA EN486, partial sequence
Seq. No.
                  420336
Seq. ID
                  uC-osrocyp016f12b1
Method
                  BLASTX
NCBI GI
                  q2119129
BLAST score
                  335
E value
                  2.0e-31
Match length
                  106
                  59
% identity
NCBI Description ribosomal protein L36a.e.c14, cytosolic - yeast
                   (Saccharomyces cerevisiae) >gi 1302130 emb CAA96049
                   (Z71438) ORF YNL162w [Saccharomyces cerevisiae]
```

Seq. No. 420337

Seq. ID uC-osrocyp016g01b1

Method BLASTX NCBI GI g5091623 BLAST score 297 9.0e-27 E value 78 Match length 78 % identity

NCBI Description (AC007454) Similar to gb U93048 somatic embryogenesis receptor-like kinase from Daucus carota, contains 4 PF_00560 Leucine Rich Repeat domains and a PF 00069

Eukaryotic protein kinase domain. [Arabidopsis thaliana]

NCBI GI

```
Seq. No.
                   420338
Seq. ID
                   uC-osrocyp016g02b1
Method
                   BLASTX
NCBI GI
                   g1931647
BLAST score
                   403
E value
                   4.0e-39
Match length
                   124
% identity
                   61
NCBI Description
                  (U95973) endomembrane protein EMP70 precusor isolog
                   [Arabidopsis thaliana]
Seq. No.
                   420339
Seq. ID
                   uC-osrocyp016g03b1
Method
                  BLASTX
NCBI GI
                  q5777631
BLAST score
                   485
E value
                  7.0e-49
Match length
                  140
% identity
                   70
NCBI Description (AJ245900) CAA303719.1 protein [Oryza sativa]
Seq. No.
                   420340
Seq. ID
                  uC-osrocyp016g04b1
Method
                  BLASTX
NCBI GI
                  q2760327
BLAST score
                  791
E value
                  1.0e-84
Match length
                  170
% identity
NCBI Description (AC002130) F1N21.12 [Arabidopsis thaliana]
Seq. No.
                   420341
Seq. ID
                  uC-osrocyp016g05b1
Method
                  BLASTN
NCBI GI
                  g459268
BLAST score
                  167
E value
                  9.0e-89
Match length
                  398
% identity
                  86
NCBI Description Z.mays mRNA Transcribed Sequence
Seq. No.
                  420342
                  uC-osrocyp016g06a1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g2384759
BLAST score
                  184
E value
                  3.0e-99
Match length
                  188
% identity
                  99
NCBI Description Oryza sativa GDP dissociation inhibitor protein OsGDI2
                  (OsGDI2) mRNA, complete cds
Seq. No.
                  420343
Seq. ID
                  uC-osrocyp016g10b1
Method
                  BLASTX
```

55190

g1708191



BLAST score 204 6.0e-16 E value Match length 70 % identity 54

NCBI Description HEXOSE CARRIER PROTEIN HEX6 >gi 467319 (L08188) hexose

carrier protein [Ricinus communis]

Seq. No. 420344

Seq. ID uC-osrocyp016g11b1

Method BLASTX NCBI GI g2384760 BLAST score 728 E value 3.0e-77Match length 142 98 % identity

NCBI Description (AF016897) GDP dissociation inhibitor protein OsGDI2 [Oryza

sativa]

Seq. No. 420345

Seq. ID uC-osrocyp016g12b1

Method BLASTX NCBI GI q4337027 BLAST score 244 E value 3.0e-26Match length 122

58 % identity

(AF123254) MFP2 [Arabidopsis thaliana] NCBI Description

Seq. No. 420346

Seq. ID uC-osrocyp016h01a1

Method BLASTN NCBI GI q3618307 BLAST score 135 E value 5.0e-70 Match length 139 % identity 99

NCBI Description Oryza sativa mRNA for zinc finger protein, complete cds,

clone:C60910

420347 Seq. No.

uC-osrocyp016h01b1 Seq. ID

Method BLASTN NCBI GI q3618307 BLAST score 139 2.0e-72 E value Match length 220 98 % identity

NCBI Description Oryza sativa mRNA for zinc finger protein, complete cds,

clone:C60910

420348 Seq. No.

uC-osrocyp016h04b1 Seq. ID

Method BLASTX g3249066 NCBI GI BLAST score 505 4.0e-51 E value Match length 180

% identity NCBI Description (AC004473) Similar to S. cerevisiae SIK1P protein gb 984964. ESTs gb F15433 and gb AA395158 come from this gene. [Arabidopsis thaliana] 420349 Seq. No. Seq. ID uC-osrocyp016h06b1 Method BLASTN NCBI GI g3885887 BLAST score 277 E value 1.0e-154 Match length 285 % identity 99 Oryza sativa high mobility group protein (HMG) mRNA, NCBI Description complete cds Seq. No. 420350 Seq. ID uC-osrocyp016h07b1 Method BLASTX NCBI GI q1841464 BLAST score 438 E value 1.0e-43Match length 99 % identity 50 NCBI Description (Y11002) LIM-domain SF3 protein [Nicotiana tabacum] >gi 5932420 gb AAD56951.1_AF184886_1 (AF184886) LIM domain protein WLIM2 [Nicotiana tabacum] Seq. No. 420351 Seq. ID uC-osrocyp016h08b1 Method BLASTX NCBI GI q2708624 BLAST score 224 2.0e-18 E value Match length 69 % identity 64 NCBI Description (AF036618) acetyl-CoA synthetase [Arabidopsis thaliana] Seq. No. 420352 Seq. ID uC-osrocyp016h09b1 Method BLASTX NCBI GI g1890573 BLAST score 456 E value 2.0e-45 Match length 109 % identity 81 NCBI Description (X93173) xyloglucan endotransglycosylase (XET) [Hordeum vulgare] Seq. No. 420353 Seq. ID uC-osrocyp016h10b1 Method BLASTX NCBI GI g2981475 BLAST score 158 E value 1.0e-10 Match length 102 % identity 38

```
NCBI Description
                  (AF053084) putative cinnamyl alcohol dehydrogenase [Malus
                  domestica]
                  420354
Seq. No.
Seq. ID
                  uC-osrocyp016h11b1
Method
                  BLASTX
NCBI GI
                  q6041851
BLAST score
                  223
E value
                  4.0e-18
Match length
                  68
                  65
% identity
NCBI Description (AC009853) unknown protein [Arabidopsis thaliana]
                  420355
Seq. No.
                  uC-osrocyp016h12a1
Seq. ID
Method
                  BLASTN
NCBI GI
                  q3885887
BLAST score
                  189
E value
                  1.0e-102
Match length
                  189
                  100
% identity
NCBI Description Oryza sativa high mobility group protein (HMG) mRNA,
                  complete cds
Seq. No.
                  420356
Seq. ID
                  uC-osrocyp017a01a1
Method
                  BLASTN
NCBI GI
                  g736271
BLAST score
                  34
                  1.0e-09
E value
                  50
Match length
                  92
% identity
NCBI Description O.sativa hsp70 gene for heat shock protein
Seq. No.
                  420357
Seq. ID
                  uC-osrocyp017a01b1
Method
                  BLASTN
NCBI GI
                  g736271
BLAST score
                  33
                  4.0e-09
E value
Match length
                  41
                  95
% identity
NCBI Description O.sativa hsp70 gene for heat shock protein
                  420358
Seq. No.
                  uC-osrocyp017a02b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g113261
BLAST score
                  746
E value
                  2.0e-79
Match length
                  153
                  97
% identity
NCBI Description ACTIN 7 > gi 71637 pir ATRZ7 actin 7 - rice
                  >gi_20333_emb_CAA33872 (X15863) actin [Oryza sativa]
Seq. No.
                  420359
Seq. ID
                  uC-osrocyp017a05b1
```

Seq. ID

Method

NCBI GI



```
Method
                  BLASTX
NCBI GI
                  g3912917
BLAST score
                  634
                  3.0e-66
E value
Match length
                  145
                  85
% identity
                  (AF001308) putative NAK-like ser/thr protein kinase
NCBI Description
                  [Arabidopsis thaliana]
                  420360
Seq. No.
Seq. ID
                  uC-osrocyp017a06a1
Method
                  BLASTX
NCBI GI
                  g2293568
BLAST score
                  237
                  8.0e-20
E value
                  51
Match length
                  88
% identity
NCBI Description (AF012897) HvB12D homolog [Oryza sativa]
Seq. No.
                  420361
Seq. ID
                  uC-osrocyp017a06b1
Method
                  BLASTX
                  g2293568
NCBI GI
BLAST score
                  452
E value
                  5.0e-45
                  89
Match length
                  97
% identity
NCBI Description (AF012897) HvB12D homolog [Oryza sativa]
Seq. No.
                  420362
Seq. ID
                  uC-osrocyp017a07a1
Method
                  BLASTX
                  q1076746
NCBI GI
BLAST score
                  157
E value
                  2.0e-10
Match length
                  60
                  60
% identity
                  heat shock protein 70 - rice (fragment)
NCBI Description
                  >gi_763160_emb_CAA47948_ (X67711) heat shock protein 70
                  [Oryza sativa]
Seq. No.
                  420363
Seq. ID
                  uC-osrocyp017a07b1
Method
                  BLASTX
NCBI GI
                  q1076746
BLAST score
                  839
E value
                  3.0e-90
Match length
                  167
% identity
                  99
NCBI Description
                  heat shock protein 70 - rice (fragment)
                  >gi_763160_emb_CAA47948 (X67711) heat shock protein 70
                  [Oryza sativa]
Seq. No.
                  420364
```

55194

uC-osrocyp017a09a1

BLASTX

g1620982

Seq. No.

420369

```
BLAST score
                   316
E value
                   4.0e-29
Match length
                   66
% identity
                   98
                   (Y08860) 40S ribosomal protein S5 [Nicotiana
NCBI Description
                  plumbaginifolia]
                   420365
Seq. No.
Seq. ID
                   uC-osrocyp017a09b1
Method
                   BLASTX
NCBI GI
                   g3043428
BLAST score
                   505
E value
                   3.0e-51
Match length
                   113
% identity
                   82
NCBI Description
                  (AJ005346) 40S ribosomal protein S5 [Cicer arietinum]
Seq. No.
                   420366
Seq. ID
                   uC-osrocyp017a10a1
Method
                  BLASTX
NCBI GI
                   g1076746
BLAST score
                   166
E value
                   1.0e-11
Match length
                   61
% identity
                   61
NCBI Description
                  heat shock protein 70 - rice (fragment)
                   >gi_763160_emb_CAA47948_ (X67711) heat shock protein 70
                   [Oryza sativa]
                   420367
Seq. No.
                  uC-osrocyp017a10b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1076746
BLAST score
                   413
E value
                   8.0e-60
Match length
                  136
                   91
% identity
NCBI Description
                  heat shock protein 70 - rice (fragment)
                   >gi_763160 emb CAA47948 (X67711) heat shock protein 70
                   [Oryza sativa]
                   420368
Seq. No.
Seq. ID
                  uC-osrocyp017a11a1
Method
                  BLASTX
NCBI GI
                   g4103987
BLAST score
                   339
E value
                  7.0e-32
Match length
                  77
% identity
                  84
NCBI Description
                  (AF030516) 5,10-methylenetetrahydrofolate
                  dehydrogenase-5,10-methenyltetrahydrofolate cyclohydrolase
                   [Pisum sativum] >gi_6002383_emb_CAB56756.1 (AJ011589)
                   5,10-methylenetetrahydrofolate dehydrogenase:
                   5,10-methenyltetrahydrofolate cyclohydrolase [Pisum
                  sativum]
```

```
Seq. ID
                  uC-osrocyp017a11b1
Method
                  BLASTX
NCBI GI
                  q4103987
BLAST score
                  331
E value
                  7.0e-31
                  114
Match length
                  59
% identity
NCBI Description
                  (AF030516) 5,10-methylenetetrahydrofolate
                  dehydrogenase-5,10-methenyltetrahydrofolate cyclohydrolase
                  [Pisum sativum] >gi 6002383 emb CAB56756.1 (AJ011589)
                  5,10-methylenetetrahydrofolate dehydrogenase:
                  5,10-methenyltetrahydrofolate cyclohydrolase [Pisum
                  sativum]
                  420370
Seq. No.
Seq. ID
                  uC-osrocyp017b02a1
Method
                  BLASTN
NCBI GI
                  q5441876
BLAST score
                  408
                  0.0e + 00
E value
                  491
Match length
% identity
                  98
                  Oryza sativa genomic DNA, chromosome 2, clone:P0437H03
NCBI Description
                  (contig b)
                  420371
Seq. No.
Seq. ID
                  uC-osrocyp017b02b1
Method
                  BLASTN
NCBI GI
                  q5441876
BLAST score
                  534
                  0.0e + 00
E value
Match length
                  542
                  100
% identity
NCBI Description Oryza sativa genomic DNA, chromosome 2, clone:P0437H03
                   (contig b)
                  420372
Seq. No.
                  uC-osrocyp017b03a1
Seq. ID
Method
                  BLASTN
                  g2984708
NCBI GI
BLAST score
                  63
                  1.0e-26
E value
Match length
                  122
                  88
% identity
NCBI Description
                  Zea mays DnaJ-related protein ZMDJ1 (mdJ1) gene, complete
                  cds >gi 5996689 gb AR066473.1 AR066473 Sequence 2 from
                  patent US
Seq. No.
                  420373
                  uC-osrocyp017b03b1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g2984708
                  49
BLAST score
E value
                  2.0e-18
                  100
Match length
                  87
% identity
```

NCBI Description Zea mays DnaJ-related protein ZMDJ1 (mdJ1) gene, complete

cds >gi_5996689_gb_AR066473.1_AR066473 Sequence 2 from
patent US

Seq. No. 420374

Seq. ID uC-osrocyp017b05a1

Method BLASTN
NCBI GI g3885887
BLAST score 372
E value 0.0e+00
Match length 380
% identity 99

NCBI Description Oryza sativa high mobility group protein (HMG) mRNA,

complete cds

Seq. No. 420375

Seq. ID uC-osrocyp017b05b1

Method BLASTN
NCBI GI g3885887
BLAST score 316
E value 1.0e-177
Match length 336
% identity 99

NCBI Description Oryza sativa high mobility group protein (HMG) mRNA,

complete cds

Seq. No. 420376

Seq. ID uC-osrocyp017b06a1

Method BLASTX
NCBI GI g5441894
BLAST score 158
E value 2.0e-10
Match length 99
% identity 39

NCBI Description (AP000367) EST AU030111(E50640) corresponds to a region of

the predicted gene.; hypothetical protein [Oryza sativa]

Seq. No. 420377

Seq. ID uC-osrocyp017b07b1

Method BLASTX
NCBI GI g3355480
BLAST score 312
E value 2.0e-28
Match length 156
% identity 35

NCBI Description (AC004218) Medicago nodulin N21-like protein [Arabidopsis

thalianal

Seq. No. 420378

Seq. ID uC-osrocyp017b08a1

Method BLASTX
NCBI GI g4966345
BLAST score 143
E value 9.0e-09
Match length 32
% identity 84

NCBI Description (AC006341) Similar to gb_Y12014 RAD23 protein isoform II

from Daucus carota. This gene is probably cut off. EST



gb_AA651284 comes from this gene. [Arabidopsis thaliana]

Seq. No. 420379

Seq. ID uC-osrocyp017b08b1

Method BLASTX
NCBI GI g1914685
BLAST score 301
E value 3.0e-27
Match length 73
% identity 79

NCBI Description (Y12014) RAD23 protein, isoform II [Daucus carota]

Seq. No. 420380

Seq. ID uC-osrocyp017b09b1

Method BLASTX
NCBI GI g3193302
BLAST score 218
E value 1.0e-17
Match length 97
% identity 48

NCBI Description (AF069298) contains similarity to a protein kinase domain

(Pfam: pkinase.hmm, score: 166.20) and to legume lectins

beta domain (Pfam: lectin_legB.hmm, score: 139.32)

[Arabidopsis thaliana]

Seq. No. 420381

Seq. ID uC-osrocyp017b10b1

Method BLASTX
NCBI GI g6014937
BLAST score 210
E value 7.0e-17
Match length 84
% identity 52

NCBI Description UROPORPHYRINOGEN DECARBOXYLASE PRECURSOR (UPD) >gi 2651307

(AC002336) putative uroporphyinogen decarboxylase

[Arabidopsis thaliana]

Seq. No. 420382

Seq. ID uC-osrocyp017b12a1

Method BLASTX
NCBI GI 94504771
BLAST score 335
E value 2.0e-31
Match length 83
% identity 81

NCBI Description integrin beta 4 binding protein

>gi_3122258_sp_P56537_IF6_HUMAN EUKARYOTIC TRANSLATION INITIATION FACTOR 6 (EIF-6) (B4 INTEGRIN INTERACTOR) (CAB)

(P27(BBP)) (B(2)GCN HOMOLOG) >gi_2809383 (AF022229)

translation initiation factor 6 [Homo sapiens]

>gi_2910997_emb_CAA72243_ (Y11435) b4 integrin interactor
[Homo sapiens] >gi_3335506 (AF047433) b(2)gcn homolog [Homo

sapiens]

Seq. No. 420383

Seq. ID uC-osrocyp017b12b1

Method BLASTX

E value

7.0e-31

```
NCBI GI
                  g6016330
BLAST score
                  458
E value
                  1.0e-51
                  133
Match length
                  80
% identity
                  EUKARYOTIC TRANSLATION INITIATION FACTOR 6 (EIF-6)
NCBI Description
                  >gi 3355311 emb CAA08809 (AJ009737) eukaryotic translation
                  initiation factor 6 [Beta vulgaris]
                  420384
Seq. No.
Seq. ID
                  uC-osrocyp017c02a1
                  BLASTX
Method
NCBI GI
                  g836954
BLAST score
                  155
                  3.0e-10
E value
                  44
Match length
                  59
% identity
NCBI Description (U20948) receptor protein kinase [Ipomoea trifida]
Seq. No.
                  420385
Seq. ID
                  uC-osrocyp017c07a1
Method
                  BLASTX
NCBI GI
                  g3941480
BLAST score .
                  211
                  8.0e-17
E value
                  52
Match length
                  69
% identity
                  (AF062894) putative transcription factor [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  420386
Seq. ID
                  uC-osrocyp017c09a1
Method
                  BLASTX
NCBI GI
                  g129591
BLAST score
                  215
E value
                  3.0e-17
Match length
                  39
                  100
% identity
NCBI Description PHENYLALANINE AMMONIA-LYASE >gi 295824 emb CAA34226
                  (X16099) phenylalanine ammonia-lyase [Oryza sativa]
                  420387
Seq. No.
                  uC-osrocyp017c09b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q82496
BLAST score
                  682
                  7.0e-72
E value
Match length
                  153
                  87
% identity
NCBI Description phenylalanine ammonia-lyase (EC 4.3.1.5) - rice
Seq. No.
                  420388
                  uC-osrocyp017c11a1
Seq. ID
Method
                  BLASTN
                  g5410347
NCBI GI
BLAST score
                  70
```

```
142
Match length
                  87
% identity
                  Sorghum bicolor BAC clone 110K5, partial sequence
NCBI Description
                  420389
Seq. No.
Seq. ID
                  uC-osrocyp017c11b1
                  BLASTN
Method
                  g5410347
NCBI GI
BLAST score
                  98
                  1.0e-47
E value
                  258
Match length
                  84
% identity
NCBI Description Sorghum bicolor BAC clone 110K5, partial sequence
                  420390
Seq. No.
                  uC-osrocyp017c12a1
Seq. ID
                  BLASTX
Method
NCBI GI
                  g4741198
BLAST score
                  185
E value
                  9.0e-14
                  51
Match length
                  78
% identity
                  (AL049746) putative protein [Arabidopsis thaliana]
NCBI Description
                  420391
Seq. No.
Seq. ID
                  uC-osrocyp017d02b1
                  BLASTX
Method
NCBI GI
                  g2982463
BLAST score
                  322
E value
                  1.0e-29
Match length
                  141
% identity
                  51
                 (AL022223) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  420392
                  uC-osrocyp017d03b1
Seq. ID
                  BLASTX
Method
NCBI GI
                  q4836950
BLAST score
                  310
                  3.0e-28
E value
Match length
                  165
% identity
                  40
NCBI Description (AC006085) Hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  420393
                  uC-osrocyp017d06b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4433618
BLAST score
                  231
E value
                  5.0e-19
                  115
Match length
% identity
                  47
                  (AF107585) putative myosin heavy chain [Dendrobium grex
NCBI Description
                  Madame Thong-IN]
                  420394
Seq. No.
                  uC-osrocyp017d07a1
Seq. ID
```

```
BLASTN
Method
                  g1753084
NCBI GI
                  430
BLAST score
                  0.0e+00
E value
                   451
Match length
                  99
% identity
                  Oryza sativa clone OSE2 leucine zipper protein mRNA,
NCBI Description
                  complete cds
                   420395
Seq. No.
                  uC-osrocyp017d08b1
Seq. ID
                  BLASTX
Method
                   g3176687
NCBI GI
BLAST score
                   687
                   2.0e-72
E value
                   188
Match length
                   61
% identity
                   (AC003671) Strong similarity to trehalose-6-phosphate
NCBI Description
                   synthase homolog from A. thaliana chromosome 4 contig
                   gb Z97344. ESTs gb H37594, gb_R65023, gb_H37578 and
                   gb R64855 come from this gene. [Arabidopsis thaliana]
                   420396
Seq. No.
                   uC-osrocyp017e01b1
Seq. ID
                   BLASTX
Method
                   g4775271
NCBI GI
                   555
BLAST score
                   6.0e-57
E value
                   153
Match length
                   73
% identity
                  (AJ131214) SF2/ASF-like splicing modulator Srp30, variant 1
NCBI Description
                   [Arabidopsis thaliana]
                   420397
Seq. No.
Seq. ID
                   uC-osrocyp017e02b1
                   BLASTX
Method
                   q433970
NCBI GI
                   227
BLAST score
                   7.0e-19
E value
Match length
                   77
% identity
NCBI Description (Z28649) polyubiquitin [Acetabularia cliftonii]
                   420398
Seq. No.
Seq. ID
                   uC-osrocyp017e03a1
Method
                   BLASTN
                   g2331130
NCBI GI
BLAST score
                   63
                   7.0e-27
E value
Match length
                   111
% identity
                   89
                   Oryza sativa glycine-rich protein (OSGRP1) mRNA, complete
NCBI Description
```

Seq. No. 420399

Seq. ID uC-osrocyp017e04a1

Method BLASTN

```
g2586089
NCBI GI
BLAST score
                  37
                  2.0e-11
E value
                  65
Match length
                  89
% identity
                  Oryza longistaminata receptor-like kinase protein (Xa21),
NCBI Description
                  family member F, pseudogene sequence
                  420400
Seq. No.
                  uC-osrocyp017e06b1
Seq. ID
Method
                  BLASTX
                  g1706328
NCBI GI
BLAST score
                  756
                  1.0e-80
E value
                  166
Match length
                  89
% identity
                  PYRUVATE DECARBOXYLASE ISOZYME 2 (PDC) >gi 1009710 (U27350)
NCBI Description
                  pyruvate decarboxylase 2 [Oryza sativa] >gi 1777455
                   (U38199) pyruvate decarboxylase 2 [Oryza sativa]
                  420401
Seq. No.
Seq. ID
                  uC-osrocyp017e07a1
                  BLASTX
Method
NCBI GI
                  q4415931
BLAST score
                  383
                  8.0e-37
E value
                  120
Match length
                   59
% identity
                  (AC006418) unknown protein [Arabidopsis thaliana]
NCBI Description
                   >qi 4559393 gb AAD23053.1 AC006526 18 (AC006526) unknown
                  protein [Arabidopsis thaliana]
                   420402
Seq. No.
                   uC-osrocyp017e07b1
Seq. ID
Method
                   BLASTX
                   q4415931
NCBI GI
BLAST score
                   255
                   9.0e-22
E value
Match length
                   115
% identity
                   48
NCBI Description
                   (AC006418) unknown protein [Arabidopsis thaliana]
                   >qi 4559393 gb AAD23053.1 AC006526 18 (AC006526) unknown
                   protein [Arabidopsis thaliana]
Seq. No.
                   420403
                   uC-osrocyp017e08a1
Seq. ID
Method
                   BLASTN
                   g2331130
NCBI GI
                   208
BLAST score
                   1.0e-113
E value
                   208
Match length
                   100
% identity
NCBI Description Oryza sativa glycine-rich protein (OSGRP1) mRNA, complete
                   cds
```

420404

uC-osrocyp017e08b1

Seq. No.

Seq. ID

Match length

% identity

142 87



```
BLASTX
Method
NCBI GI
                  g2293480
BLAST score
                  449
                  1.0e-44
E value
                  89
Match length
                  98
% identity
NCBI Description (AF011331) glycine-rich protein [Oryza sativa]
                  420405
Seq. No.
Seq. ID
                  uC-osrocyp017e10b1
Method
                  BLASTX
NCBI GI
                  q2618696
BLAST score
                  153
E value
                  7.0e-10
                  93
Match length
                  32
% identity
NCBI Description (AC002510) hypothetical protein [Arabidopsis thaliana]
                  420406
Seq. No.
Seq. ID
                  uC-osrocyp017e11a1
Method
                  BLASTX
NCBI GI
                  q2924247
BLAST score
                  285
E value
                  2.0e-25
Match length
                  109
% identity
                  48
NCBI Description (Y07782) expansin [Oryza sativa]
                  420407
Seq. No.
Seq. ID
                  uC-osrocyp017e11b1
Method
                  BLASTX
                  g4027891
NCBI GI
BLAST score
                  550
                  2.0e-56
E value
Match length
                  136
                  72
% identity
NCBI Description (AF049350) alpha-expansin precursor [Nicotiana tabacum]
Seq. No.
                  420408
Seq. ID
                  uC-osrocyp017e12b1
Method
                  BLASTX
NCBI GI
                  q3132478
BLAST score
                  304
E value
                  1.0e-27
Match length
                  150
% identity
                  37
NCBI Description (AC003096) bZIP-like protein [Arabidopsis thaliana]
                  420409
Seq. No.
Seq. ID
                  uC-osrocyp017f01b1
Method
                  BLASTX
NCBI GI
                  g5916445
BLAST score
                  691
                  5.0e-73
E value
```

55203

NCBI Description (AC007633) putative protein [Arabidopsis thaliana]

```
Seq. No.
                  420410
                  uC-osrocyp017f02a1
Seq. ID
Method
                  BLASTN
NCBI GI
                  q6013290
                  131
BLAST score
                  2.0e-67
E value
                  223
Match length
                  90
% identity
NCBI Description Oryza sativa polyubiquitin (RUBQ2) gene, complete cds
                  420411
Seq. No.
Seq. ID
                  uC-osrocyp017f02b1
Method
                  BLASTX
                  q82512
NCBI GI
                   682
BLAST score
                   6.0e-72
E value
Match length
                  142
                   42
% identity
                  ubiquitin precursor - rice (fragment)
NCBI Description
                   >gi_218189_dbj_BAA02241_ (D12776) poly-ubiquitin [Oryza
                   satīva]
                   420412
Seq. No.
                   uC-osrocyp017f03a1
Seq. ID
                   BLASTX
Method
                   q2224915
NCBI GI
                   350
BLAST score
                   5.0e-33
E value
Match length
                   113
                   59
% identity
NCBI Description (U95968) beta-expansin [Oryza sativa]
                   420413
Seq. No.
Seq. ID
                   uC-osrocyp017f03b1
                   BLASTX
Method
NCBI GI
                   g2224915
BLAST score
                   318
                   3.0e-29
E value
Match length
                   87
                   60
% identity
NCBI Description (U95968) beta-expansin [Oryza sativa]
                   420414
Seq. No.
                   uC-osrocyp017f07a1
Seq. ID
Method
                   BLASTN
NCBI GI
                   g3885887
BLAST score
                   341
                   0.0e+00
E value
Match length
                   377
% identity
                   98
NCBI Description Oryza sativa high mobility group protein (HMG) mRNA,
                   complete cds
                   420415
Seq. No.
                   uC-osrocyp017f07b1
Seq. ID
Method
                   BLASTX
```

```
NCBI GI
                  g3885888
BLAST score
                  215
E value
                  3.0e-17
                  87
Match length
                  57
% identity
NCBI Description (AF093632) high mobility group protein [Oryza sativa]
Seq. No.
                  420416
                  uC-osrocyp017f08b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2688824
BLAST score
                  151
                  8.0e-10
E value
                  90
Match length
% identity
                  46
NCBI Description
                  (U93273) putative auxin-repressed protein [Prunus
                  armeniaca]
                  420417
Seq. No.
                  uC-osrocyp017f09b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2979560
BLAST score
                  154
                  5.0e-10
E value
Match length
                  61
                  51
% identity
                  (AC003680) unknown protein [Arabidopsis thaliana]
NCBI Description
                   420418
Seq. No.
                  uC-osrocyp017f10a1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4220481
BLAST score
                  186
                  8.0e-14
E value
                  79
Match length
                  39
% identity
NCBI Description
                 (AC006069) unknown protein [Arabidopsis thaliana]
                  420419
Seq. No.
                  uC-osrocyp017f10b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4220481
                  244
BLAST score
E value
                  1.0e-20
Match length
                  110
% identity
                   49
NCBI Description
                 (AC006069) unknown protein [Arabidopsis thaliana]
Seq. No.
                  420420
                  uC-osrocyp017f11a1
Seq. ID
Method
                  BLASTN
NCBI GI
                  q303858
BLAST score
                  394
E value
                  0.0e+00
Match length
                  402
% identity
                  100
NCBI Description Rice mRNA for brain specific protein (S94 gene), complete
```

Seq. ID Method



cds

```
Seq. No.
                   420421
Seq. ID
                   uC-osrocyp017f11b1
Method
                   BLASTX
NCBI GI
                   q543711
BLAST score
                   305
E value
                   8.0e-28
Match length
                   64
                   98
% identity
                  14-3-3-LIKE PROTEIN S94 >gi 419796 pir S30927 14-3-3
NCBI Description
                  protein homolog - rice >gi 303859 dbj BAA03711 (D16140)
                  brain specific protein [Oryza sativa]
Seq. No.
                   420422
Seq. ID
                   uC-osrocyp017g04b1
Method
                  BLASTX
NCBI GI
                   q4204265
BLAST score
                   408
E value
                   1.0e-39
Match length
                   108
% identity
                   69
NCBI Description
                  (AC005223) 45643 [Arabidopsis thaliana]
                   420423
Seq. No.
                  uC-osrocyp017g05a1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4008156
BLAST score
                   224
                   3.0e-18
E value
                   68
Match length
% identity
                   68
NCBI Description
                  (AB008845) NADH dependent Glutamate Synthase [Oryza sativa]
                   420424
Seq. No.
                  uC-osrocyp017g05b1
Seq. ID
Method
                  BLASTX
NCBI GI
                   g4008156
BLAST score
                   677
E value
                  2.0e-71
Match length
                  141
% identity
                  91
NCBI Description
                  (AB008845) NADH dependent Glutamate Synthase [Oryza sativa]
                   420425
Seq. No.
                  uC-osrocyp017g06a1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4490316
BLAST score
                  336
E value
                  2.0e-31
Match length
                  98
% identity
                  58
NCBI Description
                  (AL035678) nucellin-like protein [Arabidopsis thaliana]
Seq. No.
                  420426
```

55206

uC-osrocyp017g09a1

BLASTX

Match length

49

```
NCBI GI
                   g6016698
BLAST score
                   173
E value
                   2.0e-12
Match length
                   40
% identity
                  72
                  (AC009991) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   420427
                  uC-osrocyp017g09b1
Seq. ID
Method
                  BLASTX
NCBI GI
                   q6016698
BLAST score
                   458
E value
                   9.0e-46
Match length
                  124
% identity
                   69
NCBI Description
                  (AC009991) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   420428
                   uC-osrocyp017g10a1
Seq. ID
Method
                  BLASTX
NCBI GI
                   q2688828
BLAST score
                   198
E value
                   3.0e-15
Match length
                   91
                   48
% identity
NCBI Description
                   (U97530) ethylene-forming-enzyme-like dioxygenase [Prunus
                  armeniaca]
Seq. No.
                   420429
                  uC-osrocyp017g10b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q5430761
BLAST score
                   145
                  1.0e-14
E value
                  148
Match length
                   36
% identity
                  (AC007504) Similar to ethylene-forming-enzyme-like
NCBI Description
                  dioxygenase [Arabidopsis thaliana]
                   420430
Seq. No.
                  uC-osrocyp017h01b1
Seq. ID
Method
                  BLASTN
NCBI GI
                   g4874281
                  36
BLAST score
E value
                   1.0e-10
                   44
Match length
                   95
% identity
NCBI Description
                  Arabidopsis thaliana chromosome II BAC F8D23 genomic
                  sequence, complete sequence
                   420431
Seq. No.
Seq. ID
                   uC-osrocyp017h02b1
Method
                  BLASTX
NCBI GI
                  q1304128
BLAST score
                   215
E value
                   2.0e-17
```

BLAST score

212

% identity (D63791) polyubiquitin [Homo sapiens] NCBI Description Seq. No. 420432 uC-osrocyp017h03a1 Seq. ID Method BLASTX NCBI GI g829283 BLAST score 368 4.0e-35 E value Match length 86 % identity 88 NCBI Description (Z15018) heat shock protein hsp82 [Oryza sativa] Seq. No. 420433 Seq. ID uC-osrocyp017h03b1 Method BLASTX NCBI GI g417154 BLAST score 284 E value 2.0e-25 Match length 67 % identity 85 NCBI Description HEAT SHOCK PROTEIN 82 >gi 100685 pir S25541 heat shock protein 82 - rice (strain Taichung Native One) >gi_20256_emb_CAA77978_ (Z11920) heat shock protein 82 (HSP82) [Oryza sativa] 420434 Seq. No. Seq. ID uC-osrocyp017h05a1 Method BLASTX NCBI GI q549063 BLAST score 261 1.0e-22 E value 58 Match length 86 % identity NCBI Description TRANSLATIONALLY CONTROLLED TUMOR PROTEIN HOMOLOG (TCTP) >gi_1072464_pir__A38958 IgE-dependent histamine-releasing factor homolog - rice >gi_303835_dbj_BAA02151 (D12626) 21kd polypeptide [Oryza sativa] 420435 Seq. No. uC-osrocyp017h05b1 Seq. ID Method BLASTX NCBI GI g549063 BLAST score 268 3.0e-46 E value Match length 102 96 % identity NCBI Description TRANSLATIONALLY CONTROLLED TUMOR PROTEIN HOMOLOG (TCTP) >gi_1072464_pir__A38958 IgE-dependent histamine-releasing factor homolog - rice >gi_303835_dbj_BAA02151_ (D12626) 21kd polypeptide [Oryza sativa] Seq. No. 420436 Seq. ID uC-osrocyp017h06a1 Method BLASTX NCBI GI g462195

```
E value
                   6.0e-17
Match length
                  50
                  84
% identity
                  PROTEIN TRANSLATION FACTOR SUI1 HOMOLOG (GOS2 PROTEIN)
NCBI Description
                  >gi 100682 pir S21636 GOS2 protein - rice
                  >gi 20238 emb CAA36190 (X51910) GOS2 [Oryza sativa]
                  >gi 3789950 (AF094774) translation initiation factor [Oryza
                  satival
                  420437
Seq. No.
                  uC-osrocyp017h06b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q462195
BLAST score
                  316
                   5.0e-29
E value
                  74
Match length
% identity
                  82
                  PROTEIN TRANSLATION FACTOR SUI1 HOMOLOG (GOS2 PROTEIN)
NCBI Description
                  >gi_100682_pir__S21636 GOS2 protein - rice
                  >gi 20238 emb CAA36190 (X51910) GOS2 [Oryza sativa]
                  >gi 3789950 (AF094774) translation initiation factor [Oryza
                  sativa]
Seq. No.
                  420438
                  uC-osrocyp017h07b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2894607
BLAST score
                  375
E value
                  6.0e-36
Match length
                  102
                  65
% identity
NCBI Description
                  (AL021889) NAM (no apical meristem)-like protein
                   [Arabidopsis thaliana]
Seq. No.
                   420439
                  uC-osrocyp017h10b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2493318
BLAST score
                  234
                  2.0e-19
E value
Match length
                  99
                  47
% identity
                 BLUE COPPER PROTEIN PRECURSOR >gi 562779 emb CAA80963
NCBI Description
                   (Z25471) blue copper protein [Pisum sativum]
                  >gi 1098264 prf 2115352A blue Cu protein [Pisum sativum]
                  420440
Seq. No.
Seq. ID
                  uC-osrocyp017h12b1
Method
                  BLASTX
NCBI GI
                  g2501494
BLAST score
                  145
E value
                  6.0e-09
```

Match length 148 % identity 27

NCBI Description FLAVONOL 3-O-GLUCOSYLTRANSFERASE 5 (UDP-GLUCOSE FLAVONOID

3-O-GLUCOSYLTRANSFERASE 5) >gi_542015_pir__s41951

UTP-glucose glucosyltransferase - cassava



>gi_453249_emb_CAA54612_ (X77462) UTP-glucose
glucosyltransferase [Manihot esculenta]

Seq. No. 420441

Seq. ID uC-osrocyp021a02b1

Method BLASTX
NCBI GI g4587518
BLAST score 759
E value 6.0e-81
Match length 170
% identity 86

NCBI Description (AC007060) Strong similarity to F19I3.8 gi_3033381 putative

UDP-galactose-4-epimerase from Arabidopsis thaliana BAC gb_AC004238 and is a member of PF_01370 the NAD dependent

epimerase/dehydratase family. EST gb_AA59

Seq. No. 420442

Seq. ID uC-osrocyp021a04b1

Method BLASTX
NCBI GI 94586062
BLAST score 206
E value 4.0e-16
Match length 94
% identity 50

NCBI Description (AC007020) unknown protein [Arabidopsis thaliana]

Seq. No. 420443

Seq. ID uC-osrocyp021a05b1

Method BLASTX
NCBI GI g3913437
BLAST score 239
E value 1.0e-42
Match length 145
% identity 72

NCBI Description PUTATIVE PRE-MRNA SPLICING FACTOR ATP-DEPENDENT RNA

HELICASE >gi_1402875_emb_CAA66825_ (X98130) RNA helicase [Arabidopsis thaliana] >gi_1495271_emb_CAA66613_ (X97970)

RNA helicase [Arabidopsis thaliana]

Seq. No. 420444

Seq. ID uC-osrocyp021a06b1

Method BLASTN
NCBI GI 94097337
BLAST score 59
E value 3.0e-24
Match length 67
% identity 97

NCBI Description Oryza sativa metallothionein-like protein mRNA, complete

cds

Seq. No. 420445

Seq. ID uC-osrocyp021a11b1

Method BLASTX
NCBI GI g2791806
BLAST score 389
E value 2.0e-37
Match length 119

% identity

100

sativa]

% identity NCBI Description (AF041433) bet3 [Mus musculus] Seq. No. 420446 Seq. ID uC-osrocyp021a12b1 Method BLASTN NCBI GI q4097337 BLAST score 348 E value 0.0e + 00Match length 415 100 % identity NCBI Description Oryza sativa metallothionein-like protein mRNA, complete Seq. No. 420447 Seq. ID uC-osrocyp021b01b1 Method BLASTX NCBI GI g3548801 BLAST score 173 E value 3.0e-12 Match length 85 % identity 38 (AC005313) putative transmembrane protein [Arabidopsis NCBI Description thaliana] >gi_4335768_gb_AAD17445_ (AC006284) putative integral membrane protein [Arabidopsis thaliana] Seq. No. 420448 Seq. ID uC-osrocyp021b02b1 Method BLASTX NCBI GI q2662343 BLAST score 648 E value 5.0e-68 Match length 127 % identity 98 NCBI Description (D63581) EF-1 alpha [Oryza sativa] Seq. No. 420449 Seq. ID uC-osrocyp021b03b1 Method BLASTX NCBI GI g5081779 BLAST score 774 E value 1.0e-82 Match length 150 % identity 94 NCBI Description (AF150630) cellulose synthase [Gossypium hirsutum] Seq. No. 420450 Seq. ID uC-osrocyp021b04b1 Method BLASTX NCBI GI g585338 BLAST score 779 E value 3.0e-83 Match length 154

55211

>gi 391879 dbj BAA01181 (D10335) adenylate kinase-b [Oryza

NCBI Description ADENYLATE KINASE B (ATP-AMP TRANSPHOSPHORYLASE)

```
Seq. No.
                   420451
Seq. ID
                   uC-osrocyp021b06b1
Method
                  BLASTX
                  g3044214
NCBI GI
BLAST score
                   234
E value
                   9.0e-20
                   55
Match length
                  76
% identity
NCBI Description (AF057044) acyl-CoA oxidase [Arabidopsis thaliana]
Seq. No.
                   420452
Seq. ID
                  uC-osrocyp021b12b1
Method
                  BLASTX
NCBI GI
                  g4263786
BLAST score
                   591
                  2.0e-61
E value
Match length
                  131
% identity
                   85
                  (AC006068) putative acyl coenzyme A oxidase, peroxisomal
NCBI Description
                  component [Arabidopsis thaliana]
Seq. No.
                   420453
                  uC-osrocyp021c03b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g5762457
BLAST score
                  215
E value
                  5.0e-19
Match length
                  82
                  58
% identity
NCBI Description
                  (AF176040) ubiquitin-conjugating enzyme UBC2
                   [Mesembryanthemum crystallinum]
                   420454
Seq. No.
Seq. ID
                  uC-osrocyp021c06b1
Method
                  BLASTX
NCBI GI
                  g3023713
BLAST score
                  326
E value
                  2.0e-30
Match length
                  72
                  88
% identity
NCBI Description
                  ENOLASE (2-PHOSPHOGLYCERATE DEHYDRATASE)
                   (2-PHOSPHO-D-GLYCERATE HYDRO-LYASE) (OSE1) >gi_780372
                   (U09450) enolase [Oryza sativa]
Seq. No.
                  420455
Seq. ID
                  uC-osrocyp021c08b1
Method
                  BLASTN
NCBI GI
                  q2463334
BLAST score
                  60
                  6.0e-25
E value
Match length
                  236
% identity
                  83
NCBI Description Oryza sativa mRNA for ribosomal protein S4
                  420456
Seq. No.
Seq. ID
                  uC-osrocyp021c11b1
```

```
Method
                   BLASTX
NCBI GI
                   q1708924
BLAST score
                   609
E value
                   2.0e-63
Match length
                   143
% identity
                   84
NCBI Description MALATE OXIDOREDUCTASE (MALIC ENZYME) (ME) (NADP-DEPENDENT
                  MALIC ENZYME) (NADP-ME) >gi 515759 (L34836) malate
                  dehydrogenase (NADP+) [Vitis vinifera]
Seq. No.
                   420457
Seq. ID
                  uC-osrocyp021c12b1
Method
                  BLASTX
NCBI GI
                  g3023713
BLAST score
                   660
E value
                  2.0e-69
Match length
                  142
% identity
                  89
NCBI Description ENOLASE (2-PHOSPHOGLYCERATE DEHYDRATASE)
                   (2-PHOSPHO-D-GLYCERATE HYDRO-LYASE) (OSE1) >gi 780372
                   (U09450) enolase [Oryza sativa]
Seq. No.
                  420458
Seq. ID
                  uC-osrocyp021d02b1
Method
                  BLASTX
NCBI GI
                  g2281649
BLAST score
                  296
E value
                  5.0e-27
Match length
                  77
% identity
                  71
NCBI Description
                 (AF003105) AP2 domain containing protein RAP2.12
                  [Arabidopsis thaliana]
Seq. No.
                  420459
Seq. ID
                  uC-osrocyp021d12b1
Method
                  BLASTX
NCBI GI
                  g5091510
BLAST score
                  254
E value
                  1.0e-21
Match length
                  53
                  91
% identity
NCBI Description
                 (AB023482) Similar to Arabidopsis thaliana gamma-adaptin 1
                  mRNA, complete cds.(AF061286) [Oryza sativa]
Seq. No.
                  420460
Seq. ID
                  uC-osrocyp021e02b1
Method
                  BLASTX
NCBI GI
                  g6056419
BLAST score
                  153
E value
                  2.0e-10
Match length
                  47
                  72
% identity
NCBI Description
                  (AC009525) 60S ribosomal protein L22 [Arabidopsis
                  thaliana]
Seq. No.
                  420461
Seq. ID
                  uC-osrocyp021e12b1
```

```
Method
                  BLASTX
NCBI GI
                  g2660675
BLAST score
                  567
                   2.0e-58
E value
Match length
                  139
                  81
% identity
                   (ACO02342) similar to DNA-damage-inducible protein P
NCBI Description
                   [Arabidopsis thaliana]
                   420462
Seq. No.
Seq. ID
                  uC-osrocyp021f02b1
                   BLASTX
Method
NCBI GI
                   q2921323
                   379
BLAST score
                   1.0e-36
E value
                   116
Match length
                   64
% identity
                  (AF034112) beta-1,3-glucanase 7 [Glycine max]
NCBI Description
                   420463
Seq. No.
                   uC-osrocyp021f03b1
Seq. ID
                   BLASTX
Method
                   q4586021
NCBI GI
BLAST score
                   214
                   9.0e-18
E value
                   68
Match length
                   59
% identity
                  (AC007170) putative cytoplasmic aconitate hydratase
NCBI Description
                   [Arabidopsis thaliana]
                   420464
Seq. No.
                   uC-osrocyp021g02b1
Seq. ID
                   BLASTX
Method
NCBI GI
                   g129591
BLAST score
                   317
                   2.0e-29
E value
Match length
                   63
                   100
% identity
                  PHENYLALANINE AMMONIA-LYASE >gi 295824 emb_CAA34226_
NCBI Description
                   (X16099) phenylalanine ammonia-lyase [Oryza sativa]
                   420465
Seq. No.
                   uC-osrocyp021g12b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g5912299
                   738
BLAST score
                   4.0e-86
E value
                   166
Match length
                   99
% identity
NCBI Description (AJ133787) gigantea homologue [Oryza sativa]
                   420466
Seq. No.
                   uC-osrocyp021h11b1
Seq. ID
                   BLASTX
Method
                   g2498731
NCBI GI
                   478
BLAST score
```

6.0e-48

E value

BLAST score

E value

184

4.0e-14

```
Match length
                  156
% identity
                  59
                  PROBABLE NADP-DEPENDENT OXIDOREDUCTASE P1
NCBI Description
                  >gi_1362013 pir S57611 zeta-crystallin homolog -
                  Arabidopsis thaliana >gi_886428 emb CAA89838 (Z49768)
                  zeta-crystallin homologue [Arabidopsis thaliana]
Seq. No.
                  420467
Seq. ID
                  uC-osrocyp021h12b1
Method
                  BLASTX
NCBI GI
                  g2498731
BLAST score
                  404
                  7.0e-43
E value
                  155
Match length
                  56
% identity
NCBI Description
                 PROBABLE NADP-DEPENDENT OXIDOREDUCTASE P1
                  >gi 1362013 pir S57611 zeta-crystallin homolog -
                  Arabidopsis thaliana >gi_886428 emb CAA89838 (Z49768)
                  zeta-crystallin homologue [Arabidopsis thaliana]
Seq. No.
                  420468
Seq. ID
                  uC-osrocyp024a06b1
Method
                  BLASTX
NCBI GI
                  q3386621
BLAST score
                  248
E value
                  2.0e-21
Match length
                  62
                  77
% identity
NCBI Description (AC004665) unknown protein [Arabidopsis thaliana]
Seq. No.
                  420469
Seq. ID
                  uC-osrocyp024a07b1
Method
                  BLASTX
NCBI GI
                  q5059115
BLAST score
                  411
E value
                  3.0e-40
Match length
                  121
% identity
                  64
NCBI Description (AF132212) OPDA-reductase homolog [Arabidopsis thaliana]
Seq. No.
                  420470
Seq. ID
                  uC-osrocyp024a11b1
Method
                  BLASTX
NCBI GI
                  q4835757
BLAST score
                  289
E value
                  4.0e-26
Match length
                  107
% identity
                  49
NCBI Description
                  (AC007202) EST gb AA404917 comes from this gene.
                  [Arabidopsis thaliana]
Seq. No.
                  420471
Seq. ID
                  uC-osrocyp024b08b1
Method
                  BLASTX
NCBI GI
                  q2104681
```

```
59
Match length
% identity
                  64
                  (X97907) transcription factor [Vicia faba]
NCBI Description
                  420472
Seq. No.
Seq. ID
                  uC-osrocyp024d03b1
                  BLASTX
Method
NCBI GI
                  g1657621
BLAST score
                  185
                  3.0e-15
E value
                  69
Match length
                  64
% identity
                  (U72505) G6p [Arabidopsis thaliana] >gi_3068711 (AF049236)
NCBI Description
                  putative acyl-coA dehydrogenase [Arabidopsis thaliana]
                  >gi 5478795_dbj_BAA82478.1_ (AB017643) Short-chain acyl CoA
                  oxidase [Arabidopsis thaliana]
                  420473
Seq. No.
Seq. ID
                  uC-osrocyp024e02b1
                  BLASTX
Method
                  g129591
NCBI GI
BLAST score
                  161
                  2.0e-11
E value
                  30
Match length
                  100
% identity
NCBI Description PHENYLALANINE AMMONIA-LYASE >gi 295824 emb CAA34226
                  (X16099) phenylalanine ammonia-Tyase [Oryza sativa]
                  420474
Seq. No.
Seq. ID
                  uC-osrocyp024e08b1
Method
                  BLASTX
NCBI GI
                  q3819164
                  355
BLAST score
                  1.0e-33
E value
Match length
                  121
% identity
                  (AJ012318) cytosolic chaperonin, delta-subunit [Glycine
NCBI Description
                  max]
Seq. No.
                  420475
                  uC-osrocyp024f03b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1853974
BLAST score
                  224
                  7.0e-19
E value
Match length
                  43
                  95
% identity
NCBI Description (D14481) putative peroxidase [Oryza sativa]
Seq. No.
                  420476
Seq. ID
                  uC-osrocyp024g03b1
Method
                  BLASTX
NCBI GI
                  g6093997
BLAST score
                  365
                  5.0e-35
E value
Match length
                  82
```

% identity

```
NCBI Description
                  60S RIBOSOMAL PROTEIN L11 >gi 2570507 (AF022736) ribosomal
                  protein [Oryza sativa]
Seq. No.
                   420477
Seq. ID
                  uC-osrocyp025a02a1
                  BLASTX
Method
                   q100689
NCBI GI
BLAST score
                   195
                   7.0e-15
E value
                   74
Match length
                   54
% identity
                  ribosomal protein L10.e, cytosolic - rice (fragment)
NCBI Description
                   >gi_20312_emb_CAA45905_ (X64621) unknown [Oryza sativa]
                   420478
Seq. No.
                   uC-osrocyp025a03a1
Seq. ID
Method
                   BLASTX
NCBI GI
                   q4581156
BLAST score
                   287
                   1.0e-25
E value
                   61
Match length
                   92
% identity
                  (AC006919) putative pyruvate kinase [Arabidopsis thaliana]
NCBI Description
                   420479
Seq. No.
Seq. ID
                   uC-osrocyp025a06a1
                   BLASTX
Method
                   q4760700
NCBI GI
BLAST score
                   182
E value
                   2.0e-13
Match length
                   71
                   54
% identity
                  (AB024437) peroxidase 1 [Scutellaria baicalensis]
NCBI Description
                   420480
Seq. No.
                   uC-osrocyp025a07a1
Seq. ID
Method
                   BLASTX
                   g549986
NCBI GI
BLAST score
                   320
                   1.0e-29
E value
                   69
Match length
                   90
% identity
                   (U13149) possible apospory-associated protein [Pennisetum
NCBI Description
                   ciliare]
                   420481
Seq. No.
                   uC-osrocyp025a08a1
Seq. ID
                   BLASTN
Method
                   g3885887
NCBI GI
                   451
BLAST score
                   0.0e + 00
E value
                   459
Match length
                   100
% identity
NCBI Description Oryza sativa high mobility group protein (HMG) mRNA,
                   complete cds
                   420482
Seq. No.
```

```
Seq. ID
                  uC-osrocyp025a09a1
Method
                  BLASTX
NCBI GI
                  g129591
BLAST score
                  208
E value
                  2.0e-16
Match length
                  39
                  97
% identity
NCBI Description PHENYLALANINE AMMONIA-LYASE >gi 295824 emb CAA34226
                  (X16099) phenylalanine ammonia-Tyase [Oryza sativa]
Seq. No.
                  420483
Seq. ID
                  uC-osrocyp025a10a1
Method
                  BLASTX
NCBI GI
                  g129591
BLAST score
                  265
                  5.0e-23
E value
                  49
Match length
                  98
% identity
NCBI Description
                 PHENYLALANINE AMMONIA-LYASE >gi 295824 emb CAA34226
                  (X16099) phenylalanine ammonia-lyase [Oryza sativa]
Seq. No.
                  420484
Seq. ID
                  uC-osrocyp025b03a1
Method
                  BLASTX
NCBI GI
                  q231587
BLAST score
                  182
E value
                  3.0e-13
                  47
Match length
% identity
                  77
NCBI Description ATP SYNTHASE BETA CHAIN, MITOCHONDRIAL PRECURSOR
                  >gi 283001 pir S25304 H+-transporting ATP synthase (EC
                  3.6.1.34) beta chain precursor, mitochondrial - rice
                  >gi_218147_dbj_BAA01372_ (D10491) mitochondrial F1-ATPase
                  [Oryza sativa]
                  420485
Seq. No.
Seq. ID
                  uC-osrocyp025b04a1
Method
                  BLASTX
NCBI GI
                  g629864
BLAST score
                  348
E value
                  7.0e-33
Match length
                  75
                  95
% identity
NCBI Description histone H2B - garden asparagus >gi 563329 emb CAA57778
                  (X82362) histone 2B [Asparagus officinalis]
                  420486
Seq. No.
Seq. ID
                  uC-osrocyp025b06a1
Method
                  BLASTX
NCBI GI
                  g601871
BLAST score
                  775
E value
                  8.0e-83
                  150
Match length
                  97
% identity
NCBI Description
                 (L34039) manganese superoxide dismutase [Oryza sativa]
```

420487

Seq. No.

Method

NCBI GI

BLASTX

g129591

```
Seq. ID
                  uC-osrocyp025b07a1
Method
                  BLASTX
                  g267056
NCBI GI
BLAST score
                  442
                  8.0e-44
E value
Match length
                  86
                  98
% identity
                  SUCROSE SYNTHASE 1 (SUCROSE-UDP GLUCOSYLTRANSFERASE 1)
NCBI Description
                  >gi 100710 pir S25526 sucrose synthase (EC 2.4.1.13) -
                  rice >gi 20374 emb CAA78747 (Z15028) sucrose synthase
                  [Oryza sativa]
                  420488
Seq. No.
                  uC-osrocyp025b09a1
Seq. ID
                  BLASTX
Method
NCBI GI
                  g4585901
BLAST score
                  345
                  2.0e-32
E value
Match length
                  156
% identity
                  47
                  (AC007133) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                  420489
Seq. No.
                  uC-osrocyp025b11a1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g5410347
BLAST score
                  62
                  4.0e-26
E value
Match length
                  142
% identity
                  86
NCBI Description Sorghum bicolor BAC clone 110K5, partial sequence
                  420490
Seq. No.
                  uC-osrocyp025c03a1
Seq. ID
Method
                  BLASTX
                  g1350969
NCBI GI
                  400
BLAST score
                  8.0e-39
E value
Match length
                  75
                  96
% identity
                 40S RIBOSOMAL PROTEIN S26 (S31) >gi 971284 dbj BAA07208_
NCBI Description
                   (D38011) ribosomal protein S31 [Oryza sativa]
                  420491
Seq. No.
                  uC-osrocyp025c07a1
Seq. ID
                  BLASTN
Method
NCBI GI
                  g20365
                  112
BLAST score
                  3.0e-56
E value
Match length
                  172
                  93
% identity
NCBI Description O.sativa RSs1 gene for sucrose synthase
                  420492
Seq. No.
                  uC-osrocyp025d01a1
Seq. ID
```



BLAST score 250 E value 3.0e-21 Match length 46 % identity 100

PHENYLALANINE AMMONIA-LYASE >gi 295824 emb CAA34226 NCBI Description (X16099) phenylalanine ammonia-lyase [Oryza sativa]

420493 Seq. No.

uC-osrocyp025d02a1 Seq. ID

Method BLASTX NCBI GI g4325345 BLAST score 262 E value 1.0e-22 Match length 86 24 % identity

NCBI Description (AF128393) similar to thioredoxin-like proteins (Pfam: PF00085, Score=42.9, E=1.4e-11, N=1); contains similarity to dihydroorotases (Pfam: PF00744, Score=154.9, E=1.4e-42,

N=1) [Arabidopsis thaliana]

Seq. No. 420494

uC-osrocyp025d03a1 Seq. ID

Method BLASTX NCBI GI g1170937 BLAST score 272 6.0e-24 E value Match length 51 % identity 96

NCBI Description S-ADENOSYLMETHIONINE SYNTHETASE 1 (METHIONINE

ADENOSYLTRANSFERASE 1) (ADOMET SYNTHETASE 1)

>gi 450549 emb CAA81481 (Z26867) S-adenosyl methionine

synthetase [Oryza sativa]

Seq. No. 420495

uC-osrocyp025d04a1 Seq. ID

BLASTN Method g20332 NCBI GI BLAST score 49 E value 2.0e-18 49 Match length 100 % identity

NCBI Description O.sativa RAc7 gene for actin

420496 Seq. No.

uC-osrocyp025d06a1 Seq. ID

Method BLASTX NCBI GI g1352347 BLAST score 255 E value 6.0e-22 60 Match length % identity 82

NCBI Description ELONGATION FACTOR 1-BETA A1 (EF-1-BETA)

>gi_480620_pir__S37103 translation elongation factor eEF-1 beta-A1 chain - Arabidopsis thaliana (cv. Colombia)

>gi_398608_emb_CAA52751_ (X74733) elongation factor-1 beta

Al [Arabidopsis thaliana]

```
Seq. No.
                   420497
Seq. ID
                  uC-osrocyp025d09a1
Method
                  BLASTX
NCBI GI
                  g4887020
BLAST score
                  155
                  4.0e-10
E value
                  36
Match length
                  78
% identity
NCBI Description (AF123508) Nt-iaa28 deduced protein [Nicotiana tabacum]
                  420498
Seq. No.
Seq. ID
                  uC-osrocyp025e02a1
Method
                  BLASTX
NCBI GI
                  g4567203
                  250
BLAST score
                  3.0e-21
E value
Match length
                  55
                  87
% identity
NCBI Description
                  (AC007168) putative beta-hydroxyacyl-ACP dehydratase
                   [Arabidopsis thaliana]
                   420499
Seq. No.
Seq. ID
                  uC-osrocyp025e08a1
                  BLASTX
Method
NCBI GI
                  g1184112
BLAST score
                  471
                  3.0e-47
E value
Match length
                  122
                  77
% identity
NCBI Description (U46138) Zn-induced protein [Oryza sativa]
                   420500
Seq. No.
                  uC-osrocyp025e12a1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g6016736
BLAST score
                  163
E value
                   4.0e-11
Match length
                   45
% identity
                   60
NCBI Description (AC009325) unknown protein [Arabidopsis thaliana]
Seq. No.
                   420501
                  uC-osrocyp025f01a1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2088651
BLAST score
                  156
E value
                   3.0e-10
Match length
                  56
                  54
% identity
NCBI Description (AF002109) hypersensitivity-related gene 201 isolog
                   [Arabidopsis thaliana]
                   420502
Seq. No.
                  uC-osrocyp025f02a1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3540199
```

521

BLAST score

```
E value
                   4.0e-53
Match length
                   150
                   67
% identity
                   (AC004260) Putative monosaccharide transport protein
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                   420503
Seq. ID
                   uC-osrocyp025f07a1
Method
                   BLASTX
NCBI GI
                   g3201612
BLAST score
                   335
E value
                   3.0e-31
Match length
                  161
% identity
NCBI Description (AC004669) putative 2A6 protein [Arabidopsis thaliana]
Seq. No.
                   420504
Seq. ID
                  uC-osrocyp025f08a1
Method
                  BLASTX
                  q2494132
NCBI GI
BLAST score
                  194
E value
                  1.0e-14
Match length
                   92
% identity
NCBI Description
                  (AC002376) Contains similarity to human dimethylaniline
                  monooxygenase (gb M64082). [Arabidopsis thaliana]
Seq. No.
                  420505
Seq. ID
                  uC-osrocyp025f10a1
Method
                  BLASTX
NCBI GI
                  q3080427
BLAST score
                  761
E value
                  3.0e-81
Match length
                  159
% identity
                  88
NCBI Description (AL022604) putative protein [Arabidopsis thaliana]
Seq. No.
                  420506
Seq. ID
                  uC-osrocyp025g01a1
Method
                  BLASTX
NCBI GI
                  g1136122
BLAST score
                  368
                  4.0e-35
E value
Match length
                  74
% identity
                  97
NCBI Description (X91807) alfa-tubulin [Oryza sativa]
Seq. No.
                  420507
Seq. ID
                  uC-osrocyp025g03a1
Method
                  BLASTX
NCBI GI
                  g4586246
BLAST score
                  276
E value
                  2.0e-24
Match length
                  105
% identity
                  47
```

NCBI Description (AL049640) putative protein [Arabidopsis thaliana]

Match length

402

```
Seq. No.
                   420508
Seq. ID
                  uC-osrocyp025g04a1
Method
                  BLASTX
NCBI GI
                  g1184112
BLAST score
                  208
E value
                  2.0e-16
Match length
                  98
% identity
                  53
NCBI Description (U46138) Zn-induced protein [Oryza sativa]
Seq. No.
                  420509
Seq. ID
                  uC-osrocyp025g07a1
Method
                  BLASTX
NCBI GI
                  g6041858
BLAST score
                  192
E value
                  1.0e-14
Match length
                  53
                  72
% identity
NCBI Description (AC009853) unknown protein [Arabidopsis thaliana]
Sea. No.
                  420510
Seq. ID
                  uC-osrocyp025g10a1
Method
                  BLASTX
NCBI GI
                  g2501812
BLAST score
                  145
E value
                  5.0e-09
Match length
                  46
% identity
NCBI Description (U91509) glycolate oxidase [Arabidopsis thaliana]
Seq. No.
                  420511
                  uC-osrocyp025g11a1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4371292
BLAST score
                  192
E value
                  2.0e-14
Match length
                  57
% identity
                  61
NCBI Description (AC006260) unknown protein [Arabidopsis thaliana]
                  420512
Seq. No.
Seq. ID
                  uC-osrocyp025h04a1
Method
                  BLASTX
NCBI GI
                  q1045614
BLAST score
                  456
E value
                  1.0e-45
Match length
                  117
% identity
                  75
NCBI Description (U37088) beta-ketoacyl-CoA synthase [Simmondsia chinensis]
Seq. No.
                  420513
Seq. ID
                  uC-osrocyp025h05a1
Method
                  BLASTN
NCBI GI
                  g6016845
BLAST score
                  180
E value
                  2.0e-96
```

```
% identity
NCBI Description Oryza sativa genomic DNA, chromosome 1, clone:P0711E10
                  420514
Seq. No.
Seq. ID
                  uC-osrocyp025h10a1
Method
                  BLASTN
NCBI GI
                  g1314048
BLAST score
                  454
                  0.0e + 00
E value
                  454
Match length
                  100
% identity
NCBI Description O.sativa mRNA for archain/delta-COP
                  420515
Seq. No.
Seq. ID
                  uC-osrocyp025h11a1
                  BLASTX
Method
NCBI GI
                  g3193301
                  250
BLAST score
E value
                  3.0e-21
Match length
                  74
                  65
% identity
                  (AF069298) Arabidopsis putative chloroplast outer envelope
NCBI Description
                  86-like protein T10P11.19 (GB: AC002330) [Arabidopsis
                  thaliana]
                   420516
Seq. No.
Seq. ID
                  uC-osrocyp026a05a1
                  BLASTN
Method
NCBI GI
                  g5091496
BLAST score
                   64
                   2.0e-27
E value
                  167
Match length
                   47
% identity
                  Oryza sativa genomic DNA, chromosome 6, clone P0680A03,
NCBI Description
                   complete sequence
Seq. No.
                   420517
                   uC-osrocyp026a06a1
Seq. ID
                   BLASTN
Method
NCBI GI
                   q425794
BLAST score
                   201
E value
                   1.0e-109
Match length
                   201
                   100
% identity
NCBI Description Rice mRNA for heat shock protein 82 (gene name AD167),
                  partial cds
Seq. No.
                   420518
Seq. ID
                   uC-osrocyp026a09a1
Method
                   BLASTN
NCBI GI
                   g710307
BLAST score
                   42
E value
                   4.0e-14
                  117
Match length
                   85
% identity
```

NCBI Description Avena sativa victorin binding protein mRNA, complete cds

```
420519
Seq. No.
Seq. ID
                  uC-osrocyp026b01a1
Method
                  BLASTX
NCBI GI
                  g1143864
BLAST score
                  269
                  1.0e-23
E value
                  48
Match length
                  100
% identity
NCBI Description (U28047) beta glucosidase [Oryza sativa]
                  420520
Seq. No.
                  uC-osrocyp026b07a1
Seq. ID
                  BLASTN
Method
NCBI GI
                  g1408221
                  43
BLAST score
                  8.0e-15
E value
                  83
Match length
                  88
% identity
NCBI Description Sorghum bicolor pathogenesis-related protein (PR-10) mRNA,
                  complete cds
Seq. No.
                  420521
Seq. ID
                  uC-osrocyp026b10a1
                  BLASTX
Method
                  g1184112
NCBI GI
BLAST score
                  406
                  1.0e-42
E value
                  111
Match length
                  82
% identity
NCBI Description (U46138) Zn-induced protein [Oryza sativa]
Seq. No.
                  420522
Seq. ID
                  uC-osrocyp026c02a1
Method
                  BLASTX
NCBI GI
                  q829283
BLAST score
                  268
                  2.0e-23
E value
Match length
                  69
                  81
% identity
NCBI Description (Z15018) heat shock protein hsp82 [Oryza sativa]
Seq. No.
                  420523
                  uC-osrocyp026c04a1
Seq. ID
                  BLASTN
Method
NCBI GI
                  q6006355
BLAST score
                  326
E value
                  0.0e + 00
Match length
                  378
% identity
                  97
NCBI Description Oryza sativa genomic DNA, chromosome 6, clone:P0493C11
Seq. No.
                  420524
Seq. ID
                  uC-osrocyp026c08a1
Method
                  BLASTX
                  q535454
NCBI GI
BLAST score
                  239
```

4.0e-20

E value

56 Match length % identity (U13940) cysteine proteinase [Alnus glutinosa] NCBI Description 420525 Seq. No. Seq. ID uC-osrocyp026c09a1 BLASTX Method NCBI GI q129916 235 BLAST score 1.0e-19 E value 53 Match length 91 % identity PHOSPHOGLYCERATE KINASE, CYTOSOLIC >gi_66911_pir__TVWTGY NCBI Description phosphoglycerate kinase (EC 2.7.2.3), cytosolic - wheat >gi_21835_emb_CAA33302_ (X15232) phosphoglycerate kinase (AA 1 - 401) [Triticum aestivum] 420526 Seq. No. Seq. ID uC-osrocyp026c10a1 Method BLASTX NCBI GI q100812 BLAST score 235 1.0e-19 E value 51 Match length 92 % identity ubiquitin precursor - wheat (fragment) NCBI Description >gi 21816 emb CAA40138 (X56803) ubiquitin [Triticum aestivum] >gi 21900 emb CAA39938 (X56601) ubiquitin [Triticum aestivum] 420527 Seq. No. uC-osrocyp026c11a1 Seq. ID BLASTN Method q20241 NCBI GI BLAST score 102 6.0e-50 E value Match length 352 89 % identity NCBI Description O. sativa (rice) root-specific GOS9 gene Seq. No. 420528 uC-osrocyp026d02a1 Seq. ID Method BLASTX q2668744 NCBI GI BLAST score 173 2.0e-12 E value 48 Match length % identity 71 NCBI Description (AF034946) ubiquitin conjugating enzyme [Zea mays] 420529 Seq. No. uC-osrocyp026d04a1 Seq. ID Method BLASTN g561664 NCBI GI 37 BLAST score 3.0e-11 E value 41 Match length

Match length

% identity

62

76

```
98
% identity
                  Rice mRNA, partial homologous to ribosomal protein S3
NCBI Description
                  coding sequence >gi 3106635 dbj D42355 D42355 Rice callus
                  cDNA, AK042
                  420530
Seq. No.
Seq. ID
                  uC-osrocyp026d07a1
                  BLASTN
Method
NCBI GI
                  g3885887
BLAST score
                  179
                  3.0e-96
E value
                  243
Match length
                  93
% identity
                  Oryza sativa high mobility group protein (HMG) mRNA,
NCBI Description
                  complete cds
                  420531
Seq. No.
Seq. ID
                  uC-osrocyp026d11a1
Method
                  BLASTX
NCBI GI
                  q5231210
                  359
BLAST score
E value
                  2.0e-37
                  84
Match length
                  78
% identity
                  (AF159061) serine/threonine protein phosphatase PP2A-3
NCBI Description
                  catalytic subunit [Oryza sativa subsp. indica]
                  420532
Seq. No.
Seq. ID
                  uC-osrocyp026e02a1
Method
                  BLASTX
                  g115881
NCBI GI
BLAST score
                  145
E value
                  3.0e-09
                  80
Match length
                  41
% identity
NCBI Description CARBOXYPEPTIDASE B >gi_67539_pir__CPCYB carboxypeptidase B
                  (EC 3.4.17.2) - broad-fingered crayfish
                  >gi 223890 prf__1004229A CPase B [Astacus astacus]
Seq. No.
                  420533
                  uC-osrocyp026e08a1
Seq. ID
Method
                  BLASTN
                  g6013290
NCBI GI
BLAST score
                  173
                  1.0e-92
E value
Match length
                  221
                  95
% identity
NCBI Description Oryza sativa polyubiquitin (RUBQ2) gene, complete cds
Seq. No.
                  420534
Seq. ID
                  uC-osrocyp026e11a1
Method
                  BLASTX
NCBI GI
                  q4038034
BLAST score
                  248
E value
                  6.0e-21
```

NCBI Description

```
Seq. No.
                  420535
Seq. ID
                  uC-osrocyp026f01a1
                  BLASTX
Method
NCBI GI
                  q6006369
                  596
BLAST score
E value
                  7.0e-62
                  119
Match length
                  96
% identity
                  (AP000559) ESTs C99670(E21043), C99671(E21043),
NCBI Description
                  AU078262(R10938), AU078261(R10938), D15282(C0402) correspond
                  to a region of the predicted gene.; Similar to arginine
                  decarboxylase (U52851) [Oryza sativa]
                  420536
Seq. No.
Seq. ID
                  uC-osrocyp026f02a1
Method
                  BLASTX
NCBI GI
                  q1076746
BLAST score
                  166
                  1.0e-11
E value
                  76
Match length
                  50
% identity
                  heat shock protein 70 - rice (fragment)
NCBI Description
                  >gi 763160 emb CAA47948_ (X67711) heat shock protein 70
                   [Oryza sativa]
                   420537
Seq. No.
Seq. ID
                  uC-osrocyp026f11a1
Method
                  BLASTX
NCBI GI
                  q5777629
BLAST score
                  190
                   9.0e-17
E value
Match length
                   52
% identity
                   96
NCBI Description (AJ245900) CAA303717.1 protein [Oryza sativa]
Seq. No.
                   420538
Seq. ID
                   uC-osrocyp026f12a1
Method
                  BLASTN
NCBI GI
                   g20280
BLAST score
                   57
                   8.0e-24
E value
                  89
Match length
% identity
                   91
NCBI Description Rice gene for phenylalanine ammonia-lyase (EC 4.3.1.5)
                   420539
Seq. No.
                  uC-osrocyp026g01a1
Seq. ID
Method
                  BLASTX
                  g5262775
NCBI GI
BLAST score
                   209
                   1.0e-16
E value
                   62
Match length
                   61
% identity
NCBI Description (AL080282) putative protein [Arabidopsis thaliana]
```

(AC005936) unknown protein [Arabidopsis thaliana]

```
420540
Seq. No.
Seq. ID
                  uC-osrocyp026g12a1
                  BLASTX
Method
NCBI GI
                  g401238
BLAST score
                  345
                  4.0e-33
E value
Match length
                  81
% identity
                  UBIQUITIN-ACTIVATING ENZYME E1 3 >gi 170686 (M90664)
NCBI Description
                  ubiquitin activating enzyme [Triticum aestivum]
                  420541
Seq. No.
Seq. ID
                  uC-osrocyp026h05a1
                  BLASTX
Method
                  q6056375
NCBI GI
                  232
BLAST score
                  1.0e-19
E value
Match length
                  78
% identity
                  55
                  (AC009894) Similar to serine/threonine kinases [Arabidopsis
NCBI Description
                  thaliana]
                   420542
Seq. No.
Seq. ID
                  uC-osrocyp026h09a1
                  BLASTX
Method
                  q1346804
NCBI GI
BLAST score
                   630
                   9.0e-66
E value
Match length
                   133
% identity
                   83
                 PROFILIN 2 >gi 1008443 emb CAA61944 (X89826) profilin
NCBI Description
                   [Triticum aestivum]
Seq. No.
                   420543
                  uC-osrocyp027a01a1
Seq. ID
Method
                   BLASTN
                   q2160781
NCBI GI
BLAST score
                   374
                   0.0e+00
E value
Match length
                   406
% identity
                   98
NCBI Description Oryza sativa putative ammonium transporter OsAMT1p (OsAMT1)
                   mRNA, complete cds
Seq. No.
                   420544
                   uC-osrocyp027a01b1
Seq. ID
                   BLASTX
Method
NCBI GI
                   g2160782
BLAST score
                   310
                   6.0e-36
E value
                   104
Match length
% identity
                  (AF001505) putative ammonium transporter OsAMT1p [Oryza
NCBI Description
                   sativa]
```

420545

uC-osrocyp027a04b1

Seq. No.

Seq. ID

```
BLASTX
Method
NCBI GI
                  q131755
                  567
BLAST score
                  2.0e-58
E value
Match length
                  144
% identity
                  76
                  PPLZ12 PROTEIN >gi 81843 pir S14688 hypothetical protein
NCBI Description
                  pPLZ12 - large-leaved lupine >gi 19501 emb CAA36070
                  (X51768) pPLZ12 gene product (AA 1-184) [Lupinus
                  polyphyllus]
                  420546
Seq. No.
Seq. ID
                  uC-osrocyp027a05a1
                  BLASTN
Method
NCBI GI
                  q5006854
BLAST score
                  189
E value
                  1.0e-102
Match length
                  325
% identity
                  90
                  Oryza sativa homeodomain leucine zipper protein (hox5)
NCBI Description
                  mRNA, complete cds
                  420547
Seq. No.
Seq. ID
                  uC-osrocyp027a05b1
                  BLASTN
Method
                  g5006854
NCBI GI
                  77
BLAST score
                  3.0e-35
E value
Match length
                  142
% identity
                  100
NCBI Description
                  Oryza sativa homeodomain leucine zipper protein (hox5)
                  mRNA, complete cds
Seq. No.
                  420548
                  uC-osrocyp027a07b1
Seq. ID
Method
                  BLASTX
                  g2462834
NCBI GI
BLAST score
                  246
E value
                  8.0e-21
                  99
Match length
                   47
% identity
                  (AF000657) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  420549
                  uC-osrocyp027a08a1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g5263337
BLAST score
                  254
E value
                  9.0e-22
Match length
                  68
                   69
% identity
                  (AC007727) Strong similarity to gb_X96932 ascorbate
NCBI Description
                  oxidase-related protein PS60 from Nicotiana tabacum and is
                  a member of the PF_00394 Multicopper oxidase family. This
                  gene is cut off. [Arabidopsis thaliana]
```

420550

Seq. No.